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Title:
Perfect score:
Sequence:
                                                              Database :
                                                                                       Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                  Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                                                               Searched:
                                                                                                                                                                                                                                                                         Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                Run on:
                                                                                                                                                                                              Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                            OM protein -
                                                                                                                                                                                                                                                                                                                                                                                                                          protein search, using sw model
4321
                                                                                                                                                                                                                                                                                                  January 12, 2004, 08:12:09; Search time 19.0439 Seconds (without alignments) 1661.397 Million cell updates/sec
                                                                                                                                                                                                                          283308 seqs, 96168682 residues
                                                                                                                                                                                                                                                                            BLOSUM62
                                                                                                                                                                                                                                                         Gapop 10.0 , Gapext 0.5
                                                            PIR_76:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.
pir1:
pir2:*
pir3:**
                                                                                                                                                                                                283308
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	8	7	6	υ	4	ω	2	_		Result
97.5	98	131.5	135.5	139.5	145.5	147	147.5	150	151.5	158	160.5	163	163.5	164.5	165.5	166.5	168	168.5	169.5	170	172	173	175	176.5	182	184	196	213	0.000	2010
5.6	5.7	7.6	7.9	8.1	8.4	8.5	8.5		8.8	9.2	9.3	9.4	9.5	9.5	9.6	9.6	9.7			9.8	10.0	10.0	0	0	10.5	10.7	11.4	12.3	Maccii	
476	3938	992	170	635	423	1228	215	196	245	193	246	224	674	253	743	680	245	680	674	744	245	744	744	253	253	215	244	219	тепест	
2	N	N	N	N	N	N	N	N	4سر	N	N	N	N	ν	H	Ľ	N	N	N	N	H	_	μ	N	ب	N	N	N	100	1
T29083	T42761	T08772	B57131	A57131	A55797	A57384	C48150	A48150	CIHUQA	A37873	S29328	A60032	\$13301	I49560	S23779	CCHUID	S19018	S31216	S23297	S15435	CIHUQC	A34246	S23298	S49158	CIHUQB	B48150	JC4708	T14782	115	;
3-isopropylmalate	Bassoon protein -	hypothetical prote	alpha	collagen alpha 2(V	collagen precursor	multimerin, endoth	hibernation-relate	n-relat			complement subcomp	Œ		œ	collagen alpha 1(V	collagen alpha 1(x	complement subcomp	alpha 1		collagen alpha 1(v	nt subco	alpha	_	complement protein	complement subcomp	22		hypothetical prote	pescription	<b>3</b>

45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30
91.5	92.5	92.5	93	93	93	93.5	94	94	94	94	94	94	94	94.5	95
5.3	υ •	5.4	5.4	5.4	5.4	5.4	5.4	5.4	5.4	5.4	5.4	5.4	5.4	5.5	5 5
13055	1334	420	1239	481	462	686	7463	1045	913	913	810	495	495	619	495
N	N	N	<u>_</u>	N	N	ᆫ	N	2	N	N	N	N	N	N	_
T16580	T50568	E75130	QQBE10	B75480	B75306	VGBENA	T36248	A39199	B97369	AB2587	B84185	D85755	E90863	A87499	G64878
ical		hypothetical prote	BOLF1 protein - hu	hypothetical prote	probable cycloprop	glycoprotein H pre	CDA peptide synthe	endoglucanase B (E	translation initia	translation initia	cytochrome-like pr	aldehyde dehydroge	aldehyde dehydroge	hypothetical prote	aldehyde dehydroge

## ALIGNMENTS

RESULT 2  JC4708  JC4708  gelatin-binding 28K protein precursor - human N;Alternate names: adipose specific collagen-like factor C;Species: Homo sapiens (man) C;Date: 10-May-1996 #sequence_revision 19-Jul-1996 #text_change 20-Sep-1999 C;Accession: JC4708; JC4944 R;Maeda, K; Okubo, K; Shimomura, I; Funahashi, T; Matsuzawa, Y; Matsubara, K. Biochem. Biophys. Res. Commun. 221, 286-289, 1996 A;Title: cDNA cloning and expression of a novel adipose specific collagen-like factor, A;Reference number: JC4708; MUID:96224171; PMID:8619847 A;Accession: JC4708	Oy 306 KSGFLVYRD 314  Db 203 FSGFLVYSD 211	QY 246 KLMKONDEVQAMIYDDGASRRREMQSQSVMLALRRGDAVMLLSHDHDGYGAYSNHGKYIT 305	Qy 186 SLVGSDAGPGPRHQPLAFDTEFVNIGGDFDAAAGVFRCRLPGAYFFSFTLGKLPRKTLSV 245	QY 138 GAPHYALGAPGATFSGYLVYADADADAPARGPPAPPEPRSAFSAARTR 185	Query Match 12.3%; Score 213; DB 2; Length 219; Best Local Similarity 34.9%; Pred. No. 4.3e-10; Matches 66; Conservative 18; Mismatches 83; Indels 22; Gaps 6;	RESULT 1 T14782 T14782 Typothetical protein DKFZp586B0621.1 - human (fragment) C;Species: Homo sapiens (man) C;Species: Homo sapiens (man) C;Accession: T14782 R;Ottenwaelder, B.; Obermaier, B.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S. submitted to the Protein Sequence Database, August 1999 A;Reference number: Z18184 A;Accession: T14782 A;Accession: T14782 A;Kolecule type: mRNA A;Residues: 1-219 <ott> A;Cross-references: EMBL:AL110261 A;Experimental source: adult uterus; clone DKFZp586B0621 C;Genetics: A;Note: DKFZp586B0621.1 C;Superfamily: complement C1q carboxyl-terminal homology</ott>
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A;Title: Isolation and characterization of GBP28, a A;Reference number: JC4944; MUID:97103474; PMID:894 A;Accession: JC4944 A;Molecule type: protein A;Molecule type: protein A;Molecule type: protein A;Molecule type: protein is an endogenous factor that C;Comment: This protein is an endogenous factor that C;Genetics: A;Genetics: 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Status: preliminary
A;Molecule type: prottein
C;Superfamily: complement subcomponent Ciq chain A; complen
C;Keywords: glycoprotein; hibernation; plasma
F;1-28/Domain: signal sequence #status predicted <SIG>F;29-215/Product: hibernation-related protein HP-25 #status
F;91-214/Domain: complement Ciq carboxyl-terminal homology
                                                                                                                                                                                                                                                                  A; Note: the source is designated as Tamias asiaticus in G A; Note: sequence extracted from NCBI backbone (NCBIN:1259 R; Kondo, N.; Kondo, J. Biol. Chem. 267, 473-478, 1992 A; Title: Identification of novel blood proteins specific A; Reference number: A41752; MUID:92112696; PMID:1730610 A; Accession: B41752
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Species: Eutamias sibirico
C;Date: 16-Feb-1994 #sequeno
C;Accession: B481752
C;Accession: B481752
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848150
hibernation_related protein HP-25 precursor - Siberian chipmunk
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                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: GB:D12975; NID:g287469; PIDN:BAA02352.1; PID:g287470 A;Note: the source is designated as Tamias asiaticus in Genbank entry TMSHP25, A;Note: sequence extracted from NCBI backbone (NCBIN:125946, NCBIP:125947)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R;Takamatsu, N.; Ohba, K.; Kondo, J.; Kondo, N.; Shiba, T. Mol. Cell. Biol. 13, 1516-1521, 1931
A;Tile: Hbernation-associated gene regulation of plasma A;Reference number: A48150; MUID:93180798; PMID:8441393
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: mRNA; protein A; Residues: 1-215 < TAK>
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Best Local S
Matches 54
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;Residues: 1-244 <MAE>
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R;Reid, K.B.M.; Thompson, E.O.P.
Blochem. J. 173, 863-868, 1978
A;Title: Amino acid sequence of the N-terminal 108 amino A;Reference number: A90301; MUID:79041552; PMID:708376
A;Accession: A90301
                                                                                                                                                                                                                                                                                                                                                                                                          A;ACCEBBLOWN
A;ACCEBBLOWN
A;Molecule type: protein
A;Residues: 'E',29-84,'D',86-99,'P',101-135
A;Residues: 'E',29-84,'D',86-99,'P',101-135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement subcomponent Clq chain B precursor [validated] N;Alternate names: complement subcomponent Clq beta chain
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                                                     A;Molecule type: protein
A;Residues: 136-253 <RE4>
A;Residues: 136-253 <RE4>
A;Note: 176-Glx may also be present
A;Note: 176-Glx may also be present of complement is a
C;Comment: The first component of complement is a
the C;Comment: The Clx (enzyme), Cls (proenzyme), and the
C;Comment: The Clx subcomponent is composed of nin
(see PIR:C1HUQC) chain. Equimolar amounts of the A
                                                                                                                                                                                           R;Reid, K.B.M.; Gagnon, J.; Frampton, J.
Biochem. J. 203, 559-569, 1982
A;Title: Completion of the amino acid sequences of the A
A;Reference number: A90315, MUID:82283890; PMID:6981411
A;Accession: B90315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Biochem. J. 179, 367-371, 1979
A; Title: Complete amino acid sequences of A; Reference number: A90304; MUID:80020137;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: mRNA
A; Residues: 28-253 cRE1>
A; Cross-references: EMEL:XO3084
A; Note: the authors translated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Biochem. J. 231, 729-735, 1985
A;Title: Molecular cloning and characterization of the
A;Reference number: A23422; MUID:86076906; PMID:3000358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Species: Homo sapiens (man)
C;Date: 22-May-1981 #sequence revision 31-May-1996 #text_change
C;Accession: B23422; A23422; B90304; A90301; B90315; A03206
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A; Residues: 'HS', 1-32 <REI>
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A;Gene: GDB:C1QB
A;Cross-references:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Accession: B23422
                                                                                                                                                                                                                                                                                               A;Molecule type: protein
A;Residues: 28-99,'P',101-195 <RE3>
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position:

1p36.3-1p34.1

GDB:119043;

OMIM: 120570

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collagen alpha 1(VIII) chain - chicken C;Species: Gallus gallus (chicken) C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999 C;Accession: S23298 R;Ninomiya, Y:; Castagnola, P.; Gerecke, D.; Gordon, M.K.; Jacenko, O.; LuV. maguchi, N.; Olsen, B.R.
in Extracellular Matrix Genes, Sandell L.J. and Boyd C.D., eds., pp.79-114,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Superfamily: complement subcomponent Clq chain A; complement Clq carboxyl-terminal C;Keywords: complement pathway; glycoprotein; heterodimer; hydroxylysine; hydroxypro F;1-27/Domain: signal sequence #status predicted <SIG>F;28-253/Froduct: complement subcomponent Clq chain B #status experimental <MAT>F;38-253/Froduct: complement subcomponent Clq chain B mature experimental complement clq carboxyl-terminal homology <ClQ>F;28-253/Froduct: complement Clq carboxyl-terminal homology <ClQ>F;28-253/Froduct: complement Clq carboxyl-terminal homology <ClQ>F;28/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status experimental F;35,36,65,83,86,101,104,107/Modified site: 4-hydroxyproline (Pro) #status F;59,62,77,92,98,110/Modified site: 5-hydroxylysine (Lys) #status experimental F;59,62,79,27,98,110/Msidied site: carbohydrate (Lys) (covalent) #status experimental
                                                                                                                                             RESULT
S23298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-253 <SCH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement protein Clq beta chain precursor - C;Species: Rattus norvegicus (Norway rat) C;Date: 16-Feb-1995 #sequence_revision 12-May-C;Accession: S49158 R;Schwaeble, W.; Petry, F.; Loos, M. submitted to the EMBL Data Library, March 1993 submitted to the EMBL Data Library, March 1993
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S49158
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                                                                                                                                                                                                                         CDYAQ-NTFQVTTGGVVLKLEQEEVVHLQATD-KNSLLGVEGANSIFTGFLLFPDMD
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                                                                                                                                                                                                                                                                                                            IRFEKVITNVNDNYEPRSGKFTCKVPGLYYFTYHASSRGNLCVNIVRGRDRDRMQKVLTF
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Pred. No. 1.7e-07;
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                         SAVLLLRPGDRVFLQMPSEQAAGLYAGQYVHSSFSGYLLYP
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A;Reference number: A34246; MUID:89380199; PMID:2476437
A;Accession: A34246
A;Molecule type: mRNA
A;Residues: 1-744 <YAM's
A;Cross-references: GB:J05042; NID:g164895; PIDN:AAA31204.1; PID:g164896
A;Cross-references: GB:J05042; NID:g164895; PIDN:AAA31204.1; PID:g164896
C;Superfamily: collagen alpha 1(VIII) chain; complement C1q carboxyl-tern
F;1-20/Domain: signal sequence #status predicted <SIG's
F;21-744/Product: collagen alpha 1(VIII) chain #status predicted <MAT's
F;21-117/Region: amino-terminal nonhelical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  collagen alpha 1(VIII) chain precursor - rabbit C;Species: Oryctolagus cuniculus (domestic rabbit) C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 C;Accession: A34246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       F;118-571/Region: interrupted helical F;572-744/Region: carboxyl-terminal nonhelical F;617-743/Domain: complement Clg carboxyl-term
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        J. Biol. Chem. 264, 16022-16029, 1989
A;Title: The cloning and sequencing of alphal(VIII) collagen omains similar to those of type X collagen.
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A; Residues: 1-744 <NIN>
A; Residues: 1-744 <NIN>
C; Superfamily: collagen alpha 1(V
F; 617-743/Domain: complement Clq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R;Yamaguchi, N.; Benya, P.D.; van der Rest, M.; Ninomiya, J. Biol. Chem. 264, 16022-16029, 1989
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     617-743/Domain: complement Clq carboxyl-terminal homology
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                                                                                                                                                                                                                                                                                                                           136 LHGAPHYALGAPGATFSGYLVYADADADAPA-RGPPAPPEPRS-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         136 LHGAPHYALGAPGATFSGYLVYADADADAPA-RGPPAPPEPRS----------
                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
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                                                                                                                                                         LGIDGVKTPHAYAAKK-----GKNGGPAYEMPAFTAELTAPFPPVGAPIKFDRLLYNGRQ
                                                                                                                                                                                                              ----AFSAARTRSLVGSDAGPG------
                                                                                                                                                                                                                                                                      LHGPP---
SVMLALRRGDAVWLLSHDHDGYGAYSNHGKYITFSGFLVYP
                                                     NYNPQTGIFTCEVPGVYYFAYHV-HCKGGNVWVALFKNNEPVM-YTYDEYKKGFLDQASG
                                                                                                       DFDAAAGVFRCRLPGAYFFSFTLGKLPRKTLSVKLMKNRDEVQAMIYDDGASRRREMQSQ
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                                                                                                                                                                                                                                                                                                                                                                                                      Score 173; DB 1;
Pred. No. 3.4e-06;
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ccheв 77;
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A; Map position:
A; Introns: 60/3
A; Introns: 60/3
C; Superfamily: cc
C; Keywords: comp
F; 1-28/Domain: s:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Keywords: complement pathway; glycoprotein; homodimer; hydroxylysine F;1-28/Domain: signal sequence #status predicted <SIG>
F;29-245/Product: complement subcomponent Clq chain B #status predicte F;31-114/Domain: collagenous, triple helix <COL>
F;121-244/Domain: complement Clq carboxyl-terminal homology <ClQ>
F;121-244/Domain: complement Clq carboxyl-terminal homology <ClQ>
F;32/Disulfide bonds: interchain #status experimental
F;36,39,42,45,54,63,81,93,96,99,105/Modified site: 4-hydroxyproline (1F;37,72,75/Modified site: 5-hydroxylysine (Lys) #status experimental
F;75/Binding site: carbohydrate (Lys) (covalent) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Molecule type: protein
A;Residues: 29-56,'p',58-65,'K',67-71,'p',73-83,'K',85-86,'D',88-89,'N',91-122 <REI>C;Comment: The first component of complement is a calcium-dependent complex of the three ivation of CIr (enzyme), Cls (proenzyme), and the other eight components of complement. C;Comment: The Clq subcomponent is composed of nine subunits, six of which are disulfide dimers of the C chain. Equimolar amounts of the A, B, and C chains are found after reductions.
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A; Title: Characterization and organization
A; Reference number: S14350; MUID:91174759;
                                                                            RESULT
S15435
collagen alpha 1(VIII) chain precursor - C;Species: Homo sapiens (man) C;Date: 13-Jan-1995 #sequence_revision 1
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A;Cross-references: GDB:128132; OMIM:120575
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A;Accession: S14351
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Best Local S
Matches 67
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                                                                                                                                                                      GVLLRLQVGEEVWLAVNDY - - YDMVGIQGSDSVFSGFLLFPD
                                                                                                                                                                                                                                                                                                             DEDAAAGVERCRLEGAYEESETLGKLERKTLSVKLMKNRDEVQAMIYDDGASRRREMQSQ
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    #sequence_revision 13-Jan-1995
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23.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 172; DB 1;
Pred. No. 1.1e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                      human
                                                                                                                                                                                                                                                                 -HTANLCVLLYRSGVKVVTFCGHTSKTNQVNSG
                                                                                                                                                                                                                                                                                                                                                               -----QTHQPPAPNSLIRFNAVLTNPQG
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PMID:1706597
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    #text_change 13-Aug-1999
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R;Muragaki, Y.; Mattei, M.G.; Yamaguchi, N.; Olsen, B.R.; Ninomiya, Y. Eur. J. Biochem. 197, 615-622, 1991
A;Title: The complete primary structure of the human alpha-1(VIII) chain A;Reference number: S15435; MUID:91231001; PMID:2029894
                                                                                                                                                                                                                                                                                                                                                                                         F;118-571/Region: interrupted helical
F;572-744/Region: carboxyl-terminal nonhelical
F;617-743/Domain: complement Clq carboxyl-terminal homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Superfamily: collagen alpha 1(VIII) chain; complement F;1-20/Domain: signal sequence #status predicted <SIG>F;21-744/Product: collagen alpha 1(VIII) chain #status F;21-117/Region: amino-terminal nonhelical
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A; Residues: 1-744 < MUR>
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Best Local (
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                                      278
  708
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  LRPGDRVFLQMPSEQAAGLYAGQYVHSSFSGYLLYP
                                                                                                                                                           LGIDGVKPPHATGAKKGKNGGPAYEMPAFTAELTAPFPPVGGPVKFNKLLYNGRQNYNPQ
                                      LRRGDAVWLLSHDHDGYGAYSNHGKYITFSGFLVYP
                                                                             TGIFTCEVPGVYYFAYHV-HCKGGNVWVALFKNNEPVM-YTYDEYKKGFLDQASGSAVLL
                                                                                                                    AGVFRCRLPGAYFFSFTLGKLPRKTLSVKLMKNRDEVQAMIYDDGASRRREMQSQSVMLA 277
                                                                                                                                                                                                                                      LHGPP----GKPGA-----LGPQGQPGLPGPPGPPGPPGPPAVMPPTPPPQGEYLPDMG 589
                                                                                                                                                                                               -AFSAARTRSLVGSDAGP--GPRHQPLAFDTE----FVNIGG--
                                                                                                                                                                                                                                                                                                                    Conservative
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                                                                                                                                                                                                                                                                                                                                      Score 170;
Pred. No.
                                                                                                                                                                                                                                                                                                                  Pred. No. 6e-17; Mismatches
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                                          313
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collagen alpha 1(X) chain precursor - chicken
N;Alternate names: type X collagen
C;Species: Gallus gallus (chicken)
C;Date: 07-Oct-1994 #sequence revision 10-Nov-1995 #text\_change 13-Aug-1999
C;Accession: S23297; A31896; S65594; S77711; I50218
R;Ninomiya, Y; Castaggola, P.; Gerecke, D.; Gordon, M.K.; Jacenko, O.; LuVi maguchi, N.; Olsen, B.R. in Extracellular Matrix Genes, A;Title: The molecular biology A;Molecule type: mRNA A;Residues: 1-74 <NIN> R;LuValle, P.; Ninomiya, Y.; Rosenblum, N.; J. Biol. Chem. 263, 18378-18385, 1988 J.;Title: The type X collagen gene. Intron: A;Reference number: A31896; MUID:89054019; A;Accession: A31896 A;Accession: S23297 A; Reference number: S22243 preliminary Sandell L.J. and Boyd C.D., eds., pp.79-114, Academic of collagens with short triple-helical domains. O.; LuValle,

'O' :-

3 Pr

N.D.; Olsen,

B. R

sequences split; PMID:2461368

the

5'-untranslated

region

A;Molecule type: mRNA
A;Residues: 1-75 <LUV>
R;Ninomiya, Y:, Gordon, M.; van der Rest, M.
J. Biol. Chem. 261, 5041-5050, 1986
A;Title: The developmentally regulated type
A;Reference number: I50218; MUID:86168227; E
A;Accession: \$65594

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Schmid,

H ., gene

Linsenmayer,

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Olsen,

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,48-89,'L

X collagen PMID:3082876

A;Molecule type: DNA A:Residues: 'T',9,'D',11-12,'EDQMKLYILFTM',30-31,'TCKSGRAFTTYMILQNVMADLVSSHT'

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A;Molecule type: DNA
A;Residues: 1-680 <KON>
A;Cross references: EMBL: Z21610; NID: g49793; PIDN: CAA79736.1; PID: g49794
R;Elima; K; Eerola, I; Rosati, R.; Metsaeranta, M.; Garofalo, S.; Perac
Biochem. J. 289, 247-253, 1993
A;Title: The mouse collagen X gene: complete nucleotide sequence, exon st
A;Reference number: S28807; MUID: 93143676; PMID: 8424763
A;Accession: S28807
                                                                                              R;Apte, S.S.; Olsen, B.R.
Matrix 13, 165-179, 1993
A;Title: Characterization of the mouse type
A;Reference number: S30127; MUID:93261348; F
A;Accession: S30127
                                                                                                                                                                                                                                                                                                                                          A;Molecule type: DNA
A;Residues: 1-285, 'A','287-680 <ELI>
A;Cross-references: EMBL:X67348; NID:g50480; PIDN:CAA47763.1; PID:g50481
A;Cross-references: EMBL:X67348; NID:g50480; PIDN:CAA47763.1; PID:g50481
R;Elima, K.; Metsaeranta, M.; Kallio, J.; Peraelae, M.; Berola, I.; Garo: Biochim. Biophys. Acta 1130, 78-80, 1992
Biochim. Biophys. Acta 1130, 78-80, 1992
A;Title: Specific hybridization probes for mouse alpha-2(IX) and alpha-1
A;Reference number: S22215; MUID:92182017; PMID:1543751
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A;Residues: 104-112,'X',114-117;453-466 <NIN2>
C;Superfamily: collagen alpha 1(VIII) chain; complement Clq carboxyl-terminal homology C;Keywords: coiled coil; extracellular matrix; glycoprotein; homotrimer; hydroxyproline F;1-18/Domain: signal sequence #status predicted <SIG>
F;547-673/Domain: complement Clq carboxyl-terminal homology <ClQ>
F;547-673/Domain: complement Clq carboxyl-terminal homology <ClQ>
F;545,456/Modified site: hydroxyproline (Pro) #status experimental F;611/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                              A; Molecule type: mRNA
A; Residues: 385-450, 'K', 452-627
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                                                 A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Title: Intron-exon structure, alternative use of promoter and A;Reference number: S31216; MUID:93238750; PMID:8477738
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A;Cross-references: EMBL:X63013; NID:g49795; PIDN:CAA44741.1;
                                                                                                                                                                                                                                                                                                   A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                  A; Accession:
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A;Accession: S77711
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ollagen alpha 1(X) chain precursor - mouse

/Species: Mus musculus (house mouse)

/Date: 30-Sep-1993 #sequence revision 30-Sep-1993 #text change 13-Aug-1999

/Date: 30-Sep-1993 #text change 13-Aug-1999

/Accession: S31216; S28807; S22215; S30127; I48299; S26397; S31830

/Mhomana .T T . Roof-Handford, R.P.; G.
                                                                         Status: preliminary
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s: 1-12,'F',14-26,'S',28-247,'L',249-285,'A',287-305,'F',307-416,'S',418-499,
.S.; Seldin, M.F.; Hayashi, M.; Olsen, B.R.
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1; Mismatches
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C;Accession: S19018
R;Petry, F.; Reid, K.B.M.; Loos, M.
J. Immunol. 147, 3988-3993, 1991
A;Title: Gene expression of the A- and B-chain A;Reference number: S19018; MUID:92043789; PMII A;Accession: S19018
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement subcomponent Clq chain A precursor - C;Species: Mus musculus (house mouse) C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1903
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A;Molecule type: DNA
A;Residues: 52-247,'L',249-285,'A',287-305,'F',307-416,'S',418-499,'L',501-566
A;Residues: 52-247,'L',249-285,'A',287-305,'F',307-416,'S',418-499,'L',501-566
A;Residues: 52-247,'L',249-285,'A', Balian, G.
A;Summers, T.A.; Irwin, M.H.; Mayne, R.; Balian, G.
R;Summers, T.A.; Irwin, M.H.; Mayne, R.; Balian, G.
J. Biol. Chem. 263, 581-587, 1988
A;Tille: Monoclonal antibodies to type X collagen. Biosynthetic studies using A;Reference number: S26397; MUID:88087150; PMID:2826450
                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: mRNA
A; Residues: 1-245 < PET>
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A; Introns: 51/3
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A;Title: Cloning of the human and mouse type X collagen genes and mapping of the mouse A;Reference number: 148299; MUID:92267014; PMID:1587271
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                                                                                                                                                                                                                                                                                                                                    Cross-references: EMBL:X58861; NID:g50226; PIDN:CAA41664.1; PID:g50227; Cuperfamily: complement subcomponent Clq chain A; complement Clq carbo
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                                                                                   LGDSGPQGLKGVKGNPGNIRDQPRPAFSAIRQNPM--TLGNVVIFDKVLTNQESPYQNHT
                                                                                                                                        LGLLGPAACWALGPTPGPGSSELRSAFSAARTTPLEGTSEMAVTFDKVYVNIGGDFDVAT
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PMID:1940381
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A;Molecule type: DNA
A;Residues: 'TIPFYGWVCWVCLL',52-680 <APT>
A;Residues: 'TIPFYGWVCWVCLL',52-680 <APT>
A;Ross-references: EMBL:X65120; NID:923129
A;Note: the initial difference is probably due to translation of an R;Apte, S:; Mattei, M.G.; Olsen, B.R.
R;Apte, S:; Mattei, M.G.; Olsen, B.R.
FEBS Lett. 282, 393-396, 1991
A;Title: Cloning of human alpha-1(X) collagen DNA and localization
A;Reference number: S15826; MUID:91243838; PMID:2037056
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A; Residues: 561-447, 'G', 649-666 < AP2>
A; Crestdues: 561-647, 'G', 649-666 < AP2>
A; Cross-references: EMBL: X58879; NID: 930013; PIDN: CAA41686.1;
A; Chomas, J. T.; Cresswell, C.J.; Rash, B.; Nicolai, H.; Jones
Biochem. J. 280, 617-623, 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R;Apte, S.S. submitted to the EMBL Data Library, A;Reference number: $30085 A;Accession: $30086
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C;Genetics:
A;Gene: GDB:COL10A1
A;Cross-references:
                                                             A;Residues: 520-597, D', 599-680 <WALDA;Cross-references: GB:568531; NID:9545180; PIDN:AAC60615.1; PID:9545181 A;Cross-references: GB:568531; NID:9545180; PIDN:AAC60615.1; PID:9545181 A;Note: mutant sequence from patrict with metaphyseal chondrodysplasia t; A;Note: a second mutant sequence with 614-Pro is also described C;Comment: Prolines and lysines at the third position of the tripeptide ed and subsequently O-glycosylated.
                                                                                                                                                                                A; Molecule type: mRNA
A; Residues: 520-597,'I
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                                                                                                                                                                                                                                                                                                                        A;Title:
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                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: mRNA
A; Residues: 547-656 <1
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A; Residues: 1-26, 'T', 28-680 < THO>
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                                                                                                                                                                                                                                                                                                                   J. Hum. Genet. :
itle: Amino acid
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  GDB:128635; OMIM:120110
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S23779
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R;Muragaki, Y.; Shiota, C.;
Eur. J. Biochem. 207, 895-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ş
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C; Accession: $23779
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A; Residues: 1-743 < MUR>
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C/Superfamily: collagen alpha 1(VIII) chain; complement Clq carboxy C/Keywords: coiled coil; extracellular matrix; glycoprotein; homotr: F;1-18/Domain: signal sequence #status predicted <SIG> F;19-680/Product: collagen alpha 1(X) chain #status predicted <MAT> F;19-56/Domain: amino-terminal nonhelical #status predicted <NC2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          F;57-519/Region: interrupted helical #status predicted F;520-680/bomain: amino-terminal nonhelical #status predicted F;520-680/bomain: complement C1g carboxyl-terminal homology << F;553-679/bomain: complement C1g carboxyl-terminal homology << F;617/Binding site: carbohydrate (Asn) (covalent) #status pred
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Description: structural component
                                                                                                                                                                                                                                                                                                                                                                               145 GAPGATFSGYLVYADADADAPARGPPAPPEPRSAFSAARTRSLVGSDAGPGPRHQ----
                                                                                                        PRIGIFICQIPGIYYFSYHV-HVKGTHVWVGLYKNGTPVM-YTYDEYTKGYLDQASGSAI
                                                                                                                                                        AAAGVFRCRLPGAYFFSFTLGKLPRKTLSVKLMKNRDEVQAMIYDDGASRRREMQSQSVM
                                                                                                                                                                                                              GFIKAGQRPSLSGTPLVSANQGVTGMPVSAFTVILSKAYPAIGTPIPFDKILYNRQQHYD
                                                  LALRRGDAVWLLSHDHDGYGAYSNHGKYITFSGFLVYP
                                                                                                                                                                                                                                                                                                                         GSPGP--PGPAGIATKGLNGPT-GPPGPPGPPGPP---GHSGEPGLPGPPGPPGPPGQAVMPE
IDLTENDOVWLOLPNAESNGLYSSEYVHSSFSGFLVAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6q21-6q22
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 166.5;
Pred. No. 1e-0
22; Mismatches
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; homotrimer; hydro
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Eur. J. Biochem. 207, 895-902, 1992
A;Title: Alpha-1(VIII)-collagen gene transcripts encode
A;Reference number: S23779; MUID:92362626; PMID:1499564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               collagen alpha 1(VIII) chain - mouse C; Species: Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: EMBL:X66976; NID:g50493; PIDN:CAA47387.1; PID:g1359953 C;Superfamily: collagen alpha 1(VIII) chain; complement C1q carboxyl-terminal
                                       AAGVFRCRLPGAYFFSFTLGKLPRKTLSVKLMKNRDEVQAMIYDDGASRRREMQSQSVML
                                                                                                                                                                                                           LHGAPHYALGAPGATFSGYLVYADADADAPARGPPAPPEPRSAFSAARTRSLVGS----DA
QTGIFTCEVPGVYYFAYHV-HCKGGNVWVALFKN-NEPMMYTYDEYKKGFLDQASGSAVL
                                                                                 GLGIDGVKTPHAYAGKKGKHGGPAYEMPAFTAELTVPFPPVGAPVKFDKLLYNGRQNYNP
                                                                                                                                                                                                                                                                                                                                      complement Clq carboxyl-terminal homology
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                                                                                                                                                                                                                                                                         9.6%;
25.8%;
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                                                                                                                                                                                                                                                   Score 165.5;
Pred. No. 1.4e
23; Mismatches
                                                                                                                                                                  -LGPQGQPGLPGPPGPPGPPAVMPTPSPQGEYLPDM
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A;Residues: 1-114,'R',116-253 <PET>
A;Cross-references: Bmb:x16874; NID:g50222; PIDN:CAA34757.1; PID:g50223
A;Cross-references: Embcomponent C1q chain A; complement C1q carboxyl-terminal hom F;1-25/Domain: signal sequence #status predicted <SIG>
F;26-253/Product: complement subcomponent C1q chain B #status predicted <MAT>
F;121-249/Domain: complement C1q carboxyl-terminal homology <C1Q>
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Search completed: January 12, 2004, 08:16:41 Job time : 22.0439 secs
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R;Wood, L.; Pulaski, S.; Vogeli, G.
Immunol. Lett. 17, 59-62, 1988
A;Title: cDNA clones coding for the complete murine B chain of complement Clq: Nucleotid A;Reference number: I49527; MUID:88168728; PMID:3258283
A;Accession: I49527
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Best Local
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                                                                                                                    195 VTFCDYAQNTFQVTTGGVVLKLEQEEVVHLQATD-KNSLLGIEGANSIFTGFLLFPDMDA 253
                                                                                                                                                                                 105 AFDEQRRPGARRAASQSAMLQLDYGDTVWLRLHGAPHYALGAPGAT--FSGYLVYADADA 162
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50; Conserv
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                                                                                                                                                                                                                                                                                                                EMAVTFDKVYVNIGGDFDVATGQFRCRVPGAYFFSFTAGKAPHKSLSVMLVRNRDEVQAL 104
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Maximum Match 100%
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Maximum DB seq length: 2000000000
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RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altechul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Altechul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hong L.,

RA Hopkins R.F., Jordan R., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

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RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Hopkins R.F., Jones S.J.M., Marra M.A.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

"Generation and initial analysis of more than 15,000 full-length

RT human and mouse cDNA sequences.";
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Q9BXCI; Q9GZR4;

28-FEB-2003 (Rel. 41, Created)

28-FEB-2003 (Rel. 42, Last sequence update)

15-SEP-2003 (Rel. 42, Last annotation update)

Complement-clq tumor necrosis factor-related protein 1 precursor (G protein coupled receptor interacting protein) (GIP).

CIQTNPI OR CTRP1.
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Ishibashi T., Kanehori K., Yosida M., Watanabe S., Ishida S., Ono Y. Hotuta T., Hiraoka S., Murakawa K., Takiguchi S., Kusano J., Watanabe M., Fujimori K., Tanai H., Ishida M., Yamashita H., Chiba Sugiyama T., Irie R., Otsuki T., Sato H., Wakamatsu A., Ishii S., Yamamoto J., Isono Y., Kawai-Hio Y., Saito K., Nishikawa T., Kimura K., Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K., Wagatsuma M., Takahashi-Fujii A., Oshima A., Sugiyama A., Kawakami J., Suzuki Y., Sugano S., Nagahari K., Masuho Y., Nagai K., Isogai T.;
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Mammalia; Eutheria; Primates;
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Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
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Best Local S
Matches 77
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EMBL; AF232905; AAG44303.1; A
EMBL; AF2329840; AAK17964.1;
EMBL; BC021553; AAK21553.1;
EMBL; AK055541; BAB70947.1;
Genew; HGNC:14324; C1QTNF1.
                                            'S_HUMAN STANDARD
COTS_HUMAN STANDARD
Q9BXJO; Q9UEX4;
28-FEB-2003 (Rel. 41, C
28-FEB-2003 (Rel. 41, I
28-FEB-2003 (Rel. 41, II
28-FEB-2003 (Rel. 41, II
Complement-clq tumor ne
C1QTNF5 OR CTRP5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "NEDO human cDNA sequencing project.";
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases
-:- SIMILARITY: Contains 1 collagenous domain.
-:- SIMILARITY: Contains 1 CIQ domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CONFLICT
CONFLICT
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Collagen;
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00386; Cld; 1.
Pfam; PF01391; Collagen; 1.
SMART; SM00110; ClO; 1.
PROSITE; PS01113; ClQ; FALSE_NEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro;
            Eukaryota; Metazoa;
Mammalia; Eutheria;
                                    Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                         129
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                       TRSLVGSDAGEGERH-----OPLAFDTEFVNIGGDFDAAAGVFRCRLEGAYFESETLGKL
                                                                                                                                                                                                                                                                                                                                                       GDT---VWLRLHGAP----HYALGAPGATFSGYLVYADADADAPARGPPAPPEPRSAFSAAR
                                                                                                                                                                                                                                                                                                                                                                                                      RCRVPGAYFFSFTAGKAPHKSLSVMLVRNRDEVQALAFDEQRRPGARRAASQSAMLQLDY
                                                                                                                                                                                                                                                                                                                                                                                RCCDPGTSMYPATA--VPQINITILKGEKGDR----
                                                                                                                                                                                                                                                                                                                                 GKTGSAGARGHTGPKGQKGSMGAPGERCKSH--YA---
                                                                                                                                                                                  SEELDTYITFSGYLV
                                                                                                                                                                                                                                NQKETYLHIMKNEEEVVILFAQVG--DRSIMOSQSLMLELREQDQVWVRLYKGERENAIF
                                                                                                                                                                                                                                                        PRKTLSVKLMKNRDEVQAMIYDDGASRRREMQSQSVMLALRRGDAVWLLSHDHDGYGAYS
                                                                                                                                                                                                                                                                                KK------PMHSNHYYQTVIFDTEFVNLYDHFNMFTGKFYCYVPGLYFFSLNVHTW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IPR001073; Clq.
IPR000087; Collagen.
                                                                                                                                                                                                           NH--GKYITFSGFLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                241
281 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                       STANDARD;
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281
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281
22
241
            Chordata;
Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                              12.5%;
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                                                           , Last sequence update)
, Last annotation update)
necrosis factor-related
                                                                                                 Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RELATED PROTEIN : COLLAGEN-LIKE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                L -> P (IN REF. 1).
R -> Q (IN REF. 1).
; 49E248CB88ACFB7C
                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 215; DB 1;
Pred. No. 2.7e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POTENTIAL.
COMPLEMENT-C1Q TUMOR
             Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (See http://www.isb-sib.ch/announce/
                                                                                                                           243
                                                              protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 281;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
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                                                               տ
                                                               precursor
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RESULT
CQT2_HU
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Best Local (
                                                  28-FEB-2003
28-FEB-2003
15-SEP-2003
                                                                                                              _HUMAN
                                    28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Complement-clq tumor necrosis factor-related
                                                                                     CQT2_HUMAN
Q9BXJ5;
                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; E
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Pfam; PF01391; Collagen; 1.
PF1391; COMPLEMNTC1Q.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL;
PIR; ]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for com
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
Sheppard P.O., Humes J.M.;
"Homo sapiens complement-olg tumor necrosis factor-related protein.";
Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
               Homo
                           C1QTNF2 OR CTRP2
                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AF329841; AAK17965.1; -. EMBL; AL110261; CAB53702.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (AUG-1999) to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Wiemann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SMART;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3enew; HGNC:14344; C1QTNF5.
InterPro; IPR001073; C1q.
InterPro; IPR000087; Collagen.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     T14782; T14782.
              sapiens
                                                                                                                                                                                        306
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                                                                                                                                                                                                                                      246
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SM00110; C1Q; 1.
                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                    GAPHYALGAPGATFSG---YLVYADAD----ADAPARGPPAPP----EPRSAFSAARTR 185
                                                                                                                                                                                                              DLVKNGESIASFFQFFGGWPKPASLSGGAMVRLEPEDQVWVQVGVGDYIGIYASIKTDST
                                                                                                                                                                                                                                     KLMKNRDEVQAMIYDDGASRRREMQSQSVMLALRRGDAVWLLSHDHDGYGAYSNHGKYIT
                                                                                                                                                                                                                                                                SRV--
                                                                                                                                                                                                                                                                                     SLVGSDAGPGPRHQPLAFDTEFVNIGGDFDAAAGVFRCRLPGAYFFSFTLGKLPRKTLSV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OF 25-243 FROM N.A.
                                                                                                                                                              FSGFLVYSD 235
                                                                                                                                                                                       FSGFLVYPD
Metazoa;
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97
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B
               (Human)
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                                                                                                 STANDARD;
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243
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   Chordata;
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                                                                                                                                                                                                                                                                                                                                                                                                                 MW.
                                                                                                                                                                                                                                                                                                                                                              18;
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                                                                                                                                                                                                                                                                                                                                                                                                    C1Q.
; 7CCDA65CDA7EB784 CRC64;
                                                                                                                                                                                                                                                                                                                                                                          Score 213; DB 1;
Pred. No. 3.3e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                      POTENTIAL.
COMPLEMENT-C1Q TUMOR NECROSIS FACTOR-
RELATED PROTEIN 5.
COLLAGEN-LIKE.
  Craniata; Vertebrata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mewes
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                                                                                                 285
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  Euteleostomi;
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tions on its
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RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA HOpkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Stapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Brownstein M.J., Wadin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hullyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hullyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gibbs R.A.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gibbs R.A.,
RA Richards S., Worley M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Rahby J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Rahby J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Mihting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Rodriguez A.C., Grinwood J., Schmutz J., Myers R.M.,
"Generation and initial analysis of more than 15,000 full-length
"Thuman and mouse cDNA sequences.",

Proc. Natl. Acad. Sci. U.S.A. 99:16399-16303 (2002).
                                                                                                                                                                        Query Match
Best Local S
Matches 55
                                                                                                                                                                                                                                                               DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Piddington C.S., Bishop P.;
"Homo sapiens complement-clq tumor necrosis factor-related cubmifred (DEC-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00386; Clq; 1.
Pfam; PF01391; Collagen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; BC011699; AAH11699.1; Genew; HGNC:14325; C1QTNF2.
                                                                                                                                                                                                                                                                                                                    CHAIN
                                                                                                                                                                                                                                                                                                                                       SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                        SMART;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    or send
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Strausberg R.L., Feingold E.A., Grou
Klausner R.D., Collins F.S., Wagner
                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR001073; Clq.
InterPro; IPR000087; Collagen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AF329836; AAK17960.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      entities
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- SIMILARITY: Contains 1 collagenous domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=22388257; PubMed=12477932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE=Muscle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mammalia; Eutheria;
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                    184
                                                                                                        136 GLPGPCSC-
                                                                   65
                                                                                                                                                                                                                                                                                                                                                                                      ; PR00007; COMI
SM00110; C1Q;
                                                                                                                                         7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  an email to license@isb-sib.ch).
                                                                                                                                                                                          Similarity
QLDYGDTVWLRLHGA---
                                  SGKFVCGVPGIYYFTYDITLA-NKHLAIGLVHN-GQYRIRTFD--ANTGNHDVASGSTIL
                                                                   TGQFRCRVPGAYFFSFTAGKAPHKSLSVMLVRNRDEVQALAFDEQRRPGARRAASQSAML
                                                                                                                        GLLGPAACWALGPTPGPGSSELRSAFSAA--RTTPLEGTSEMAVTFDKVYVNIGGDFDVA
                                                                                                                                                                                                                                                                                                                                                                    PS01113; C1Q; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    requires a license agreement
                                                                                                                                                                                                                                                                                                                                                  Signal.
                                                                                                                                                                                                                                               285 AA;
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143
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29952
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285
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                                                                                                    -GSGHTKSAFSVAVTKSYPRE---RLPIKFDKILMNEGGHYNAS
                                                                                                                                                                        31;
                                                                                                                                                                                                                                                              POTENTIAL.
COMPLEMENT-C1Q TUMOR N
RELATED PROTEIN 2.
COLLAGEN-LIKE.
C1Q.
                                                                                                                                                                                          Pred.
                                                                                                                                                                                                         Score 208;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Catarrhini; Hominidae;
                                                                                                                                                                                                                                               7E31FF9868D4EDFA
                                                                                                                                                                           Mismatches
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                                                                                                                                                                                          No.
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                                                                                                                                                                                          1e-09;
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                                                                                                                                                                                                          DB 1;
                                                                                                                                                                           49;
                                                                                                                                                                                                          Length 285;
                                                                                                                                                                                                                                             CRC64;
                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                    NECROSIS FACTOR-
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                                                                                                                                                                        Gaps
                                                                                                      183
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RESULT 5
     RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards J., Hoton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Hahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Bakkesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Bakkesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Botherch A., Schein J.E., Jones S.J.M., Marra M.A.,
"Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences.";

Proc. Natl. Acad. Sci. U.S. A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-SEP-2003 (Rel. 41, Last sequence update)
Complement-clq tumor necrosis factor-related |
ClQTNF6 OR CTRP6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CQT6_HUMAN
Q9BXI9;
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                                                                                                                                                                                                                                                                                                                                         use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                EMBL; AF329842; AAK17966.1; -.
EMBL; BC020551; AAH20551.1; -.
Genew; HGNC:14343; ClQTNF6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=22388257; PubMed=12477932;
Strausberg R.L., Feingold E.A., Grouse L.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                              CHAIN
                                                                                                  SIGNAL
                                                                                                                                                       PRINTS; PR00007;
                                                                                                                                                                                                          InterPro; IPR001073; Clq.
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PF01391; Collagen; 1.
                                                                                                                                  PS01113; C1Q; FALSE_NEG
                                                                                                                Signal.
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139
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complement-clq tumor necrosis fa
connol to the EMBL/GenBank/DDBJ
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                                                                                                                                                       COMPLEMNTC10
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POTENTIAL.

COMPLEMENT-C10 TUMOR NECROSIS FACTOR-
RELATED PROTEIN 6.

COLLAGEN-LIKE.

C10.

N-LINKED (GLCNAC. . .) (POTENTIAL).
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C1RF MOUSE
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                                                                                                                                                                                                                                                               Berube N.G., Swanson X.H., Bertram M.J., Kittle J.D., Didenko Baskin D.S., Smith J.R., Pereira-Smith O.M.; "Cloning and characterization of CRF, a novel Clq-related fact expressed in areas of the brain involved in motor function."; Brain Res. Mol. Brain Res. 63:233-240(1999).

1- TISSUE SPECIFICITY: EXPRESSED IN BRAINSTEM. MORE ABUNDANT OF THE NERVOUS SYSTEM INVOLVED IN MOTOR FUNCTION, SUCH AS PURKINJE CELLS OF THE CEREBELLUM, THE ACCESSORY OLIVARY NUTHER PONS AND THE RED NUCLEUS.
                                                                           EMBL; AF095155; AAC64187.1; -. MGD; MGI:1344400; Clqrf. GO; GO:0005737; C:cytoplasm; I
                                                                                                                                  entities requires a license agreement (S or send an email to license@isb-sib.ch).
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus (Mouse)
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16-OCT-2001
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                                                InterPro; IPR001073;
InterPro; IPR000087;
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87; Conserv
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Pfam; PF00386; Clq; 1. Pfam; PF01391; Collagen;

PR00007;

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APM1 OR
                                                                                                                                                                                      MEDLINE=99196984; PubMed=10095105; Saito K., Tobe T., Minoshima S., Asakawa Nakano Y., Shimizu N., Tomita M.; "Organization of the gene for gelatin-bir Gene 229:67-73(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates; NCBI_TaxID=9606;
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DOMAIN
"The human apM-1, an adipocyte-specific gene linked to the family TNF's and to genes expressed in activated T cells, is mapped to chromosome 1921.3-923, a susceptibility locus identified for family combined hyperlipidemia (FCH).";
                                                                               MEDLINE=99333693; PubMed=10403784;
Schaeffler A., Orso E., Palitzsch K.D.,
Fuerst A., Schoelmerich J., Schmitz G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=Adipose tissue;
MEDLINE=96224171; PubM
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ACRP30 OR GBP28.
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(Rel. 42, Last annotation update)
precursor (30 kDa adipocyte complement-related
ipose most abundant gene transcript 1) (apM-1)
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Yamauchi T., Kamon J., Waki H., Terauchi Y., Kubota N., Yamauchi Y., Ide T., Murakami K., Tsuboyama-Kasaoka N., Ezak Akanuma Y., Gavrilova O., Vinson C., Reitman M.L., Kagec Shudo K., Yoda M., Nakano Y., Tobe K., Nagai R., Kimura Froguel P., Kadowaki T.;
"The fat-derived hormone adiponectin reverses insulin re associated with both lipoatrophy and obesity.";
Nat. Med. 7:941-946(2001).
                                                                                                                                                                                                                                                                                                                                                                     Yazaki Y., Nagai R., Taniyama M., Matsubara K., Yoda M., Nakano Y., Kimura S., Tomita M., Kimura S., Ito C., Froguel P., Kadowaki T.; "Genetic variation in the gene encoding adiponectin is associated with an increased risk of type 2 diabetes in the Japanese population."; Diabetes 51:536-540(2002)
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Otabe S., Okada T., Eto K., Kadowaki H.,
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Ouchi N., Kihara s
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MEDLINE=20417747;
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                                                                                                                                                                                                                                   FUNCTION: IMPORTANT NEGATIVE REGULATOR IN HEMATOPOIESIS AND IMMUNE SYSTEMS; MAY BE INVOLVED IN ENDING INFLAMATORY RESPONSES THROUGH ITS INHIBITORY FUNCTIONS. INHIBITS ENDOTHELIAL NF-KAPPAB SIGNALING THROUGH A CAMP-DEPENDENT PATHWAY. INHIBITS TNF-ALPHA-INDUCED EXPRESSION OF ENDOTHELIAL ADHESTON MOLECULES. INVOLVED IN THE EXPRESSION OF FAT METABOLISM AND INSULIN SENSITIVITY. SUBUNIT: HOMOOLIGOMER (POTENTIAL).
          s SWISS-PROT entry is copyright. It is produced through a collaboratic ween the Swiss Institute of Bioinformatics and the EMBL outstation European Bioinformatics Institute. There are no restrictions on it
                                                                          diabetes type 2 and insulin resistance. SIMILARITY: Contains 1 collagenous domain. SIMILARITY: Contains 1 C1Q domain.
                                                                                                                    [MIM:605441], resulting in very low concentration of adiponectin. Decreased adiponectin plasma levels are with obesity insulin resistance, and diabetes type 2. PHARMACEUTICAL: Adiponectin might be used in the trea
                                                                                                                                                                                    TISSUE SPECIFICITY: Synthesized e secreted into plasma.
DISEASE: Defects in APM1 are the
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Shimomura I., Hotta K., Kuriyama H.,
S., Funahashi T., Matsuzawa Y.;
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Kihara S.,
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Takahashi I., Ishikav
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SMART; SM00110; ClQ; 1.
PROSITE; PS01113; ClQ; 1.
Hormone; Collagen; Signal; Repeat Polymorphism; Disease mutation; C
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EMBL; AJ131461; CABS;
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                                                                                  243
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                                                                                                                                                             184
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                                                                                                                                                                                                                                                                                                                    GLIGPKGDIGETGVPGAEGPRGFPGIQGRKGEPGEGAYVYRSAFSVGLETYVT-IPNMPI
                                                                                                                                                                                                                                                                                                                                                         GLLGP-----AACWALGP------TPGPGSSELRSAFSAARTTPLEGTSEMAV
                                                                                                                                                             FTYDQYQENNVDQ-ASGSVLLHLEVGDQVWLQVYGEGERNGLYADNDNDSTFTGFLLYHD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IPR001073; Clq.
IPR000087; Collagen.
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29.7%;
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HYDROXYLATION
HYDROXYLATION
G -> R.
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/FTId=VAR_013274.
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/FTId=VAR_013273.
R -> C (in adipor
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COLLAGEN-LIKE.
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64D8C6C1204B1018 CRC64;
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/FTId=VAR_013275.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FTId=VAR_013276
                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                   196;
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1.7e-09;
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(BY SIMILARI)
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Y SIMILARITY).
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REPRESENTATION OF THE PROPERTY OF THE PROPERTY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APMI MOUSE STANDARD;
Q60994; Q62400; Q9D6C8;
01-NOV-1997 (Rel. 35, Car
01-NOV-1997 (Rel. 35, Lau
15-SEP-2003 (Rel. 42, Lau
                                                                                                                      Yamauchi T., Kamon Mori Y., Ide T., Mu Akanuma Y., Gavrilo Shudo K., Yoda M., I Froguel P., Kadowak: "The fat-derived ho
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Adiponectin precursor (30 kDa adipocyte compit (ACRP30) (Adipocyte specific protein AdipoQ).

APMI OR ACRP30 OR ADIPOQ.

Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                of the mouse
Acrp30.";
Biochem. Biop
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MEDLINE=96070757; PubMed=7592907;
Scherer P.E., Williams S., Fogliano M.,
"A novel serum protein similar to Clq, I
adipocytes.";
J. Biol. Chem. 270:26746-26749(1995).
                                                                                                                                                                                                                                                                                                                                     Nature
[5]
                                                                                                                                                                                                                                                                                                                                                       Wynshaw-Boris A., Yoshida
Hayashizaki Y.;
"Functional annotation of
Nature 409:685-690(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N. STRAIN=C57BL/6J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PubMed=11162643;
Das K., Lin Y., Widen E.,
"Chromosomal localization,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hu E., Liang P., Spiegelman B.M.;
"AdipoQ is a novel adipose-specific gene
J. Biol. Chem. 271:10697-10703(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE=Fibroblast; MEDLINE=96209999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=10090;
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Mammalia; Eutheria; Rodentia;
                                                                                                 associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
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                                                                                                                                                                                                                                                                                MEDLINE=21372498;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=21085660;
MEDLINE=21372499;
                                                                                                                                                                                                                                                                                                        FUNCTION
                       FUNCTION
                                                                                                                           fat-derived hormone adiponectin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FROM N.A.
                                                                            1 with both lipoatrophy 7:941-946(2001).
                                                                                                                                                                     Kamon J., Waki H., Terauchi Y., Kubota P.,
Kamon J., Waki H., Tsuboyama Kasaoka N., Ezak
S T., Murakami K., Tsuboyama Kasaoka N., Ezak
Gavrilova O., Vinson C., Reitman M.L., Kagec
                                                                                                                                                     Kadowaki T
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE=Heart;
                                                                                                                                                                                                                                    PubMed=11479627;
"Terauchi Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PubMed=11217851;
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                                                                                                                                                                                                                                                                                                                                                                                 of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Commun.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Zhang Y., Scherer P.E.; expression pattern, and prome g adipocyte-specific secretory
                                                                                                                                                                                                                                                                                                                                                                                 full-length
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Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
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                                                                                                      obesity.";
                                                                                                                           reverses insulin
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produced
                                                                                                                                                                                                                                                                                                                                                                                 mouse cDNA collection.";
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Ezaki O.,
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Pfam; PF01391; Collagen; 1.
PRINTS; PR00007; COMPLEMNTC1Q.
ProDom; PD000007; Clg helix; 1.
SMART; SM00110; ClQ; 1.
PROSITE; PS01113; ClQ; 1.
PROSITE; PS01113; ClQ; 1.
                                                                                                                                                                                                                                                                                                CHAIN
DOMAIN
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                                                                                                                                                                                                                                                                                                                        Polymorphism;
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                    MGD; MGI:106675; Acrp30.

GO; GO:0005576; C:extracellular; IDA.

GO; GO:0005515; F:protein binding activity; IPI.

GO; GO:0006635; P:fatty acid beta-oxidation; IMP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; U37222; AAA80543.1; -. EMBL; U49915; AAB06706.1; -. EMBL; AF304466; AAK13417.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR001073;
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"The adipocyte-secreted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FUNCTION: IMPORTANT NEGATIVE REGULATOR IN HEMATOPOIESIS AND IMMUNE SYSTEMS; MAY BE INVOLVED IN ENDING INFLAMMATORY RESPONSES THROUGH ITS INHIBITS ENDOTHELIAL NF-KAPPAB SIGNALING THROUGH A CAMP-DEPENDENT PATHWAY. INHIBITS TNF-ALPHA-INDUCED EXPRESSION OF ENDOTHELIAL ADHESION MOLECULES. INVOLVED IN THE CONTROL OF FAT METABOLISM AND INSULIN SENSITIVITY.
                                                                                                                                                                                     RES
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INDUCTION: DURING HORMONE-INDUCED
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  75
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58; Conserv
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protein Acrp30 enhances hepatic insulin
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                                             Score 196; DB
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RA Alleschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Alleschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Alleschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Alleschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Stapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hullyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hullyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hullyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hullyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hullyk S.W.,
RA Rahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Willalon D.K., Mazny D.M., Sodergren E.D., Dickson M.C.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
C., Hatla Analysis of more than 15,000 full-length
Proc. Matl. Acad. Sci. U.S.A. 99:16999-16903 (2002).
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O75973;
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Baskin D.S., Smith J.R., Pereira-Smith O.M.;
"Cloning and characterization of CRF, a novel Clq-related factor, expressed in areas of the brain involved in motor function.";
Brain Res. Mol. Brain Res. 63:233-240(1999).
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C1q-related
This SWISS-PROT entry is copyright. It is produced through a collable between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in
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Mammalia; Eutheria;
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Koide T., Aso A., Yorihuzi T., Nagata K.;
"Conformational requirements of collagenous
"conformational protein HSP47.";
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Eukaryota; Metazoa; (
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                                                       the chaperone protein HSP47.";
Biol. Chem. 275:27957-27963(2000).
- TISSUE SPECIFICITY: EXPRESSED IN GLIAL-
SIMILARITY: Contains 1 collagenous doma
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L; BC008798; AAH08798.1; -.
GO:0007626; P:locomotory behavior;
               SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its
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115
258
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Rodentia;
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27.3%;
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C1Q-RELATED FAC
COLLAGEN-LIKE.
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; 52C51CDF59CAE2BF CRC64;
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Best Local S
Matches 57
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28-FEB-2003 (Rel. 41, C
28-FEB-2003 (Rel. 41, I
15-SEP-2003 (Rel. 42, I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CQT7_F
TISSUE=Yest18;

MEDLINE=22388257; PubMed=12477932;

Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.E. Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.F. Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Altschul S.F., Zeeberg B., Buetow K.H., Wang J., Hsieh F., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz Stapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Prange C., Casavant T.C., Scheetz S.J., Abramson R.D., Mullahy
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SEQUENCE
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Pfam; PF01391; Collagen; 1.
PRINTS; PR000007; COMPLEMNTC1Q.
SMART; SM00110; C1Q; 1.
PROSITE; PS01113; C1Q; 1.
                                                                                                                                                                                                                                                                        Piddington C.S., Sheppard P.O., Bishop P., Las "Homo sapiens complement-clq tumor necrosis for Submitted (DEC-2000) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MGD; MGI:2387350; C1ql.
GO; GO:0005515; F:proctain binding
InterPro; IPR001073; Clq.
InterPro; IPR000087; Collagen.
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                                                                                                                                                                                                        SEQUENCE FROM
TISSUE=Testis;
                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human)
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57; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PPGAPGLNAAGAI SAATYSTVPKI AFYAGLKRQHEGYEVLKFDDVVTNLGNHYDPTTGKF
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Last annotation update)
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Pred. No. 4.7e
23; Mismatches
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GLIACOLIN.
COLLAGEN-LIKE.
C1Q.
C1Q.
W; 529FBAF4B2191BC1
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Catarrhini; Hominidae,
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is factor-related
DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                          Hominidae;
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ahat N.K.,
Hsieh F.,
Hong L.,
Srt
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Best Local S
Matches 60
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1. SIMILARITY: Contains 1 Collagenous domain.
                                       -HP25_TAMSI STANDARD; PRT; 215 AA.

Q06576;
Q1-NOV-1995 (Rel. 32, Created)
Q1-NOV-1995 (Rel. 32, Last sequence update)
Q8-FEB-2003 (Rel. 41, Last annotation update)
Hibernation-associated plasma protein HP-25 precursor (specific blood complex, 25 kDa subunit)
Tamias sibirious (Siberian chipmunk) (Asian chipmunk).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eut Mammalia; Eutheria; Rodentia; Sciurognathi; Sciuridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AF329839; AAK17963.1; -. EMBL; BC022187; AAH22187.1; -. Genew; HGNC:14342; C10TNF7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the European Bioinformatics Institute. Ther use by non-profit institutions as long a modified and this statement is not removed entitles requires a license agreement (See hor send an email to license@isb-sib.ch).
Tamias.
NCBI_TaxID=64680;
[1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Collagen;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRINTS;
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Pfam; PF01391; Collagen; 2
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InterPro; IPR000087; Collagen.
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SM00110; C1Q; 1.
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                                                                                                                                                                                                                                                                                                                  PIIFNKVLFNEGEHYNPATGKFICAFPGIYYFSYDITLA
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COMPLEMENT-CIQ TUMOF
RELATED PROTEIN 7.
COLLAGEN-LIKE.
C1Q.
W; A61609FF86D26946 C
                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 185.5; DB 1
Pred. No. 6.6e-08;
2; Mismatches 60
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(See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                 -GAPGATFSGYLVYADAD
                                                        Euteleostomi;
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                                                                                                                                                                                                                                                                                                                                                                                                                                    37;
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                                                                                                                                                                                                                                                                                                                  -GQYRIKTF
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SIGNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Hibernation-associated gene regulation of plasma collagen-like domain in mammalian hibernators."; Mol. Cell. Biol. 13:1516-1521(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00386; C1q; 1.
Pfam; PF01391; Collagen; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PIR; B48150; B48150.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR001073; Clq.
InterPro; IPR000087; Collagen.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Identification of novel blood proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIMILARITY: Contains 1 collagenous domain. SIMILARITY: Contains 1 C1Q domain.
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SUBCELLULAR LOCATION: Extracellular.
TISSUE SPECIFICITY: PLASMA; SYNTHESIZED IN THE LIVER
DEVELOPMENTAL STAGE: THE PROTEIN COMPLEX DISAPPEARS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FUNCTION: PLASMA PROTEINS HP-1140 kDa COMPLEX VIA DISULFIDE
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193
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                                                                                                                                                                                                                                                                                                                                                                             1 Similarity
62; Conserv
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LK---GTESEKGITHIVFFGYLLY
                                                                                      LFQSSVKIRLM--RDGIQV------REKEAQANDSYKHAMGSVIMALGKGDKVWLESK 192
                                                                                                                                        LPRKTLSVKLMKNRDEVQAMIYDDGASRRREMQSQ-----SVMLALRRGDAVWLLSH 289
                                                                                                                                                                                                                                 AFSAARTRSLVGSDAGPGPRHQPLAFDTEFVNIGGDFDAAAGVFRCRLPGAYFFSFTLGK
                                          DHDGYGAYSNHG-KYITFSGFLVY
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213
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AND ARE
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RESULT 13
C1QB_HUMAN
ID C1QB_H
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altechul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altechul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Richards S., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., McEwan J.J., McKernan N.J., Madan A.M., Gay L.J., Hulyk S.W.,
RA Willalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Whiting M., Madan A., Young A.C., Shewchenko Y., Bouffard G.G.,
RA Whiting M., Madan A., Young A.C., Shewchenko Y., Bouffard G.G.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
"Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.",
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                P02746; Q96H17;
21-JUL-1986 (Rel. 01, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement system.";
Biochem. J. 231:729-735(1985)
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Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Complement
             TISSUE=Liver;
MEDLINE=85038855; PubMed=6208566;
                                                                                                                                                                                                                                                  Reid K.B.M., Thompson E.O.P.;
"Amino acid sequence of the N-terminal 108 amino acid B chain of subcomponent Clq of the first component of
                                                                                                                                                                                                                                                                                                                                                                                                present in subcomponent Clq
                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 26-133.
MEDLINE=80020137; PubMed=486087;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=22388257; PubMed=12477932;
Strausberg R.L., Feingold E.A., Grouse L.H.,
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                                                                                      Reid K.B.M., Gagnon J., Frampton J.;
"Completion of the amino acid sequences subcomponent C1g of the first component Biochem. J. 203:559-569(1982).
                                                                                                                                                                                                                                                                                                            SEQUENCE OF 26-193.
MEDLINE=79041552; PubMed=708376;
                                                                                                                                                                                                                                                                                                                                                                Biochem. J. 179:367-371(1979).
                                                                                                                                                                                                                                                                                                                                                                                     complement
                                                                                                                                                                                                                                                                                                                                                                                                "Complete amino acid sequences of the three collagen-like regions present in subcomponent Clq of the first component of human
                                                      SEQUENCE OF
                                                                                                                                                             MEDLINE=82283890; PubMed=6981411;
                                                                                                                                                                                SEQUENCE OF 134-251
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                                                                                                                                                                                                                                          subcomponent
                                                      224-251 FROM N.A.
                                                                                                                                                                                                                     173:863-868(1978).
Bentley D.R., Wood K.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 and characterization of the complementary DNA and e B-chain of subcomponent Clq of the human
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Primates;
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Immunobiology 199:286-294 (1998).

-!- FUNCTION: C1Q ASSOCIATES WITH THE PROENZYMES CIR AND C1S TO YIELD C1, THE FIRST COMPONENT OF THE SERUM COMPLEMENT SYSTEM. THE C1, THE FIRST COMPONENT OF THE SERUM COMPLEMENT SYSTEM. THE C2LLAGEN-LIKE REGIONS OF C1Q INTERACT WITH THE CA (2+)-DEPENDENT C1R(2)C1S(2) PROENZYME COMPLEX, AND EFFICIENT ACTIVATION OF C1 TAKES PLACE ON INTERACTION OF THE GLOBULAR HEADS OF C1Q WITH THE FC REGIONS OF IGG OR IGM ANTIBODY PRESENT IN IMMUNE COMPLEXES.
-!- SUBUNIT: C1 IS A CALCIUM-DEPENDENT TRIMOLECULAR COMPLEX OF C1Q, R AND S IN THE MOLAR RATION OF 1:2:2. C1Q SUBCOMPONENT IS COMPOSED OF NINE SUBUNITS, SIX OF WHICH ARE DISULFIDE-LINKED DIMERS OF THE A AND B CHAINS, AND THREE OF WHICH ARE DISULFIDE-LINKED DIMERS OF THE C CHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REVIEW OF C1Q DEFICIENCY MEDLINE=98450587; PubMed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Molecular basis of hereditary Clq deficiency.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DISEASE: Defects in ClQB are a cause of ClQ deficiency [MIM:120570]. It is a rare genetic disorder which is assowith recurrent infections and a high prevalence of lupus erythematosus-like symptoms. It is characterized by a los SIMILARITY: Contains 1 collarance.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIMILARITY: Contains 1 collagenous domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        O-linked glycans consist of Glc-Gal disaccharides bound
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PubMed=9777412;
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EMBL; BC005983; AAH08983.1; ALT\_INIT.
EMBL; M36778; AAC41692.1; -.
Genew; HGNC:1242; C1QB. DOMAIN DOMAIN PRINTS; PRO0007; COMPLEMS SMART; SM00110; C1Q; 1. PROSITE; PS01113; C1Q; 1. GO; GO:0005602; C:complement GO; GO:0003811; F:complement Repeat; Signal; SIGNAL 1 Pfam; PF00386; Clq; 1. Pfam; PF01391; Collagen; Complement InterPro; IPR001073; Clq. 120570; pathway; Disease mutation; COMPLEMNTCLQ Plasma; Hydroxylation; Glycoprotein; ation; Pyrrolidone carboxylic HYDROXYLATION
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HYDROXYLATION component Clq complex; activity activity; TAS PYRROLIDONE CARBOXYLIC ACID COMPLEMENT INTERCHAIN COLLAGEN-LIKE QTD. HTIM) SUBCOMPONENT, C-26 IN CHAIN TAS Collagen; acid. B CHAIN ð

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RESULT 14
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01-NOV-1995 (Rel. 3
16-OCT-2001 (Rel. 4
Complement Ciq subc
Wing M.G., Seilly D.J., Bridgman D.J., Harrison R.A.;

Wing M.G., Seilly D.J., Bridgman D.J., Harrison R.A.;

"Rapid isolation and biochemical characterization of rat C1 and C1q.";

"Rapid isolation and biochemical characterization of rat C1 and C1q.";

"Rapid isolation and biochemical characterization of rat C1 and C1s.";

"Rapid isolation and biochemical characterization of C1s. To YIELD

C1. THE FIRST COMPONENT OF THE SERUM COMPLEMENT SYSTEM. THE C1, THE FIRST COMPONENT OF THE SERUM COMPLENT ACTIVATION OF C1 TAKES PLACE ON INTERACTION OF THE GLOBULAR HADDS OF C1Q WITH THE FC REGIONS OF IGG OR IGM ANTIBODY PRESENT IN IMMUNE COMPLEXES.

-!- SUBUNIT: C1 IS A CALCIUM-DEPENDENT TRIMOLECULAR COMPLEX OF C1Q, R AND S IN THE MOLAR RATION OF 1:2:2. C1Q SUBCOMPONENT IS COMPOSED OF NINE SUBUNITS, SIX OF WHICH ARE DISULFIDE-LINKED DIMERS OF THE A AND B CHAINS, AND THREE OF WHICH ARE DISULFIDE-LINKED DIMERS OF THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C1QB_RAT
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                                                                                                                                                                                                                                                                                                    STRAIN=Sprague-Dawley; TISSUE=Spleen; MEDLINE=96062319; PubMed=7594503;
                                                                                                                                                                        MEDLINE=93218657;
                                                                                                                                                                                     SEQUENCE OF 71-79
                                                                                                                                                                                                                                                                                        Schwaeble W., Schaefer M.K.-H., Petry F.,
                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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D.J., Bridgman
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G -> D (in C1Q deficiency).
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Q -> E (IN REF. 3).
N -> D (IN REF. 3).
G -> P (IN REF. 3 AND 4).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00386; C1q; 1.
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NCBI_TaxID=13106;
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MEDLINE=95167486; PubMed=7863331;

MEDLINE=95167486; PubMed=7863331;

Molecular cloning and characterization of an inner ear-specific structural protein.";

Science 267:1031-1034(1995).
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CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; U17431; AAA69978.1; ALT_FRAME. InterPro; IPR001073; Clq. InterPro; IPR000087; Collagen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gibson T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CONCEPTUAL TRANSLATION
                                                                                                                                                                                                                                                                                                                                                                                              PRINTS; PR00007; COMPLEMNTC1Q.
ProDom; PD000007; C1g_helix; 2.
                                                                                                                                                                                                                                                                         DOMAIN
                                                                                                                                                                                                                                                                                                                                                       Extracellular matrix; Repeat;
                                                                                                                                                                                                                                                                                                                                                                      SMART; SM00110; C1Q; 1.
PROSITE; PS01113; C1Q; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00386; Clq; 1.
Pfam; PF01391; Collagen; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WITH OTHER SHORT-CHAIN COLLAGENS.
                          113 GARRAASQSAMLQLDYGDTVWLRL----HGAPHYALGAPGATFSGYLVYAD 159
                                                      310 GHWDPTLNKFNVTYPGVYLFSYHITVRNRPVRAALVVNGVRKLRTRDSLYGQDIDQ----
                                                                                                               258 LKGVRGPR-----GPKGPPGESVEQIRSAFSVGLFPSRSFP---PPSLPVKFDKVFYNGE 309
                                                                                   59 GDFDVATGQFRCRVPGAYFFSF--TAGKAPHKSL----SVMLVRNRDEVQALAFDEQRRP 112
                                                                                                                                         5 LIGLIGPAACWALGPTPGPGSS--ELRSAFSA----ARTTPLEGTSEMAVTFDKVYVNIG 58
                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                               419 AA;
                                                                                                                                                                       Conservative
ASNLALLHLTDGDQVWLETLRDWNGX--YSSSEDDSTFSGFLLYPD
                                                                                                                                                                                                                               43634 MW;
                                                                                                                                                                                10.1%;
32.7%;
                                                                                                                                                                       21;
                                                                                                                                                                                 Score 173.5; DB 1
Pred. No. 9.4e-07;
                                                                                                                                                                                                                                           N-LINKED (GLCNAC. . .) (POTENTIAL)
N-LINKED (GLCNAC. . .) (POTENTIAL)
                                                                                                                                                                                                                                                                       CIQ.
                                                                                                                                                                                                                                                                                                 NONHELICAL REGION (NC2).
TRIPLE-HELICAL REGION (COL1).
                                                                                                                                                                                                                                                                                     NONHELICAL REGION (NC1).
                                                                                                                                                                                                                                                                                                                              INNER EAR-SPECIFIC COLLAGEN.
                                                                                                                                                                                                                                                                                                                                            Collagen; Signal. POTENTIAL.
                                                                                                                                                                                                                            570CDB9675FC0F39 CRC64;
                                                                                                                                                                      Mismatches
                                                                                                                                                                                                DB 1;
                                                                                                                                                                       59;
                                                                                                                                                                       Indels 35;
                                                                                                                                                                                             Length 419;
                                                                                                                                                                       Gaps
                                                        365
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Search completed: January 12, 2004, 08:12:56 Job time : 13.8204 secs

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Database :
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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1726
1 MLPLLLGLLGPAACWALGPT......LVYPDLAPAAPPGLGASELL 329
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                                                                                                                                                                                                                                                                                                    SPTREMBL_23:*
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Copyright (c) 1993 - 2004 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Result No.	Score 1718	Query Match	Query Query Match Length 99.5 329	DB 11	ID QBIV25	Description OBiv25 homo
	1587	91.9	326	11	Q8R066	Q8r066 mus
. ω	1003.5	58.1	205	11	Q9D0W2	Q9d0w2 mus
4	997.5	57.8	205	11	Q9DCB6	Q9dcb6 mus
ري ري	230	13.3	158	4	Q9Н667	Q9h667 homo
6	230	13.3	1077	4	Q8TE71	Q8te71 homo
7	226	13.1	158	11	Q8K1I0	Q8k1i0 mus
80	220.5	12.8	182	11	Q8R1P2	Q8r1p2 mus
9	220.5	12.8	281	11	Q9QXP7	Q9qxp7 mus
10	213	12.3	243	4	Q8N6P2	Q8n6p2 homo
11	207	12.0	294	11	Q9D8U4	Q9d8u4 mus
12	205	11.9	243	11	Q8R002	Q8r002 mus
13	202	11.7	243	11	Q8K479	Q8k479 mus musculi
14	199	11.5	243	σ	Q95JD7	Q95jd7 macaca mula
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16	189	11.0	240	ע		,,,,

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	131.5		134.5	137.5	139	140	141.5	145.5	150	152	155	161	162.5	163	163	164	166	167.5	167.5	168	170	176.5	179.5	180.5	185.5	186	188
7.6 7.6	7.6	7.7	7.8	8.0	8.1	8.1		8.4		8.8	9.0	9.3	9.4	9.4	9.4	9.5	9.6	9.7	9.7	9.7	9.8	10.2	10.4	10.5	10.7	10.8	10.9
583 992	185	347	213	195	198	198	1017	705	333	197	196	173	246	224	224	295	675	744	744	245	194	289	120	264	312	287	244
44	U	4	v	1	11	1	11	4.	4.	1	11	σ	11	11	4.	1	თ	11	11	11	თ	11	11	11	11	11	11
Q96G58 Q9UG76	Q9GQV4	Q96IH6	P83425	Q8BZS3	Q8BME9	Q8BMF0	Q99K41	Q8TEJ5	Q8IUU4	Q9JHG0	Q920N0	062789	Q9ES30	Q8BGU2	Q8IUK8	Q9Z1K4	Q9N178	Q8BGL6	Q921S8	Q9DCM6	Q95J95	Q8BVD7	Q8R1Z2	Q8BKR0	Q8CHX9	Q8CFR0	Q8K3R4
Q96g58 homo sapien Q9uq76 homo sapien	stron		mytil	Bum	mus	Bum		homo			0 tam	e sue	Bru	Q8bgu2 mus musculu		rat	ED.	mus	mus	Q9dcm6 mus musculu	anis	mus	mus	mus	Bru		Q8k3r4 rattus norv

## ALIGNMENTS

B 1	Q.	DЪ	ş	Дb	8	Дb	γQ	Query M Best Lo Matches	so s	DR E			RP (	3 i					A A		RESULT Q8IV25
	181 AARTRSLVGSDAGPGPRHQPLAFDTEFVNIGGDFDAAAGVFRCRLPGAYFFSFTLGKLPR 240	121 SAMLQLDYGDTVWLRLHGAPQYALGAPGATFSGYLVYADADADAPARGPPAPPEPRSAFS 180	121 SAMLQLDYGDTVWLRLHGAPHYALGAPGATFSGYLVYADADADADARARGPPAPPEPRSAFS 180	61 FDVATGQFRCRVPGAYFFSFTAGKAPHKSLSVMLVRNRDEVQALAFDEQRRPGARRAASQ 120	61 FDVATGQFRCRVPGAYFFSFTAGKAPHKSLSVMLVRNRDEVQALAFDEQRRPGARRAASQ 120	1 MLPLLLGLLGPAACWALGPTPGPGSSELRSAFSAARTTPLEGTSEMAVTFDKVYVNIGGD 60	1 MLPLLLGLLGPAACWALGPTPGPGSSELRSAFSAARTTPLEGTSEMAVTFDKVYVNIGGD 60	Query Match 99.5%; Score 1718; DB 4; Length 329; Best Local Similarity 99.7%; Pred. No. 2.2e-134; Matches 328; Conservative 0; Mismatches 1; Indels 0; Gaps 0	SEQUENCE 329 AA; 35256 MW; 16064DA8182A6732 CRC64;	EMBL; BC035628; AAH35628.1;	Strausberg R.;	rain:	SECUTENCE FROM N.A.	Primates; Catarrhini	Rukaryota: Metazoa: Chordata: Craniata: Vertebrata: Ruteleostomi:	lar to Clq and tumor necrosis	3 (TrEMBLrel. 23, Last annotation	01-MAR-2003 (TrEMBLiel. 23, Cleated)	(Tremet sol or	Q8IV25 PRELIMINARY; PRT; 329 AA.	

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RESULT
QBR066
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Strausberg R.;
Strausberg R.;
Submitted (APR-2002) to the EMBL/Ge
Interpro; IPR001073; C1q.
R Ffam; PF00386; C1q; 2.
DR PROSITE; PS01113; C1Q; 2.
DR PROSITE; PS01113; C1Q; 2.
DR PROSITE; PS01113; C1Q; 2.
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Best Loc
Matches
Q9D0W2 PRELIMINARY
Q9D0W2;
01-JUN-2001 (TrEMBLrel.
01-JUN-2001 (TrEMBLrel.
01-QCT-2002 (TrEMBLrel.
0710001E10Rik protein.
0710001E10RIK.
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01-JUN-2002 (TrEMBLrel. 21,
01-MAR-2003 (TrEMBLrel. 23,
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Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similar to Clq and tumor necrosis factor related protein 0710001E10RIK.
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2; Mismatches
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                                                Last sequence update)
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Sciurognathi; Muridae;
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annotation update)
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
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Q9DCB6;
Q1-JUN-2001 (TrEMBLrel. 1
01-JUN-2001 (TrEMBLrel. 1
01-OCT-2002 (TrEMBLrel. 2
0710001E10R1k protein.
0710001E10R1K.
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SMART; SMOOILO; CLQ; 1.
PROSITE; PSO1113; CLQ;
SEQUENCE 205 AA; 221
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STRAIN=C57BL/6J; TISSUE=Embryo;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AK004340; BAB23268.1; MGD; MGI:1914695; 0710001E10 InterPro; IPR001073; Clq. Pfam; PF00386; Clq; 1.
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Rodentia;
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93.7%;
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Last
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Pred. No. 2e-75;
1; Mismatches
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Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                              PRT;
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                                                                                                                                                                                                                                          sequence update) annotation updat
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                                                                                                                                                                                                                                          update)
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Eukaryota; Metazoa; Mammalia; Eutheria;

Chordata; Rodentia;

Craniata; Vertebrata; Sciurognathi; Muridae;

Euteleostomi; Murinae;

SEQUENCE

N.A.

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RESULT Q94667 ID 94667 OF PAC Q9 DT OF OF PAC Q9 PA
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RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Arakawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Kadota K., Matsuda H.A., Ashburner M., Besole G., Quackenbush J.,
RA Kadota K., Matsuda H.A., Tomita M., Wagner L., Washio T.,
RA Kadota K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
Rasaki K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
Rasaki K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
Rasaki H., Sato K., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
Rasaki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
Wa Hayashizaki Y..;
Na Hayashizaki Y..;
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Best Local S
Matches 192
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PRINTS; PR00007; COMPLEUR...
SMART; SM00110; C1Q; 1.
DROSITE; PS01113; C1Q; 1.
                    TISSUE-Small intestine; Watanabe K., Kumagai A., Itakura S., Yamazaki Suzuki Y., Obayashi M., Nishi T., Shibahara T. Nakamura Y., Isogai T., Sugano S.; "NEDO human cDNA sequencing project."; Submitted (AUG-2000) to the EMBL/GenBank/DDBJ Submitted (AUG-2000)
                                                                                                                                                                                                                                                                                                                                 01-MAR-2001 (TrEMBLrel. 16, La
01-OCT-2002 (TrEMBLrel. 22, La
Hypothetical protein FLJ22569
Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q9H667;
01-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q9H667
                                                                                                                                                                                                                                                                               Eukaryota; Metazoa;
Mammalia; Eutheria;
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EMBL; AK002948; BAB22473.1; -.
MGD; MGI:1914695; 0710001E10Rik.
                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                               NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YITFSGFLVYPDLAAAGPPALKPPEL
                                                                                                                                                                                                                                                                                                                                                                                     (TrEMBLrel. 16, Created)
(TrEMBLrel. 16, Last sequence update)
(TrEMBLrel. 22, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                  Chordata;
Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   57.8%;
93.2%;
                          project.";
EMBL/GenBank/DDBJ databases
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Pred. No. 6.4e-75;
1; Mismatches 12
                                                                                                                                                                                                                                                                            Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
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Best Local S
Matches 63
                                                                                                                                                     Query Match
Best Local
                                                                                                                                          Matches
                                                                                                                                                                                      InterPro; IPR001073; Clq. Pfam; PF00386; Clq; 1. SMART; SM00110; ClQ; 1. PR0SITE; PS01113; ClQ; 1. SEQUENCE 1077 AA; 12097.
                                                                                                                                                                                                                                                                                                                                                                                 Q8TE71;
Q8TE71;
01-JUN-2002
01-JUN-2002
01-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                      EEG1L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00386; Clq; 1
PRINTS; PR0007; COMPLEMNTC1Q.
SMART; SM00110; ClQ; 1
PROSITE; PS01113; ClQ; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases EMBL; AK026222; BAB15398.1; -. EMBL; BC007520; AAH07520.1; -. InterPro; IPR001073; Clq.
                                                                                                                                                                                                                                                 Submitted (JAN-2002) to the EMBL; AY074490; AAL71549.1;
                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
Aerbajinai W., Miller J.L.;
                                                                                                                                                                                                                                                                                                                          Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hypothetical protein. SEQUENCE 158 AA; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. TISSUE=Uterus;
                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                   Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Strausberg
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1038
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                      Similarity
NHAILQLFQGDQIWLRLH----RGAIYGSSWKYSTFSGYLLYQD
                                                                   DFDAAAGVFRCRLPGAYFFSFTLGKLP-RKTLSVKLMKNRDEVQAMIYDDGASRRREMQS
                     QSVMLALRRGDAVWLLSHDHDGYGA-YSNHGKYITFSGFLVYPD
                                                                                          DVPVTNPAATILPVHVYPLPQQMRVAFSAART----SNLAPGTLDQPIVFDLLLNNLGE
                                                                                                                  DAPARGP-----PAPPEPRSAFSAARTRSLVGSDAGPGPRHQPLAFDTEFVNIGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NHAILQLFQGDQIWLRLH----RGAIYGSSWKYSTFSGYLLYQD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QSVMLALRRGDAVWLLSHDHDGYGA-YSNHGKYITFSGFLVYPD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TFDLQLGRENCPVNGTYVFIFHMLKLAVNVPLYVNLMKNEEVLVSAYANDGAP-DHETAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DFDAAAGVFRCRLPGAYFFSFTLGKLP-RKTLSVKLMKNRDEVQAMIYDDGASRRREMQS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DVPVTNPAATILPVHVYPLPQQMRVAFSAART----SNLAPGTLDQPIVFDLLLNNLGE
                                              TFDLQLGR
                                                                                                                                                                                                                                                                                                                        Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                  (TrEMBLrel. (TrEMBLrel. (TrEMBLrel.
                                                                                                                                          Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                 (Human)
                                              FNCPVNGTYVF1FHMLKLAVNVPLYVNLMKNEEVLVSAYANDGAP-DHETAS
                                                                                                                                                                                                                                                                                                                         Chordata;
Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17625 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13.3%;
                                                                                                                                                     13.3%;
                                                                                                                                                                                         120974 MW;
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21,
23,
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                                                                                                                                          16;
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                                                                                                                                                                                                                                                              EMBL/GenBank/DDBJ databases
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Last annotation updat
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Pred.
                                                                                                                                        Score 230; DB 4;
Pred. No. 2.4e-10;
6; Mismatches 63
                                                                                                                                                                                                                                                                                                                         Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      47DB10EDD6DC9760 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                         2B88BF3C47D032D6 CRC64;
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Yn 2e-11;
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                                                                                                                                                               Length 1077;
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1077
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RESULT
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Query Match
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Matches 56
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-OCT-2002 (TrEMBLrel.
01-OCT-2002 (TrEMBLrel.
01-MAR-2003 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (ARR-2002) to the EMBL; BC027523; AAH27523.1; InterPro; IPR001073; Clq. Pfam; PF00386; Clq; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similar to hypothetical Mus musculus (Mouse).
                                                                                                                    NON TER
                                                                                                                                                                              Submitted (PEB-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC023468; AAH23468.1; -.
MGD; MGI:1919254; 1600017K21Rik.
InterPro; IPR001073; C1q.
InterPro; IPR001073; Cc1q.
Pfam; PF00386; C1q; 1.
SMART; SM00110; C1Q; 1.
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SMART; SM00110; C10; 1.
PROSITE; PS01113; C10; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JUN-2002 (TrEMBLrel. 21, Creat
01-JUN-2002 (TrEMBLrel. 21, Last
01-JUN-2003 (TrEMBLrel. 23, Last
01-MAR-2003 (TrEMBLrel. 23, Last
Similar to RIKEN cDNA 1600017K21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE=Uterus;
                                                                                                                                                                                                                                                                                                                                                                                                 Strausberg R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus (Mouse)
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                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE=Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE 15
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                                Similarity
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                                                                                                                       182
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   Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chordata;
Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rodentia;
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                             12.8%;
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22, Last sequence update)
23, Last annotation updat
protein FLJ22569.
                                                                                                                              M.
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   20;
   Score 220.5;
Pred. No. 1.4e
20; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -RGAIYGSSWKYSTFSGYLLYQD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 226; DB 11
Pred. No. 4.2e-11
8; Mismatches 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sciurognathi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Craniata; Vertebrata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Craniata; Vertebrata; | Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              86E9321C99225FCB CRC64;
                                                                                                                           559C73DE9517882F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sequence update)
annotation update)
gene (Fragment).
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                                .4e-10;
                                                          DB 11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Euteleostomi;
; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12;
   9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
      Gaps
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RESULT
Q9QXP7
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                                                                                                                                                                                                                                                                      RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Aizawa K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schrimil L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Schrimil L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Blake J., Boitolli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Hovashi H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Sasaki H., Sato K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Mynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Havashizki Y.,
               Query Match
Best Local
 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q9QXP7;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Putative secreted protein ZSIG37 (1600017K21RIK protein).
ZSIG37 OR 1600017K21RIK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q9QXP7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sheppard P., Deisher T., Whitmore T., O'Hara P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus (Mouse)
                                                                                                               Pfam; PF00386; Clq; 1. Pfam; PF01391; Collagen;
                                                                                                                                                                             EMBL; AF192499; AAF06664.1; -.
EMBL; AK005484; BAB24070.1; -.
MGD; MGI:1919254; 1600017K21Rik.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=C57BL/6J; TISSUE=Placenta; MEDLINE=21085660; PubMed=11217851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                 SEQUENCE
                                                                                SMART;
                                                                                               PRINTS;
                                                                                                                                                                                                                            Nature 409:685-690(2001
                                                                                                                                            InterPro; IPR001073; Clq.
InterPro; IPR000087; Collagen.
                                                                                                                                                                                                                                                 Functional annotation of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  47
l Similarity
56; Conserv
                                                                                ; PR00007; COMPLE
SM00110; C1Q; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GAYSNHGKYITFSGFLVYPDLAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TWNQKETYLHIMKNEEEV-VILYAQ-VSDRSIMQSQSLMMELREEDEVWVRLFKGERENA 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KLPRKTLSVKIMKNRDEVQAMIYDDGASRRREMQSQSVMLALRRGDAVW--LLSHDHDGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAFSVGRKKALHSND-----YFOPVVFDTEFVNLYKHFNMFTGKFYCYVPGIYFFSLNVH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SAFSAARTRSLVGSDAGPGPRHQPLAFDTEFVNIGGDFDAAAGVFRCRLPGAYFFSFTLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (OCT-1999) to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
 Conservative
                                                                 AA,
                                                                                                 COMPLEMNTC1Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chordata;
Rodentia;
                                                                 32009 MW;
               12.8%;
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 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                               full-length
Score 220.5; DB 11;
Pred. No. 2.5e-10;
0; Mismatches 58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Mus
                                                                 C9816216DB6419E2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein.";
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                                                                                                                                                                                                                                                   mouse cDNA
                                DB 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Haldeman
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   Indels
                                                                                                                                                                                                                                                   collection.";
                                Length
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B
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                                  281;
   9
   Gaps
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RESULT 10
Q8N6P2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               밁
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local S
Matches 66
                                                                                                                                                                     01-JUN-2001
01-JUN-2001
01-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Strausberg R.;
Submitted (MAY-2002) to the EMI
EMBL; BC029485; AAH29485.1; -.
InterPro; IPR001073; C1q.
InterPro; IPR000087; Collagen.
                                                              Mus musculus (Mouse)
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                            01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
1810033K05R1k protein (RIKEN cDNA 1810033K05 gene)
1810033K05RIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Clq and tumor necrosis factor related protein 5.
                          NCBI_TaxID=10090;
[1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                        Q9D8U4;
                                                                                                                                                                                                                                                              Q9D8U4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRINTS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00386; Clq; 1.
Pfam; PF01391; Collagen; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q8N6P2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q8N6P2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            113
                                                                                                                                                                                                                                                                                                                                                                                                               306
                                                                                                                                                                                                                                                                                                                                                                                                                                                       167
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SM00110; C1Q; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SLVGSDAGPGPRHQPLAFDTEFVNIGGDEDAAAGVFRCRLPGAYFFSFTLGKLPRKTLSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GAPHYALGAPGATFSG---YLVYADAD----ADAPARGPPAPP----EPRSAFSAARTR 185
                                                                                                                                                                                                                                                                                                                                                                                                             FSGFLVYPD
                                                                                                                                                                                                                                                                                                                                                                                                                                                       DLVKNGESIASFFQFFGGWPKPASLSGGAMVRLEPEDQVWVQVGVGDYIGIYASIKTDST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KLMKNRDEVQAMIYDDGASRRREMQSQSVMLALRRGDAVWLLSHDHDGYGAYSNHGKYIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SRV----PPPSDAPLPFDRVLVNEQGHYDAVTGKFTCQVPGVYYFA-VHATVYRASLQF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GAP---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IFSDEFDTYITFSGYLVKPASEP
                                                                                                                                                                                                                                                                                                                                                                       FSGFLVYSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GAYSNHGKYITESGFLVYPDLAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TWNQKETYLHIMKNEEEV-VILYAQ-VSDRSIMQSQSLMMELREEDEVWVRLFKGERENA 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KLPRKTLSVKLMKNRDEVQAMIYDDGASRRREMQSQSVMLALRRGDAVW--LLSHDHDGY 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAFSVGRKKALHSND----YFQPVVFDTEFVNLYKHFNMFTGKFYCYVPGIYFFSLNVH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      243 AA;
                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GAPGEKGEGGRPGLPGPRGDPGPRGEAGPAGPTGPAGECSVPPRSAFSAKRSE
                                                                                                                                                                                                                                                                                                                                                                       235
                                                                                                                                                                                                                                                                                                                                                                                                             314
                                                                Chordata;
Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25326 MW; 6D9306A0EB21B44A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 213; DB 4;
Pred. No. 8.8e-10;
                                                              Craniata; Vertebrata; I
Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Catarrhini;
                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     317
                                                                                                                                                                                                                                                            294
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                                                                                                                                                                                                                                                            B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   83;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 243;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                Euteleostomi; 
Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       226
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Q8R002
    RRRRR COCC OG DIT AC
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Best Local :
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01-JUN-2002
01-JUN-2002
                                                                                                           NCBI_TaxID=10090;
                                                                                                                                              Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                            Q8R002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00386; C1q; 1.
Pfam; PF01391; Collagen; 2.
PRINTS; PR00007; COMPLEMNTC1Q.
PROSITE; PS01113; C1Q; 1.
SEQUENCE 294 AA; 30865 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AK007683; BAB25187.1; -.
EMBL; BC030324; AAH30324.1; -.
MGD; MGI:1916433; 1810033K05Rik.
SEQUENCE FROM N.A
                                          Submitted
                                                              Strausberg
                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                         Mus musculus (Mouse)
                                                                                                                                                                                                                                 Similar to
                                                                                                                                                                                                                                                         01-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (MAY-2002) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Strausberg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nature 409:685-690(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hayashizaki Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=C57BL/6J; TISSUE=Pancreas; MEDLINE=21085660; PubMed=11217851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR001073; Clq.
InterPro; IPR000087; Collagen.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     249
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     ALKEGDEVWLQIFYSEQNGLFYDPYWT----DSLFTGFLIYAD
                                          (FEB-2002)
                                                                                                                                                                                                                                   DKFZP586B0621
                                                                                                                                                                                                                                                     (TrEMBLrel. 21, Creat
(TrEMBLrel. 21, Last
(TrEMBLrel. 23, Last
                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
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                                                                                                                                              Chordata;
Rodentia;
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                                          EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                               Created)
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Pred. No. 3.
                                                                                                                                            Craniata; Vertebrata; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6D3905AE7C19E6FA CRC64;
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annotation update)
(Hypothetical 25.4
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Length Indels

294; 30;

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Euteleostomi;

Murinae;

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159

124 192 64

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RESULT 13
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                                           Query Match
Best Local S
Matches 63
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Best Local Similarity
Matches 64; Conser
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EMBL; BC025174; AAH25174.1; -.
MGD; MG1:2385958; Clqtnf5.
InterPro; IPR001073; Clq.
InterPro; IPR000087; Collagen.
Pfam; PF00386; Clq; 1.
Pfam; PF00386; Clq; 1.
SMART; SM00110; ClQ; 1.
Hypothetical protein.
SEQUENCE 243 AA; 25420 MW; 4
                                                                                                        PRINTS;
SMART; S
                                                                                                                                                                                                                                                                                                                                                                                 01-OCT-2002 (TrEMBLrel. 22, 01-OCT-2002 (TrEMBLrel. 22, 01-MAR-2003 (TrEMBLrel. 23,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Strausberg
                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                       Hum. Mol. Genet. 11:1879-1886(2002)
EMBL; AF469650; AAM89217.1; -.
                                                                                                                                                                                                                                      Nishina
                                                                                                                                                                                                                                                   Kameya S.,
                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                     Q8K479;
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                                                                                           SEQUENCE
                                                                                                                               Pfam;
                                                                                                                                          Pfam;
                                                                                                                                                    InterPro; IPR001073; Clq.
InterPro; IPR000087; Collagen.
                                                                                                                                                                                                                 mouse
                                                                                                                                                                                                                                                             MEDLINE=22135657;
                                                                                                                                                                                                                                                                          STRAIN=C57BL/6J;
                                                                                                                                                                                                                                                                                                          NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                     Complement-clq tumor
                                                                                                                                                                            MGD; MGI:2385958; Clqtnf5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ubmitted
                                                                                         n; PF00386; C1q; 1.
n; PF01391; Collagen; 2.
VTS; PR00007; COMPLEMNTC1Q.
RT; SM00110; C1Q; 1.
JENCE 243 AA; 25436 MW;
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                     138
                                                                                                                                                                                                             , a gene encoding a frizzled related retinal degeneration 6.";
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57
                                            l Similarity
63; Conserv
                                                                                                                                                                                                                                         P.M.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SAARTRSLVGSDAGPGPRHQPLAFDTEFVNIGGDFDAAAGVFRCRLPGAYFFSFTLGKLP 239
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                   GAPHYALGAPGATFSGYLVYADADADAPA-RGPPAP------
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                                          11.7%;
nilarity 32.3%;
Conservative 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
GAPGEKGEG-
                                                                                                                                                                                                                                                 PubMed=12140190;
N.L., Chang B., Heckenlively J.R.,
                                                                                                                                                                                                                                                                                                                                                                el. 22, Last sequence update)
el. 23, Last annotation update)
necrosis factor-related
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           235
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                                           Score 202; DB
Pred. No. 7.2e
17; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 205; DB 11;
Pred. No. 4.1e-09;
6; Mismatches 81
                                                                                                                                                                                                                                                                                                                       Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
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-GRPGLPGPRGEPGPRGEAGPMGAIGPAGECSVPPRSAF
                                                                                           9F4D5804349791D9
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                                                       DB 11;
.2e-09;
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Best Local S
Matches 54
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01-DEC-2001
01-DEC-2001
01-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRINTS; PRO00007; COMPLEMNTC1Q.
ProDom; PD0000007; CoNlagen; 1.
SMART; SM00110; C1Q; 1.
PROSITE; PS01112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Collagen.
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE-Adjoose tissue;
TISSUE-Adjoose tissue;
MEDLINE=21232234; PubMed=11334417;
MEDLINE=21232234; PubMed=11334417;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Circulating concentrations of the adipocyte protein adiponed decreased in parallel with reduced insulin sensitivity during progression to type 2 diabetes in rhesus monkeys.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Macaca mulatta (Rhesus macaque).
Eukaryota; Metazoa; Chordata; Cr
Mammalia; Eutheria; Primates; Ca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q95JD7
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Pfam; PF01391; Collagen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AF404407; AAK92202.1; -. InterPro; IPR001073; Clq. InterPro; IPR000087; Collagen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Diabetes 50:1126-1133(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hansen B.C., Matsuzawa Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cercopithecinae; Macaca.
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242
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Pred. No. 1.3e-08;
31; Mismatches 61
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RESULT Q8BRW2

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Search completed: January 12, 2004, 08:19:07 Job time : 49.3114 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                      the RIKEN Genome Exploration Research Group Phase I & II Team; than Alysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDDNs."; Nature 420:563-573 (2002). EMBL; AK041214; BAC30866.1; -. SEQUENCE 247 AA; 26751 MW; 0D3FA64C789CAEF3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QBBRW2 PRELIMINARY; PRT; 247 AA.
QBBRW2;
01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Adipocyte complement related protein of 30 kDa.
Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Aorta and vein;
MEDLINE=22354683; PubMed=12466851;
The FANTOM Consortium,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=10090;
                                                                                                                                     246 TN 247
                                                                                                        160 AD 161
                                                                                                                                                                                                          134 RFTKIFYNQQNHYDGSTGKFYCNIPGLYYFSY-----HITVYMKDVKVSLFK-KDKAVL 186
                                                                                                                                                                                                                                49 TFDKVYVNIGGDFDVATGQFRCRVPGAYFFSFTAGKAPH-----KSLSVMLVRNRDEVQA 103
                                                                                                                                                                                                                                                                               75 GLLGPKGETGGVGMTGAEGPRGFPGTPGRKGEPGEAAYVYRSAFSVGLETRVT-VPNVPI 133
                                                                                                                                                                                                                                                                                                                  7 GLLGP-----AACWALGP----TPG----PGSSE--LRSAFSAARTTPLEGTSEMAV 48
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Result
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Copyright (c) 1993 - 2004 Compugen Ltd.
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Adipocyte compleme
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## ALIGNMENTS

RESULT 1 AAB61606 11-JAN-2001. Peptide Human; zacrp4; complement factor Clq domain; chromosome llqll; energy balance; cellular metabolic reaction; autocrine factor; development; cell proliferation; differentiation; cell surviva 01-JUL-1999; 28-JUN-2000; 2000WO-US17692 WO200102565-A2 Domain Human ZACRP4. 05-APR-2001 AAB61606 standard; Protein; 329 AA Domain Key Homo sapiens AAB61606; (first entry) 99US-0346502 /label= Clq\_domain\_#1 160..328 /label= Signal\_peptide 17..159 Location/Qualifiers 'label= C1q\_domain\_#2

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RESULT 2
ABG79643
ID ABG77
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                      Human; SECP; secreted protein; cell proliferative disorder; actinic keratosis; arreriosclerosis; bursitis; hepatitis; cancer; actinic keratosis; arreriosclerosis; bursitis; hepatitis; cancer; autoimmune disorder; inflammatory disorder; AIDS; asthma; allergy; acquired immunodeficiency syndrome; anaemia; atopic dermatitis; cardiovascular disorder; congestive heart failure; vascular tumour; ischaemic heart disease; myocardial infarction; epilepsy; stroke; hypertensive heart disease; meurological disorder; cerebral neoplasm; Alzheimer's disease; developmental disorder; renal tubular acidosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel secreted protein ZACRP4 polypeptides having tandem C1g globular domains, useful for studying cell-cell communication and regulation of cellular processes -
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DB; AAF28672.
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ilarity 100.0%;
Conservative (
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   muscular
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Pred. No. 1.2e-154;
); Mismatches 0;
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                                                                                                                                                                                                                                                                                                                     CC (SECP1-24), proteins 90% identical to them and active fragments of them. CC (SECP1-24), proteins 90% identical to them and active fragments of them. CC Also included are nucleic acids encoding the SECP proteins, a recombinant CC polynucleotide comprising a promoter sequence operably linked to the conclusion acid, a cell transformed with the recombinant polynucleotide, and creating for anti-gonists and modulators of anti-SECP antibody, and screening for anti-gonists and modulators of CC SECP function or expression. The SECP proteins and nucleic acids are cuseful in the diagnosis, treatment and prevention of cell proliferative (e.g. actinic keratosis, arteriosclerosis, burstiis, hepatitis or CC cander), autoimmune/inflammatory (e.g. AIDS (acquired immunodeficiency CC syndrome), asthma, anaemia, allergies or atopic dermatitis), CC cardiovascular (e.g. congestive heart failure, ischaemic heart disease, compocation, hypertensive heart disease, or vascular tumours), CC meurological (e.g. epilepsy, stroke, cerebral meoplasms, or Alzheimer's CC syndrome, Duchenne and Becker muscular dystrophy, or hypothyroidism) CC diseases, many other diseases and disorders are listed in the
                                                                                                                                                                    Query Match
Best Local S
Matches 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26-FEB-2001;
07-SEP-2001;
21-DEC-2001;
                                                                                                                                                                                                                                                                             specification. These may also be used in assessing the effects of exogenous compounds on the expression of nucleic acid and amino ac sequences of the secreted proteins. The present sequence represent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New human secreted proteins and nucleic acids useful in diagnosing, treating and preventing cell proliferative, autoimmune/inflammatory, cardiovascular, neurological, and developmental disorders -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lee
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08-FEB-2001;
                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1;
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Y, Yang J, Thang
EA, Richardson
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DB; ABS64954
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SAMLQLDYGDTVWLRLHGAPHYALGAPGATFSGYLVYADADADAPARGPPAPPEPRSAFS
                                             FDVATGQFRCRVPGAYFFSFTAGKAPHKSLSVMLVRNRDEVQALAFDEQRRPGARRAASQ
                                                           FDVATGOFRCRVPGAYFFSFTAGKAPHKSLSVMLVRNRDEVQALAFDEQRRPGARRAASQ
                                                                                                        MLPLLLGLLGPAACWALGPTPGPGSSELRSAFSAARTTPLEGTSEMAVTFDKVYVNIGGD
                                                                                                                          MLPLLLGLLGPAACWALGPTPGPGSSELRSAFSAARTTPLEGTSEMAVTFDKVYVNIGGD
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                                                                                                                                                                                                                                   329
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; 2001US-268112P.
; 2001US-271639P.
; 2001US-317818P.
; 2001US-343553P.
                                                                                                                                                                     Conservative
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2001US-267924P.
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dson TW, Ba
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                                                                                                                                                                                                                                                                invention.
                                                                                                                                                                                  98.9%;
99.4%;
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                                                                                                                                                                     Score 1707; I
Pred. No. 7.6e
0; Mismatches
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Lal PG,
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Honchell
                                                                                                                                                                    DB 23;
.6e-153;
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D, Walia NK, Lee
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to the
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SAMLQLDYGDTVWLRLLGAPQYALGAPGATFSGYLVYADADADAPARGPPAPPEPRSAFS

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                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                            The present invention relates to cDNAs encoding TANGO 244, TANGO 246, TANGO 275, TANGO 300 and MANGO 245 proteins.

The nucleic acids, proteins and protein modulators are useful treating colonic disorders, inflammatory diseases, tumors, renal disorders, liver disorders, lung disorders, autoimmune dallergic diseases, cardiovascular diseases, brain disorders, allergic diseases, cardiovascular diseases, brain disorders, and protein disorders.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               autoimmune;
pancreatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TANGO; MANGO; colon;
autoimmune; allergy;
                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                            degenerative diseases placental, pancreatic,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; Fig 25; 262pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-050127/06.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (MILL-) MILLENNIUM PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29-JUN-2000; 2000WO-US18184
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             04-APR-2001
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                                                                                                                                                                                                           318;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ted cDNAs encoding TANGO 244, TANGO 246, TANGO 275, TANGO 300 and 245 proteins, useful in the treatment of inflammatory diseases idiopathic ulcerative colitis), tumors, renal disorders and liver
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MANGO 245
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                                                                                                                                     MLPLLLGLLGPAACWALGPTPGPGSSELRSAFSAARTTPLEGTSEMAVTFDKVYVNIGGD
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                        FDVATGQFRCRVPGAYFFSFTAGKAPHKSLSVMLVRNRDEVQALAFDEQRRPGARRAASQ
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FDAATGQFRCRVPGAYFFSFTVGKAPHKSLSVMLVRNHDEVQALAFDEQRRPSARRAASQ
                                                                                                       MLPLLLGLLGPAACWALGPAPGPGSSELRSAFSAARTTPLEGASEMAVTFDKVYVNIGGD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (e.g.
                                                                                                                                                                                                                                                                                                                  329 AA;
                                                                                                                                                                                                              Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
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96.7%;
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cardiovascular; brain; degenerative; placental;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fraser
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                                                                                                                                                                                                           Score 1666; DB 22;
Pred. No. 5.7e-149;
1; Mismatches 10;
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Best Loca
Matches
                                                  Query Match
                                                                                                                                                                                                           The present invention relates to cDNAs encoding TANGO 244, TANGO 246, TANGO 275, TANGO 300 and MANGO 245 proteins. The nucleic acids, proteins and protein modulators are useful for treating colonic disorders, inflammatory diseases, tumors, renal disorders, liver disorders, lung disorders, autoimmune diseaslergic diseases, cardiovascular diseases, brain disorders, allergic diseases, cardiovascular diseases, brain disorders,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TANGO; MANGO; colon; inflammation; tumor; renal; liver; lung;
autoimmune; allergy; cardiovascular; brain; degenerative; placental;
pancreatic; skeletal; muscle.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Isolated cDNAs encoding TANGO 244, TANGO 246, TANGO 275, TANGO 300 a. MANGO 245 proteins, useful in the treatment of inflammatory diseases (e.g. idiopathic ulcerative colitis), tumors, renal disorders and li
                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; Fig 23; 262pp; English
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                                                                                                                                                                                    degenerative diseases placental, pancreatic, skeletal and
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Score 1567; Di
Pred. No. 1.4e
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1.4e-139;
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KW cell signal processing; metabolic pathway modulation; metabolic disorder;

KW obesity; diabetes; infectious disease; neurodegenerative disorder; acne;

KW Alzheimer's disease; Parkinson's disease; immune disorder; cancer;

KW haematopoietic disorder; cirrhosis; pancreatitis; learning defect;

KW memory defect; infertility; congenital heart defect; hair growth;

KW gigmentation disorder; endocrine disorder; respiratory disease; health;

KW gastro-intestinal disease; reproductive; neurological disease; health;

KW memory transplantation; endocrine disease; allergy; inflammation;

KW mephrological disorder; uninary system disorder; allergy; inflammation;

KW metarological disorder; EGF-related protein; SCUBE1; TEN-M4;

KW meuropsychiatric disorder; EGF-related protein; SCUBE1; TEN-M4;

KW adipocyte complement-related C1g tumour necrosis factor; out at first;

KW beta adrenergic receptor kinase; EphAs/ehk-2; glucose transporter;

KW type 1a membrane sushi-containing domain; butyrophilin;
                                                                                                                                                                                              19-DEC-2000; 2000US-265704P.
20-DEC-2000; 2000US-257314P.
02-MAY-2001; 2001US-288153P.
29-MAY-2001; 2001US-294075P.
24-JUL-2001; 2001US-307506P.
10-AUG-2001; 2001US-31153P.
29-AUG-2001; 2001US-315617P.
14-SEP-2001; 2001US-322358P.
                                                                                              Gangolli EA
Stone DJ,
Spytek KA,
Novel isolated NOVX polypeptide useful for treating cardiomyopathy, atherosclerosis, metabolic disorders, diabetes, obesity, infectious
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DB; ABS52097.
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                                                                                            i EA,  Patturajan I
J,  Anderson D,  SI
KA,  Casman SJ,  Bo
                                                                                                                                                                 CURAGEN CORP
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                                                                                              n M, Vernet CAM, Malyankar UM, Kekuda
Shimkets RA, Burgess CE, Zerhusen BD,
Boldog FL, Smithson G, Li L, Ji W;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; Page 31; 318pp; English
                                                                                                                                                                                                                                                AAB61466 standard; protein; 334
                                                                                                                                                                                                                                                                                                                                                                                        211
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MLPLLLGLLGPAACWALGPTPGPGSSELRSAFSAARTTPLEGTSEMAVTFDKVYVNIGGD
                                                                                                                                                                                                                                                                                                                           MLPLLLGLLGPAACWALGPTPGPGSSELRSAFSAARTTPLEGTSEMAVTFDKVYVNIGGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AARTRSLVGSDAGPGPRHQPLAFDTEFVNIGGDFDAAAGVFRCRLPGAYFFSFTLGKLPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FDVATGQFRCRVPGAYFFSFTAGKAPHKSLSVMLVRNRDEVQALAFDEQRRPGARRAASQ
                                                                                                                                                                                                                                                                                                                                                                                                          KTLSVKLMKNRDEVQAMIYDDGASRRREMQSQSVMLALRRGDAVWLLSHDHDGYGAYSNH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SAMLQLDYGDTVWLRLHGAPHYALGAPGATFSGYLVYADA----
                                                                                                                                                                                                                                                                                                                                                                                       KTLSVKLMKNRDEVQAMIYDDGASRRREMQSQSVMLALRRGDAVWLLSHDHDGYGAYSNH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FDVATGQFRCRVPGAYFFSFTAGKAPHKSLSVMLVRNRDEVQALAFDEQRRPGARRAASQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              299. AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 89.2%; ilarity 90.6%; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                    - DAGPGPRHQPLAFDTEFVNIGGDFDAAADVFRCRLPGAYFFSFTLGKLPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 1540; DB 23;
Pred. No. 4e-137;
0; Mismatches 1;
                                                                                                                                                                                                                                                  ΑA
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                                                                                                                                                                                                                                                                                                                                                          329
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TANGO; MANGO; colon; inflammation; to autoimmune; allergy; cardiovascular; pancreatic; skeletal; muscle.

ar; brain;

renal;

liver; lung

placental;

Human MANGO 245 mature protein

04-APR-2001

(first entry)

WO200100672-A1

Homo

sapiens

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Best Local
             haematopoietic disorder; cirrhosis; pancreatitis; learning def
memory defect; infertility; congenital heart defect; hair grow
pigmentation disorder; endocrine disorder; respiratory disease
gastro-intestinal disease; reproductive; neurological disease;
    gastro-intestinal
bone marrow trans
                                                                     Alzheimer's disease; Parkinson's disease; immune disorder; cancer;
                                                                                    cell signal processing; metabolic pathway modulation; metabolic disobsesity; diabetes; infectious disease; neurodegenerative disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  treating colonic disorders, inflammatory diseases, tumors, renal disorders, liver disorders, lung disorders, autoimmune diseases, allergic diseases, cardiovascular diseases, brain disorders, degenerative diseases placental, pancreatic, skeletal and muscle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Isolated cDNAs encoding TANGO 244, TANGO 246, TANGO 275, TANGO 300 and MANGO 245 proteins, useful in the treatment of inflammatory diseases (e.g. idiopathic ulcerative colitis), tumors, renal disorders and liver
                                                                                                                                             Adipocyte complement-related Clq
                                                                                                                                                                           05-NOV-2002
                                                                                                                                                                                                                                  ABG70384 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The nucleic acids,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TANGO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29-JUN-2000;
                                                                                                   n; NOVX;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    284;
                                                                                                                                                                                                                                                                                                                                                                  181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     resent invention relates to cDNAs encoding TANGO 244, 246, TANGO 275, TANGO 300 and MANGO 245 proteins. ucleic acids, proteins and protein modulators are useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MILLENNIUM PHARM
                                                                                                                                                                                                                                                                                                                              QAMIYDDGASRREMQSQSVMLALRRGDAVWLLSHDHDGYGAYSNH
                                                                                                                                                                                                                                                                                                                                                                                 GPRHQPLAFDTEFVNIGGDFDAAAGVFRCRLPGAYFFSFTLGKLPRKTLSVKLMKNRDEV
                                                                                                                                                                                                                                                                                                                                                                                                                                          RLHGAPHYALGAPGATFSGYLVYADADADAPARGPPAPPEPRSAFSAARTRSLVGSDAGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AYFFSFTAGKAPHKSLSVMLVRNRDEVQALAFDEQRRPGARRAASQSAMLQLDYGDTVWL 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WALGPTPGPGSSELRSAFSAARTTPLEGTSEMAVTFDKVYVNIGGDFDVATGQFRCRVPG
                                                                                                                                                                                                                                                                                                                                                               GPRHQPLAFDTEFVNIGGDFDAAAGVFRCRLPGAYFFSFTLGKLPRKTLSVKLMKNRDEV
                                                                                                                                                                                                                                                                                                                                                                                                                       RLHGAPQYALGAPGATFSGYLVYADADADAPARGPPAPPEPRSAFSAARTRSLVGSDAGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AYFFSFTAGKAPHKSLSVMLVRNRDEVQALAFDEQRRPGARRAASQSAMLQLDYGDTVWL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WALGPTPGPGSSELRGAFSAARTTPLEGTSEMAVTFDKVYVNIGGDFDVATGQFRCRVPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (e.g. jaundice)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           334 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Page 242; 262pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                             NOVX-associated disorder; cardiomyopathy; atherosclerosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2000WO-US18184
                                                                                                                                                                           (first
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                                                                                                                                                                                                                                  Protein;
                                                                                                                                                                         entry)
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99.3%;
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                                                                                                                                                                                                                                                                                                        QSVMLALRRGDAVWLLSHDHDGYGAYSNH
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Pred. No. 2e-132;
0; Mismatches
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                                                                                                                                           Tumour Necrosis Factor-like protein
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allergy;
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                           disease; h
                                                                                                                                                                                                                                                                                                                                   300
                                                         defect;
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                            health;
                                                                                                disorder;
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61 61

FDVATGQFRCRVPGAYFFSFTAGKAPHKSLSVMLVRNRDEVQALAFDEQRRPGARRAASQ

FDVATGQFRCRVPGAYFFSFTAGKAPHKSLSVMLVRNRDEVQALAFDEQRRPGARRAASQ

MLPLLLGLLGPAACWALGPTPGPGSSELRSAFSAARTTPLEGTSEMAVTFDKVYVNIGGD

 $\vdash$ 

MLPLLLGLLGPAACWALGPTPGPGSSELRSAFSAARTTPL

LEGTSEMAVTFDKVYVNIGGD

60 60 Query Match Best Local S Matches 283

Similarity

83.7%; ilarity 86.0%; Conservative

<u>,</u>

Score 1445.5; DB 23 Pred. No. 3.2e-128; 0; Mismatches 1;

23;

Length

Indels

45; 284;

Gaps

283;

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signal processing and metabolic pathway modulation in a subject, preferably human. The invention is also useful for treating metabolic disorders (e.g. obesity), diabetes, infectious disease, neurodegenerative disorders (e.g. Alzheimer's disease, Parkinson's disease), immune disorders, haematopoietic disorders and various cancers. The molecules of the invention are also useful for treating or preventing cirrhosis, pancreatitis, learning and memory defects, infertility, congenital heart defects, acne, hair growth, pigmentation disorders, endocrine disorders, respiratory disease, gastro-intestinal diseases, reproductive, health, neurological diseases, bone marrow transplantation, endocrine diseases, allergy and inflammation, nephrological disorders urinary system disorders, neuropsychiatric disorders and age-related disorders. The present amino acid sequence represents a NOVX protein of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19-DEC-2000;
20-DEC-2000;
02-MAY-2001;
29-MAY-2001;
24-JUL-2001;
10-AUG-2001;
110-AUG-2001;
110-AUG-2001;
14-SEP-2001;
                                                                                                                                                                                                                                                                                    The
                                                                                                                                                                                                                                                                                                                                                              Novel isolated NOVX polypeptide useful for treating cardiomyopathy, atherosclerosis, metabolic disorders, diabetes, obesity, infectious disease, anorexia, neurodegenerative disorders, Alzheimer's disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         nephrological disorder; urinary system disorder; age-related disor neuropsychiatric disorder; EGF-related protein; SCUBEI; TEN-M4; adipocyte complement-related C1q tumour necrosis factor; out at fi beta adrenergic receptor kinase; EphA6/ehk-2; glucose transporter; type la membrane sushi-containing domain; butyrophilin; type la membrane-sushi domain containing.
Sequence
                               The present invention.
                                                                                                                                                                                                                                                    cardiomyopathy or atherosclerosis, where the disorder is related to
                                                                                                                                                                                                                                                                                                                  Claim 1; Page 30; 318pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Spytek
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Stone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gangolli
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              걸
                                                                                                                                                                                                                                                                  esent invention relates to new NOVX polypeptides. The invention treating or preventing a NOVX-associated disorder such
                                                                                                                                                                                                                                                                                                                                                                                                                                ABS52096.
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284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Anderson
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2000US-257314P.

2001US-288153P.

2001US-294075P.

2001US-307506P.

2001US-311590P.

2001US-311617P.

2001US-322358P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Casman
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A
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Shimkets RA, Buryes-
Shimkets RA, Buryes-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AM, "Eggs CE, Zeim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Zerhusen
                                                                                                                                                                                                                                                                                   The invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           at first;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          disorder;
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Liu
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AC AAB6
AC 
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                                                                                            Query Match
Best Local S
Matches 177
                                                                                                                                                                                                                                                              The present invention relates to cDNAs encoding TANGO 244, TANGO 245, TANGO 275, TANGO 300 and MANGO 245 proteins.

The nucleic acids, proteins and protein modulators are useful for treating colonic disorders, inflammatory diseases, tumors, renal disorders, liver disorders, living disorders, autoimmune diseases, allergic diseases, cardiovascular diseases, brain disorders, degenerative diseases placental, pancreatic, skeletal and muscle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TANGO; MANGO; colon; inflammation; tumor; renal; liver; lung; autoimmune; allergy; cardiovascular; brain; degenerative; placental; pancreatic; skeletal; muscle.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (e.g. idic
disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Holtzman
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                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Isolated cDNAs encoding TANGO 244, TANGO 246, TANGO 275, TANGO 300 and MANGO 245 proteins, useful in the treatment of inflammatory diseases (e.g. idiopathic ulcerative colitis), tumors, renal disorders and lives
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             04-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (MILL-) MILLENNIUM PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             musculus.
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                                                                                              al Similarity
177; Conser
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MLLLLLGFLGPAACWALGPA-GPGSSELRSAFSAARTTPLEGTSEMAVTFDKVYVNIGGD
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87.2%;
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Pred. No. 3.5e
4; Mismatches
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                                                                                                                DB 22;
.5e-75;
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Best Local S
Matches 144
                                                                                                                                                                                     The present invention relates to cDNAs encoding TANGO 244, TANGO 246, TANGO 275, TANGO 300 and MANGO 245 proteins. The nucleic acids, proteins and protein modulators are useful for treating colonic disorders, inflammatory diseases, tumors, renal disorders, liver disorders, lung disorders, autoimmune diseases, allergic diseases, cardiovascular diseases, brain disorders, degenerative diseases placental, pancreatic, skeletal and muscle
                                                                                                                                                                                                                                                                                                                        Isolated cDNAs encoding TANGO 244, TANGO 246, TANGO 275, TANGO 300 and MANGO 245 proteins; useful in the treatment of inflammatory diseases (e.g. idiopathic ulcerative colitis), tumors, renal disorders and liver disorders (e.g. jaundice) -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TANGO; MANGO; colon; inflammation; to autoimmune; allergy; cardiovascular; pancreatic; skeletal; muscle.
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                                                                                                                                                      Sequence
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                                                                                                                Similarity
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                                                  YADADADAPARGPPAPPEPRSAFSAARTRSLVGSDAGPGPRHQPLAFDTEFVNIGGDFDA
                                                               YADADADAPARGPPAPPEPRSAFSAARTRSLVGSDAGPGPRHQPLAFDTEFVNIGGDFDA
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                                                                                                                                                      192
                                                                                                 44.0%; So ilarity 100.0%; I Conservative 0;
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                                                                                                 Score 760; DB 22;
Pred. No. 1.1e-63;
0; Mismatches 0;
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10-AUG-2001;
10-AUG-2001;
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02-MAY-2001;
29-MAY-2001;
The present invention relates to new NOVX polypeptides. The invention is useful for treating or preventing a NOVX-associated disorder such as cardiomyopathy or atherosclerosis, where the disorder is related to cell signal processing and metabolic pathway modulation in a subject, preferably human. The invention is also useful for treating metabolic disorders (e.g. obesity), disbetes, infectious disease, neurodegenerative disorders (e.g. Alzheimer's disease, parkinson's disease), immune disorders, haematopoietic disorders and various cancers. The molecules of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         haematopoietic disorder; cirrhosis; pancreatitis; learning defect; memory defect; infertility; congenital heart defect; hair growth; pigmentation disorder; endocrine disorder; respiratory disease; health; gastro-intestinal disease; reproductive; neurological disease; bone marrow transplantation; endocrine disease; allergy; inflammation; nephrological disorder; urinary system disorder; age-related disorder; neuropsychiatric disorder; EGF-related protein; SCUBEL; TEN-M4; adipocyte complement-related Clq tumour necrosis factor; out at first; beta adrenergic receptor kinase; Epha6/ehk-2; glucose transporter;
                                                                                                                                                                        Novel isolated NOVX polypeptide useful for treating cardiomyopathy, atherosclerosis, metabolic disorders, diabetes, obesity, infectious disease, anorexia, neurodegenerative disorders, Alzheimer's disease
                                                                                                                                                                                                                                                                                                                                                                  29-AUG-2001;
14-SEP-2001;
                                                                                                                                 Claim 1;
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                                                                                                                                                                                                                                                                                              Stone
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DB; ABS52095.
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2001US-288133P.
2001US-294075P.
2001US-30750P.
2001US-311590P.
2001US-311613P.
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2001US-322358P.
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3, Li L, Ji W
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Isolated cDNAs encoding TANGO MANGO 245 proteins, useful in
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pancreatic; skeletal;
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autoimmune; allergy;
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                                                                                                                                                                                                                                                                                                                                                                      WO200100672-A1
                                                                                                                                                                                                                                                                                                                                                                                                                      Catarrhini
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Monkey MANGO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAB61473;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
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                                                                                                                                                                         MILLENNIUM PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PGLGASELL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                         DA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LAFDTEFVNIGGDFDAAAGVFRCRLFGAYFFSFTLGKLFRKTLSVKLMKNRDEVQAMIYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PGPGSSELRSAFSAARTTPLEGTSEMAVTFDKVYVNIGGDFDVATGQFRCRVPGAYFFSF 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PGLGASELL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TAGKAPHKSLSVMLVRNRDEVQALAFDEQRRPGARRAASQSAMLQLDYGDTVWLRLHGAP 140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 245 Clq
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                                                                                                                      Barnes
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cardiovascular; brain; degenerative;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              inflammation; tumor; renal; liver; lung;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 domain
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the t
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                                                                                                                         ç,
  , TANGO 246, TANGO 275, TANGO 300 and treatment of inflammatory diseases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                153;
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches 131;
                                                                                                                                                                                                                                                                                                                                       myeloid cell disorder; lymphoid cell disorder; asthma; arthritis; chronic inflammatory condition; proliferative retinopathy; atherosclerosis; coronary heart disease; arterial ischaemia; bone disorder; osteoporosis; vascular growth disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention relates to cDNAs encoding TANGO 244, TANGO 245, TANGO 300 and MANGO 245 proteins.

TANGO 275, TANGO 300 and MANGO 245 proteins.

The nucleic acids, proteins and protein modulators are useful for treating colonic disorders, inflammatory diseases, tumors, renal disorders, liver disorders, lung disorders, autoimmune diseases, renal disorders, cardiovascular diseases, brain disorders, allergic diseases, cardiovascular diseases, brain disorders,
                                                                                                                                                                                                                                                                            cell culture; drug screening; gene therapy; antiinflammatory; antiasthmatic; antiarthritic; haemostatic; antiarteriosclerot cytostatic; osteopathic; vasotropic; cardiant; virucide; anti
                                                                                                                                                                                                                                                                                                                                                                                                          Human; cytokine; cell proliferation; cell differentiation; growth factor; haematopoiesis regulation; tissue growth; immunomodulator; activin; inhibin; chemotaxis; chemokinesis; thrombolysis; oncogenesis; proliferation; metastasis; cancer; tumour; haematopoietic disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (e.g. idio
                                                                                                                                                                     09-AUG-2001.
                                                                                                                                                                                                                                  Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human secreted protein homologue,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Fig 28; 262pp; English.
                           Tang YT,
                                                                                        03-FEB-2000; 2000US-0496914.
27-APR-2000; 2000US-0560875.
                                                                                                                                      05-FEB-2001; 2001WO-US03800.
                                                                                                                                                                                                                                                                 antifungal; vulnerary;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABB11578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
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                                                           (HYSE-) HYSEQ INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         idiopathic ulcerative colitis), tumors, renal disorders and liver ders (e.g. jaundice) -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61
                                                                                                                                                                                                                                                                                                                            regeneration; wound
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AFSAARTRSLVGSDAGPGPRHQPLAFDTEFVNIGGDFDAAAGVFRCRLPGAYFFSFTLGK 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LPRKTLSVKLMKNRDEVQAMIYDDGASRRREMQSQSVMLALRRGDAVMLLSHDHDGYGAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SNHGKYITFSGFLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AFSAARTRSLVGSDAGSGPRHRPLAFDTELVNIGGDFDAAAGVFRCRLPGAYFFSFTLGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LPRKTLSVKLMKNRDEVQAMIYDDGASRRREMQSQSVMLALRRGDAVWLLSHDHDGYGAY
                          Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      134 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                             Drmanac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  peptide; 127 AA
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                                                                                                                                                                                                                                                                  antiulcer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  134
                             RT
                                                                                                                                                                                                                                                                                                                               healing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1;
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Pred. No. 1.3e-56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQ ID NO:1948.
                                                                                                                                                                                                                                                                                                                            infection; immune disorder;
                                                                                                                                                                                                                                                                                                antiarteriosclerotic,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22;
                                                                                                                                                                                                                                                                                virucide; antibacterial;
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N-PSDB; ABA08822.

Claim 20; Page 214-215; 1963pp; English

Cor polypeptides in a sample, and methods of identifying compounds which copypeptides of the invention. Although novel, many of the CO polypeptides of the invention have homology to known proteins, thereby complying an insight into their probable biological activities, and hence giving an insight into their probable biological activities, and hence compounds which the various activities, stem cell growth factor activity; differentiation activities, stem cell growth factor activity; chaematopoiesis regulatory activity; tissue growth activity; chaematopoiesis regulatory activity; tissue growth activity; chaematopoiesis receptor or ligand activities; or may be conditions, e.g., by brotein or gene there, polypeptides and nucleotides of the invention are useful for preventing, treating or ameliorating medical conditions, e.g., by protein or gene therepy. Such conditions include cancers, haematopoietic disorders (e.g., myeloid or lymphoid cell cancers, haematopoietic disorders (e.g., myeloid or lymphoid cell vascular growth. Polypeptides involved with tissue regeneration and crepair (or nucleic acids encoding them) may be used to promote wound the haling (e.g., of burns, incisions and ulcers), while those with for preventing them may be used to promote to promote cell growth factor activity may be used in cell cultures to polypeptides may be used to neuroepithelial cells. Composed with provent factor activity may be used to neuroepithelial cells can be used to augment or replace cells damaged by illness, and in drug autoimmune disease or accidental damage. The polypeptides and nucleotides and mucleotides may also be used in the diagnosis of the above conditions, and in drug careanity techniques. The present sequence represents a novel buman in drug may also be used in the diagnosis of the above conditions, and in drug careanity techniques. antibodies against the polypeptides, or polypeptides in a sample, and meti nucleotide of the invention, methods of producing the novel polypeptides, antibodies against the polypeptides, methods of detecting the nucleotides Sequences ABB10981-ABB12330 represent 1350 novel human polypeptides, and sequences ABA08225-ABA09574 represent nucleic acids encoding them. The invention also relates to vectors and recombinant host cells comprising techniques. invention The present sequence represents a novel human a

RESULT 13 AAB61477 Ş 밁 Ś В Ś XXXXXI 밁 Query Match Best Local S Matches 126 Sequence AAB61477 126; 323 203 263 121 61 <u>د س</u> Similarity LGASELL 329 ASRRREMOSOSVMLALRRGDAVWLLSHDHDGYGAYSNHGKYITFSGFLVYPDLAPAAPPG SSRRREMOSOSVMLALRRGDAVWLLSHDHDGYGAYSNHGKYITFSGFLVYPDLAPAAPPG FDTEFVNIGGDFDAAAGVFRCRLPGAYFFSFTLGKLPRKTLSVKLMKNRDEVQAMIYDDG standard; protein; 125 LGASELL FDTEFVNIGGDFDAAAGVFRCRLPGAYFFSFTLGKLPRKTLSVKLMKNRDEVQAMIYDDG 127 Conservative ΑA, 38.5%; 99.2%; Score 664; DB 22; Pred. No. 7.8e-55; 1; Mismatches ( 0 Length Indels 127; 0 Gaps 322 60 262

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04-APR-2001

(first entry)

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KW TANGG
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention relates to cDNAs encoding TANGO 244, TANGO 246, TANGO 275, TANGO 300 and MANGO 245 proteins.

The nucleic acids, proteins and protein modulators are useful for treating colonic disorders, inflammatory diseases, tumors, renal disorders, liver disorders, living disorders, autoimmune diseases, allergic diseases, cardiovascular diseases, brain disorders, altergic diseases placental, pancreatic, skeletal and muscle degenerative diseases placental, pancreatic, skeletal and muscle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    autoimmune;
pancreatic;
                                       TANGO; MANGO; colon; inflammation; tumor; renal; liver; lung; autoimmune; allergy; cardiovascular; brain; degenerative; placental; pancreatic; skeletal; muscle.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Page 246; 262pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Isolated cDNAs encoding TANGO 244, TANGO 246, TANGO 275, TANGO 300 and MANGO 245 proteins, useful in the treatment of inflammatory diseases (e.g. idiopathic ulcerative colitis), tumors, renal disorders and liver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-050127/06.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Holtzman DA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    04-JAN-2001
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autoimmune; allergy;
              Homo sapiens
                                                                                                                                                                               AAB61469 standard; protein; 126 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  disorders (e.g. jaundice) -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29-JUN-2000; 2000WO-US18184.
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                                                                                                  MANGO
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                                                                                                                                                                                                                                                                                                                             AYFFSFTAGKAPHKSLSVMLVRNRDEVQALAFDEQRRPGARRAASQSAMLQLDYGDTVWL 134
                                                                                                                                                                                                                                                                                                                                                                                   WALGPTPGPGSSELRSAFSAARTTPLEGTSEMAVTFDKVYVNIGGDFDVATGQFRCRVPG
                                                                                                                                                                                                                                                        RLHGA
                                                                                                                                                                                                                                                                                                            AYFFSFTAGKAPHKSLSVMLVRNRDEVQALAFDEQRRPGARRAASQSAMLQLDYGDTVWL
                                                                                                                                                                                                                                                                                                                                                                     WALGPTPGPGSSELRSAFSAARTTPLEGTSEMAVTFDKVYVNIGGDFDVATGQFRCRVPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   125 AA;
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                                                                                                245
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                                                                                                                          (first entry)
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                                                                                               Clq
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                inflammation; tumor; renal; liver; lung; cardiovascular; brain; degenerative; placental;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       37.7%;
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Pred. No. 1.6e-53
                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
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Best Local
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                                                                                                                   autoimmune; allergy; cardiova
pancreatic; skeletal; muscle.
          29-JUN-1999;
                              29-JUN-2000; 2000WO-US18184
                                                      04-JAN-2001
                                                                           WO200100672-A1
                                                                                                Mus musculus
                                                                                                                                            TANGO; MANGO; colon;
                                                                                                                                                                    Murine MANGO
                                                                                                                                                                                          04-APR-2001
                                                                                                                                                                                                                 AAB61489
                                                                                                                                                                                                                                      AAB61489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Isolated cDNAs encoding TANGO 244, TANGO 246, TANGO 275, TANGO 300 and MANGO 245 proteins, useful in the treatment of inflammatory diseases (e.g. idiopathic ulcerative colitis), tumors, renal disorders and lived disorders (e.g. jaundice) -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Holtzman DA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29-JUN-1999;
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                                                                                                                                                                                                                                                                                                                    FSGYLV 156
                                                                                                                                                                                                                                                                                                                                                        SVMLVRNRDEVQALAFDEQRRPGARRAASQSAMLQLDYGDTVWLRLHGAPHYALGAPGAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                 37.4%; ilarity 99.2%; Conservative
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          99US-0342687
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                                                                                                                                                                                                                                     protein;
                                                                                                                                                                                          entry)
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                                                                                                                                   cardiovascular; brain;
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                                                                                                                                             inflammation; tumor; renal; liver; lung;
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.9e-53;
                                                                                                                                   degenerative;
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Search completed: January 12, 2004, 08:15:34 Job time: 51.5798 secs
                                                                                                                                                                                                                                                                                                                                                    Query Match 37.0%;
Best Local Similarity 96.8%;
Matches 122; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention relates to cDNAs encoding TANGO 244, TANGO 246, TANGO 275, TANGO 300 and MANGO 245 proteins.

The nucleic acids, proteins and protein modulators are useful for treating colonic disorders, inflammatory diseases, tumors, renal disorders, liver disorders, lung disorders, autoimmune diseases, allergic diseases, cardiovascular diseases, brain disorders, degenerative diseases placental, pancreatic, skeletal and muscle disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Isolated cDNAs encoding TANGO 244, TANGO 246, TANGO 275, TANGO 300 and MANGO 245 proteins, useful in the treatment of inflammatory diseases (e.g. idiopathic ulcerative colitis), tumors, renal disorders and liver disorders (e.g. jaundice) -
                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Page 260-261; 262pp; English.
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                                                                                       121
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                                                                                     FSGYLV 126
                                                                                                                         FSGYLV 156
                                                                                                                                                                          SVMLVRNRDEVQALAFDEQRRPGARRAASQSAMLQLDYGDTVWLRLHGAPHYALGAPGAT 150
                                                                                                                                                                                                                                                                                                                                                                                                                                              126 AA;
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Pred. No. 1.8e-52;
3; Mismatches 1;
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Result
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Title:
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                                                                                                                                                                                                                1587
237.5
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230
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seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Published Applications AA:*

1: /cgn2_6/ptodata/1/pubpaa/US07 PUBCOMB.pep:*

2: /cgn2_6/ptodata/1/pubpaa/US06 NEW PUB.pep:*

3: /cgn2_6/ptodata/1/pubpaa/US06 NEW PUB.pep:*

4: /cgn2_6/ptodata/1/pubpaa/US07 NEW PUB.pep:*

5: /cgn2_6/ptodata/1/pubpaa/US07 NEW PUB.pep:*

6: /cgn2_6/ptodata/1/pubpaa/US08 NEW PUB.pep:*

7: /cgn2_6/ptodata/1/pubpaa/US08 PUBCOMB.pep:*

8: /cgn2_6/ptodata/1/pubpaa/US08 PUBCOMB.pep:*

9: /cgn2_6/ptodata/1/pubpaa/US08 PUBCOMB.pep:*

10: /cgn2_6/ptodata/1/pubpaa/US09 PUBCOMB.pep:*

11: /cgn2_6/ptodata/1/pubpaa/US09 PUBCOMB.pep:*

12: /cgn2_6/ptodata/1/pubpaa/US09 PUBCOMB.pep:*

13: /cgn2_6/ptodata/1/pubpaa/US09 PUBCOMB.pep:*

14: /cgn2_6/ptodata/1/pubpaa/US108 PUBCOMB.pep:*

15: /cgn2_6/ptodata/1/pubpaa/US108 PUBCOMB.pep:*

16: /cgn2_6/ptodata/1/pubpaa/US108 PUBCOMB.pep:*

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17: /cgn2_6/ptodata/1/pubpaa/US108 PUBCOMB.pep:*

16: /cgn2_6/ptodata/1/pubpaa/US108 PUBCOMB.pep:*

17: /cgn2_6/ptodata/1/pubpaa/US108 PUBCOMB.pep:*

18: /cgn2_6/ptodata/1/pubpaa/US108 PUBCOMB.pep:*
           US-10-085-167-2
1726
1 MLPLLLGLLGPAACWALGPT.....LVYPDLAPAAPPGLGASELL 329
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Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                          Length
                                                                                                                                                                                                                                                                                                                                                                          BB
    US-09-893-737-52

US-10-091-458-43

US-10-236-055A-2

US-09-738-973-185

US-09-854-133-185

US-10-144-649A-185

US-10-309-422-10

US-10-309-422-14

US-10-309-422-14

US-10-309-422-18

US-10-309-422-18

US-10-309-422-18
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US-10-236-055A-14
US-10-236-055A-16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Search time 40.0579 Seconds (without alignments) 1655.023 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                       Description
Sequence 2, Appli
Sequence 14, Appl
Sequence 15, Appl
Sequence 23, Appl
Sequence 23, Appli
Sequence 185, App
Sequence 185, App
Sequence 10, Appl
Sequence 10, Appl
Sequence 22, Appl
Sequence 21, Appl
Sequence 14, Appl
Sequence 14, Appl
Sequence 18, Appl
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281	281	281	281	281	281	281	281	281	281	281	281	281	281	281	281	281	281	281	281	281	281	281	409	1127	1126	1092	1091	1043	1042
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US-09-911-176B-2	-944-4	US-09-943-851A-78	-944-654-7	US-09-943-762-78	-432-7	-097-7	US-09-944-396-78	-015-7	-09-945-587-7	US-09-944-862-78		US-09-944-449-78	US-09-866-028-78	765-205-2	768-	US-10-241-258-44	-10-180-762-	-10-385-0	US-10-392-706-44	-392-5	-10 - 36	11-	0-236-05	-10-309-422-2	09-422-	0-309-422-2	US-10-309-422-12	-10-309-4	US-10-309-422-8
2, 1	e 78,	Ø	e 78,	e 78,	æ	e 78,	e 78,	Ø	78,	Ø	e 78,	ce 78	78,		46,	e 44	e 44	Sequence 5, Appli	e 44,	Ф 4-	e 44,	e 44	Ф 4	Φ	e 16	e 24	e 12	Sequence 20, Appl	Sequence 8, Appli

## ALIGNMENTS

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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-085-167-2
                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Holloway, James L.
APPLICANT: Lok, Si
TITLE OF INVENTION: SECRETED PROTEIN ZACRP4
FILE REFERENCE: 99-29
CURRENT APPLICATION NUMBER: US/10/085,167
CURRENT FILING DATE: 2002-02-27
PRIOR APPLICATION NUMBER: 60/141,928
PRIOR FILING DATE: 1999-07-01
NUMBER OF SEQ ID NOS: 9
SOFTWARE: FastSEQ for Windows Version 3.0
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                                                                                                                                                                                                                                                                  Query Match
Best Local Simi
Matches 329;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2, Application US/10085167 Publication No. US20030170781A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                           SEQ ID NO 2
                                                                                                                  61 FDVATGQFRCRVPGAYFFSFTAGKAPHKSLSVMLVRNRDEVQALAFDEQRRPGARRAASQ 120
                                                                                                                                        61 FDVATGQFRCRVPGAYFFSFTAGKAPHKSLSVMLVRNRDEVQALAFDEQRRPGARRAASQ 120
                                                                                                                                                                                                                  1 MLPILLGLLGPAACWALGPTPGPGSSELRSAFSAARTTPLEGTSEMAVTFDKVYVNIGGD 60
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AARTRSLVGSDAGPGPRHQPLAFDTEFVNIGGDFDAAAGVFRCRLPGAYFFSFTLGKLPR
                                                                SAMLQLDYGDTVWLRLHGAPHYALGAPGATFSGYLVYADADADAPARGPPAPPEPRSAFS
                                                                                                                                                                                            MLPLLLGLLGPAACWALGPTPGPGSSELRSAFSAARTTPLEGTSEMAVTFDKVYVNIGGD
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3.4e-154;
les 0;
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APPLICANT: Forsythe, Ian
APPLICANT: Matteon, Daniel M.
APPLICANT: Matteon, Denine
APPLICANT: Moshrefi, Mehrdad
APPLICANT: Moshrefi, Mehrdad
APPLICANT: Moshrefi, Mehrdad
APPLICANT: Parham, Christi
TITLE OF INVENTION: MAMMALIAN GENES; RELATED REF
FILE REFERENCE: DX01343K
CURRENT APPLICATION NUMBER: US/10/236,055A
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/317,988
PRIOR APPLICATION NUMBER: US 60/317,988
PRIOR FILING DATE: 2001-09-06
NUMBER OF SEQ ID NOS: 36
SOFTWARE: Patentin version 3.1
SEQ ID NO 14
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US-10-236-055A-14
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US-10-236-055A-16
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Best Local Sin
Matches 328;
Sequence 16, Application US/10236055A Publication No. US20030134328A1 GENERAL INFORMATION: APPLICANT: Basham, Beth E. APPLICANT: Forsythe, Ian
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TYPE: PRT
ORGANISM: Homo sapiens
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Pred. No. 1
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L.3e-153;
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PRIOR APPLICATION NUMBER: US 60/317,988
PRIOR FILLING DATE: 2001-09-06
NUMBER OF SEQ ID NOS: 36
SOFTWARE: Patentin version 3.1
SEQ ID NO 16
LENGTH: 326
TYPE: PRT
ORGANISM: Mus musculus
US-10-236-055A-16
                                                                                                            Sequence 52, Application US/09893737

Patent No. US20020110855A1

GENERAL INFORMATION:
APPLICANT: Sheppard, Paul O.
APPLICANT: Presnell, Scott R.
APPLICANT: Presnell, Scott R.
TITLE OF INVENTION: MAMMALIAN SECRETED PROTEINS
FILE REFERENCE: 00-41

CURRENT APPLICATION NUMBER: US/09/893,737

CURRENT FILING DATE: 2001-06-28

PRIOR APPLICATION NUMBER: US 60/215,446

PRIOR FILING DATE: 2000-06-30

NUMBER OF SEQ ID NOS: 329

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 52

LENGTH: 252

TYPE: PRT
OPCANION.
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US-09-893-737-52
                                                                              ; ORGANISM: Homo sapiens US-09-893-737-52
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Best Local S
Matches 309
Query Match
Best Local Similarity
Matches 65; Conserv
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APPLICANT: Mattson, Jeanine
APPLICANT: Moshrei, Mehrdad
APPLICANT: Moshrei, Mehrdad
APPLICANT: Parham, Christi
TITLE OF INVENTION: MAMMALIAN GENES; RELATED
FILE REFERENCE: DX01343K
CURRENT APPLICATION NUMBER: US/10/236,055A
CURRENT FILING DATE: 2003-02-28
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      Conservative
                      13.8%;
    12;
    Score 237.5; DB 1
Pred. No. 3.7e-14;
.2; Mismatches 61
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Pred. No. 4.2e-141;
2; Mismatches 15;
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                                          DB 10;
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    61;
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      Indels
                                        Length
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168 GPPAPPEPR--SAFSAARTRSLVGSDAGPGPRHQPLAFDTEFVNIGGDFDAAAGVFRCRL

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PRIOR APPLICATION NUMBER: 09/764,900
PRIOR FILING DATE: 2001-01-17
PRIOR FILING DATE: 2001-01-17
PRIOR FILING DATE: 2001-01-17
PRIOR FILING DATE: 2000-01-31
PRIOR FILING DATE: 2000-01-31
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: 60/214,886
PRIOR APPLICATION NUMBER: 60/214,886
PRIOR APPLICATION NUMBER: 60/217,487
PRIOR APPLICATION NUMBER: 60/217,487
PRIOR FILING DATE: 2000-07-11
PRIOR APPLICATION NUMBER: 60/217,487
PRIOR APPLICATION NUMBER: 60/217
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US-10-091-458-43
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CURRENT FILING DATE: 2002-03-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: Nucleic Acids, Proteins,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: 60/217,487
FILING DATE: 2000-07-11
APPLICATION NUMBER: 60/225,758
FILING DATE: 2000-08-14
APPLICATION NUMBER: 60/220,963
FILING DATE: 2000-07-26
                                                                                                     FILING DATE: 2000-09 APPLICATION NUMBER:
                                                                                                                                                                         APPLICATION NUMBER: FILING DATE: 2000-0
                                                                                                                                                                                                                                        APPLICATION NUMBER: 60/234,223
FILING DATE: 2000-09-21
APPLICATION NUMBER: 60/228,924
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APPLICATION NUMBER:
FILING DATE: 2000-0:
                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: 60/225,270 FILING DATE: 2000-08-14 APPLICATION NUMBER: 60/251,869
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: FILING DATE: 2000-0
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FILING DATE: 2000-07-07
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FILING DATE: 2000-08-22
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                                                       APPLICATION NUMBER: 60/220,964
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OR APPLICATION NUMBER: 60/249,216
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OR APPLICATION NUMBER: 60/225,759
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OR APPLICATION NUMBER: 60/237,040
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FILING DATE: 2000-11-08
APPLICATION NUMBER: 60/246,532
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APPLICATION NUMBER: 60/229,287
FILING DATE: 2000-09-01
APPLICATION NUMBER: 60/229,513
FILING DATE: 2000-09-05
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FILING DATE: 2000-12-08
APPLICATION NUMBER: 60/229,344
FILING DATE: 2000-09-01
APPLICATION NUMBER: 60/234,997
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FILING DATE: 2000-09-08
APPLICATION NUMBER: 60/229,509
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APPLICATION NUMBER: 60/229,343
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NUMBER: 60/225,268
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APPLICATION NUMBER: 60/249,211
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APPLICATION NUMBER: 60/232,397
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Best Local Similarity 38.4%;
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APPLICANT: Forsytl
APPLICANT: Gorman
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PRIOR FILING DATE: 2001-09-06
NUMBER OF SEQ ID NOS: 36
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TITLE OF INVENTION: MAMMALIAN GENES; RELATED REAGENTS
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TYPE: PRT
ORGANISM: Homo sapiens
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                                                                                                                                                                                                                          INFORMATION:
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o. US20020110563A1
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INVENTION:
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Moshrefi, Mehrdad
Parham, Christi
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Gorman, Daniel M.
               Mannion, Jane
Kalos, Michael D.
                                                 Benson, Darin
Elliot, Mark
                                                                             Secrist, Heather
Indirias, Carol
                                                                                                                                                                  Henderson, Robert
Lodes, Michael J.
                                                                                                                  Algate, Paul
                                                                                                                                    Mohamath, Raodoh
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                                                                                                                                                                                                       Steven G.
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COMPOSITIONS AND METHODS
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                                                                                  Yoseph
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; Pred. No. 3.7e-13;
16; Mismatches 63;
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RESULT 9
US-10-144-649A-185
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; Publication No. US
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                                                                                                                                                                                                                                                                                                                                                                                             ) ORGANISM: Homo sapien US-09-854-133-185
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CURRENT FILING DATE: 2001-05-11
NUMBER OF SEQ ID NOS: 735
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 185
LENGTH: 746
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Best Local !
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APPLICANT: Mohamath, Raodoh
APPLICANT: Henderson, Rober
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TITLE OF INVENTION: THE THERAPY AND DIAGNOSIS FILE REFERENCE: 210121.475C10
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CURRENT FILING DATE: 2000-12-14
NUMBER OF SEQ ID NOS: 587
SOFTWARE: FastSEQ for Windows Version 3.0
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ORGANISM: Homo sapien
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                                                                                                       707 NHAILQLFQGDQIWLRLH----RGAIYGSSWKYSTFSGYLLYQD 746
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  213 DEDAAAGVERCRLPGAYEESETLGKLP-RKTLSVKLMKNRDEVQAMIYDDGASRRREMQS
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Similarity 38.4%;
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                                                                                                                                         QSVMLALRRGDAVWLLSHDHDGYGA-YSNHGKYITFSGFLVYPD 314
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Henderson, Robert A.
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 Application US/10144649A
o. US20030118599A1
                                                                                                                                                                                                                                                                                                                         Conservative
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Pred. No. 8e-13;
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GENERAL INFORMATION:
APPLICANT: Lodes, Michael J.
APPLICANT: Wang, Tongtong
APPLICANT: Wang, Tongtong
APPLICANT: Fan, Liqun
APPLICANT: Fan, Liqun
APPLICANT: McNeill, Paul A.
APPLICANT: McNeill, THE THERAPY AND DIAGNOSIS OF ITILE OF INVENTION: THE THERAPY AND DIAGNOSIS OF ITILE REFERENCE: 210121.475C11
CURRENT APPLICATION NUMBER: US/10/144,649A
CURRENT FILING DATE: 2002-08-21
NUMBER OF SEO ID NOS: 749
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 185
LENGTH: 746
TYPE: PRT
ORGANISM: Homo sapien
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US-10-309-422-10
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                                                                                                                                                                                                                                                                                                                                                                                          SEQ ID NO 10
LENGTH: 908
                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: US/09/798,771
PRIOR APPLICATION NUMBER: US/09/798,771
PRIOR FILING DATE: 2001-03-02
PRIOR APPLICATION NUMBER: US 60/186,557
PRIOR FILING DATE: 2000-03-02
NUMBER OF SEQ ID NOS: 43
SOFTWARE: Factor
                                                                                                                                                                                                                                                                       Query Match
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Best Local
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APPLICANT: Wilganowski, N
APPLICANT: Turner, C. Ale
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                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 90
TYPE: PRT
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                                                                                                                                     755 DVPVTNPAATILPVHVYPLPQQMRVAFSAART----SNLAPGTLDQPIVFDLLLNNLGE 809
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                                                                                       213 DFDAAAGVFRCRLPGAYFFSFTLGKLP-RKTLSVKLMKNRDEVQAMIYDDGASRRREMQS 271
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Similarity 38.4%; Pred. No. 1e-12;
63; Conservative 16; Mismatches 63; Indels 2
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                                             TFDLQLGRFNCPVNGTYVFIFHMLKLAVNVPLYVNLMKNEEVLVSAYANDGAP-DHETAS
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QSVMLALRRGDAVWLLSHDHDGYGA-YSNHGKYITFSGFLVYPD 314
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Pred. No. 8e-13;
6; Mismatches
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US-10-309-422-22
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                                                                     US-10-309-422-14
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Best Local S
Matches 63
                                                                                                                                    PRIOR APPLICATION NUMBER: US 60/186,557
PRIOR FILING DATE: 2000-03-02
NUMBER OF SEQ ID NOS: 43
SOFTWARE: FastSEQ for Windows Version 4
SEQ ID NO 14
                                                                                                                                                                                                       APPLICANT: Walke, D. Wade
APPLICANT: Wilganowski, Nathaniel L.
APPLICANT: Turner, C. Alexander Jr.
APPLICANT: Turner, C. US20030139587A1el Human Proteins and Polynucleotides Encoding
TITLE OF INVENTION: NO. US20030139587A1el Human Proteins and Polynucleotides Encoding
FILE REFERENCE: LEX-0142-USA
CURRENT APPLICATION NUMBER: US/10/309,422
CURRENT FILING DATE: 2002-12-03
PRIOR APPLICATION NUMBER: US/09/798,771
PRIOR FILING DATE: 2001-03-02
PRIOR FILING DATE: 2001-03-02
                                                                                                                                                                                                                                                                                                                                                                               Sequence 14, Application US/10309422 Publication No. US20030139587A1 GENERAL INFORMATION:
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SEQ ID NO 22
LENGTH: 909
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                                  Query Match
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 Matches
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                                                                                                      LENGTH: 95
                                                                                    ORGANISM: homo sapiens
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                   Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            163 DAPARGP------PAPPEPRSAFSAARTRSLVGSDAGPGPRHQPLAFDTEFVNIGG 212
 63;
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Conservative
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                13.3%; Score 230; DB 12; 38.4%; Pred. No. 1.1e-12;
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 16;
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 Mismatches
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                                DB 12;
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 63;
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                                Length 957;
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 Indels
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 22;
 Gaps
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FILE REFERENCE: LEX-0142-USA
CURRENT APPLICATION NUMBER: US/10/309,422
CURRENT FILING DATE: 2002-12-03
PRIOR APPLICATION NUMBER: US/09/798,771
PRIOR FILING DATE: 2001-03-02
PRIOR APPLICATION NUMBER: US 60/186,557
PRIOR FILING DATE: 2000-03-02
NUMBER OF SEQ ID NOS: 43
SOFTWARE: FASSSEQ for Windows Version 4.0
SEQ ID NO 26
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US-10-309-422-26
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; TYPE: PRT
; ORGANISM: homo sapiens
US-10-309-422-26
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                                                                                                                                                                                                                                                    Sequence 18, Application US/10309422 Publication No. US20030139587A1 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sequence 26, Appublication No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 13.3%; Score 230; DB 12; Best Local Similarity 38.4%; Pred. No. 1.1e-12;
APPLICANT: Turner, C. Alexander Jr.
TITLE OF INVENTION: No. US20030139587A1el Human Proteins
FILE REFERENCE: LEX-0142-USA
CURRENT APPLICATION NUMBER: US/10/309,422
CURRENT FILING DATE: 2002-12-03
PRIOR APPLICATION NUMBER: US/09/798,771
PRIOR APPLICATION NUMBER: US/09/798,771
PRIOR PILING DATE: 2001-03-02
PRIOR PILING DATE: 2000-03-02
PRIOR FILING DATE: 2000-03-02
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                                                                                                                                                                                                          APPLICANT: Walke, D. Wade APPLICANT: Wilganowski, N
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          163 DAPARGP-----PAPPEPRSAFSAARTRSLVGSDAGPGPRHQPLAFDTEFVNIGG 212
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                                                                                                                                                                                                          Nathaniel L.
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NUMBER OF SEQ ID NOS: 43 SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 18

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RESULT 15
US-10-309-422-30
; Sequence 30, Application US/10309422
; Publication No. US20030139587A1
; GENERAL INFORMATION:
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Best Local Similarity
Thes 63; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR FILING DATE: 2000-03-02
NUMBER OF SEQ ID NOS: 43
SOSTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 30
LENGTH: 993
TYPE: PRT
ROANISM: homo sapiens
US-10-309-422-30
Search completed: January 12, 2004, 08:33:35 Job time: 42.0579 secs
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; TYPE: PRT
; ORGANISM: homo sapiens
US-10-309-422-18
                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILE REFERENCE: LEX-0142-USA
CURRENT APPLICATION NUMBER: US/10/309,422
CURRENT FILING DATE: 2002-12-03
PRIOR APPLICATION NUMBER: US/09/798,771
PRIOR FILING DATE: 2001-03-02
PRIOR APPLICATION NUMBER: US 60/186,557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Walke, D. Wade
APPLICANT: Wilganowski, Nathaniel L.
APPLICANT: Turner, C. Alexander Jr.
TITLE OF INVENTION: No. US20030139587A1el Human Proteins and Polynucleotides Encoding
                                                                                                                                                                                                                                                               840 DVPVTNPAATILPVHVYPLPQQMRVAFSAART----SNLAPGTLDQPIVPDLLLNNLGE 894
                                                                                                                                                                                                                                                                                               163 DAPARGP-------PAPPEPRSAFSAARTRSLVGSDAGPGPRHQPLAFDTEFVNIGG 212
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                                                                                       954 NHAILQLFQGDQIWLRLH----RGAIYGSSWKYSTFSGYLLYQD 993
                                                                                                                                272 QSVMLALRRGDAVWLLSHDHDGYGA-YSNHGKYITFSGFLVYPD 314
                                                                                                                                                                            895 TFDLQLGRFNCPVNGTYVFIFHMLKLAVNVPLYVNLMKNEEVLVSAYANDGAP-DHETAS 953
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Result
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Maximum DB
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Perfect score:
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Maximum Match 100%
Listing first 45 summaries
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      Pred. No.
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seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                        No. is the number of results predicted by chance to have greater than or equal to the score of the result being pure derived by analysis of the total score distribution.
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Match
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Gapop 10.0 , Gapext 0.5
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1726
1 MLPLLLGLLGPAACWALGPT.....LVYPDLAPAAPPGLGASELL 329
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     Length
     GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                            DB
  US-09-370-838-185
US-09-5118-408-44
US-09-516-855-44
US-09-511-176B-4
US-09-511-176B-2
US-09-511-176B-2
US-09-511-176B-2
US-09-511-176B-2
US-09-510-855-2
US-09-510-855-2
US-09-510-852-2
US-09-510-852-2
US-09-336-34-2
US-09-336-336-3
US-09-312-283C-295
US-09-312-283C-295
US-09-312-283C-294
US-09-312-283C-382
US-09-312-283C-382
US-09-312-283C-382
US-09-312-283C-382
US-09-312-283C-393
US-09-312-283C-393
US-09-312-283C-393
US-09-315-36-11
US-09-316-336-11
US-09-316-336-336-11
US-09-316-336-11
US-09-316-336-31
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Sequence 185, App
Sequence 44, Appl
Sequence 44, Appl
Sequence 44, Appl
Sequence 44, Appl
Sequence 2, Appli
Sequence 3, Appli
Sequence 2, Appli
Sequence 29, Appli
Sequence 295, App
Sequence 294, App
Sequence 294, App
Sequence 294, App
Sequence 107, Appl
Sequence 110, Appl
Sequence 2, Appli
Sequence 2, Appli
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QY  Db  Db  Oy  Db		RESULT 1 US-09-370- ; Sequence ; Patent N ; GENERAL ; APPLICA	2 2 2 3 3 3 4 4 4 4 4 4 4 4 4 4 4 4 4 4
163 593 213 648 272	REFERENT ENT ENT ENT ENT ENT ENT ENT ENT ENT	838- 1850 0.60 0.60 0.60 0.70 0.70 0.70 0.70 0.7	1966 11 1966 11 1966 11 1966 11 1966 11
DAPARGPPA	LAVENILUM: LUNG CANCERENCE: 210121.475C1 ERRNCE: 210121.475C1 APPLICATION NUMBER: US FILLING DATE: 1999-08-0) APPLICATION NUMBER: US FILING DATE: 1999-04-0) F SEQ ID NOS: 289 : FastSEQ for Windows ' 185 185 185 Ch 1338; 1 Similarity 38.48;	185  , Application 444425  RMATION: Reed, Steven Lodes, Michae Mohamath, Roa Secrist, Heat	
LPVHVY LP	UNG CANC 11.475C1 1099-08- UMBER: UI 11999-04- 1289-04- 289- Windows II II II II II II II II II I	tion US/0 ven G. chael J. Roadoh Heather	00 00 00 00 00 00 00 00 00 00 00 00 00
DAPARGPPAPPEPRSAFSAARTRSLVGSDAGPGF	09/370,838 09/285,323 ersion 3.0 ersion 3.0 ersion 3.0	ALIGNMENTS 9370838 FOR THERAPY AND	US-09-140-804-3 US-09-336-536-20 US-09-530-423-1 US-09-686-838B-3 US-09-9-911-176B-48 US-09-9-552-225A-4 US-09-76-976-6 US-09-76-976-6 US-09-76-9852B-6 US-09-118-408-3 US-09-118-408-8 US-09-118-408-3 US-09-686-838B-8 US-09-686-838B-8 US-09-619-740-3 US-09-619-740-3
DAPARGP	Length 746;	IS OF	Sequence 3, Appli Sequence 20, Appli Sequence 1, Appli Sequence 3, Appli Sequence 3, Appli Sequence 3, Appli Sequence 6, Appli Sequence 6, Appli Sequence 6, Appli Sequence 6, Appli Sequence 3, Appli

RESULT 2
US-09-118-408-44
; Sequence 44, Application US/09118408A
; Patent No. 6265544
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: ADIPOCYTE-SPECIFIC PROTEIN HOMOLOGS
; FILE REFERENCE: 97-30

CURRENT APPLICATION NUMBER: US/09/118,408A

60/053,154

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APPLICANT: Sheppard, Paul O.

APPLICANT: Lasser, Gerald W.
APPLICANT: Bishop, Paul D.

TITLE OF INVENTION: INHIBITORS FOR USE IN HEMOSTASIS AND TITLE OF INVENTION: IMMUNE FUNCTION

FILE REFERENCE: 99-12
CURRENT APPLICATION NUMBER: US/09/506,855
CURRENT APPLICATION NUMBER: US/09/506,855
CURRENT APPLICATION ON MEMBER: US/09/506,855
CURRENT APPLICATION NUMBER: US/09/506,855
CURRENT APPLICATION NUMBER: US/09/506,855
CURRENT APPLICATION ON MEMBER: US/09/506,855
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US-09-911-176B-44
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US-09-506-855-44
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Best Local S
Matches 56
Sequence 44, Application US/09911176B
PATENT NO. 6518403
GENERAL INFORMATION:
APPLICANT: Sheppard, Paul O.
TITLE OF INVENTION: ANTIBODIES THAT BIND AN
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SEQ ID NO 44
LENGTH: 281
TYPE: PRT
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Patent No. 644822
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Best Local
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EARLIER APPLICATION NUMBER: 60/
EARLIER FILING DATE: 1997-07-18
ENUMBER OF SEQ ID NOS: 47
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Local Similarity 39.2%;
hes 56; Conservative 20
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                                                                                                                                                                                                                                                                                                  IFSDEFDTYITFSGYLVKPASEP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KLPRKTLSVKLMKNRDEVQAMIYDDGASRRREMQSQSVMLALRRGDAVW--LLSHDHDGY 294
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39.2%; Pred. No. 2.1e-14;
tive 20; Mismatches 58
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FITTLE OF INVENTION: ADIPOCYTE-SPECIFIC PROTE
FILE REFERENCE: 97-3011
CURRENT APPLICATION NUMBER: US/09/911,176B
CURRENT FILING DATE: 2001-07-23
PRIOR APPLICATION NUMBER: 09/118,408
PRIOR FILING DATE: 1998-07-17
PRIOR APPLICATION NUMBER: 60/053,154
PRIOR APPLICATION NUMBER: 60/053,154
PRIOR APPLICATION NUMBER: 60/053,154
PRIOR PILING DATE: 1997-07-18
NUMBER OF SEQ ID NOS: 52
SOFTWARE: FASTER OF SEQ
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US-09-619-740-44
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APPLICANT: Lasser, G
APPLICANT: Bishop, F
TITLE OF INVENTION:
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Best Local
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Best Local Similarity 39.2%;
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TYPE: PRT
ORGANISM: Mus (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: 09/506,855 PRIOR FILING DATE: 2000-02-17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH:
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No. 6544946
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                                   295
                                                                                               201
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                                                                                                                                                                                                                                                           177 SAFSAARTRSLVGSDAGPGPRHQPLAFDTEFVNIGGDFDAAAGVFRCRLPGAYFFSFTLG 236
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Similarity 39.2%;
GAYSNHGKYITFSGFLVYPDLAP 317
                                                                                         TWNQKETYLHIMKNEEEV-VILYAQ-VSDRSIMQSQSLMMELREEDEVWVRLFKGERENA
                                                                                                                                               KLPRKTLSVKLMKURDEVQAMIYDDGASRRREMQSQSVMLALRRGDAVW---LLSHDHDGY 294
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Lasser, Gerald |
Bishop, Paul D.
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                                                                                                                                                                                                                                                                                                                                           Score 220.5; DB 4
Pred. No. 2.1e-14;
20; Mismatches 58
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Pred. No. 2.1e-14;
20; Mismatches 58
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IFSDEFDTYITFSGYLVKPASEP 281

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CURRENT APPLICATION NUMBER: US/09/118,408A
CURRENT FILING DATE: 1998-07-17
EARLIER APPLICATION NUMBER: 60/053,154
EARLIER FILING DATE: 1997-07-18
NUMBER OF SEQ ID NOS: 47
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 2
LENGTH: 281
TYPE: PRT
ORGANISM: Homo sapien
US-09-118-408-2
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EARLIER FILLING DATE: 1997-07-18
NUMBER OF SEQ ID NOS: 44
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 44
LENGTH: 281
TYPE: PRT
ORGANISM: Mus musculus
US-09-506-852-44
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US-09-118-408-2
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                                                                                                                                                                                                                    Query Match 12.5%; Score 215; DB 3; Length 281; Best Local Similarity 30.2%; Pred. No. 7.6e-14; Matches 77; Conservative 26; Mismatches 86; Indels
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Best Local Similarity 39.2%; Pred. No. 2.1e-14;
Matches 56; Conservative 20; Mismatches 58
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APPLICANT: Sheppard, Paul O.
TITLE OF INVENTION: ADIPOCYTE-SPECIFIC PROTEIN HOMOLOGS
FILE REFERENCE: 97-30
FILE REFERENCE: 97-30
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Patent No. 6566499
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TITLE OF INVENTION: ADIPOCYTE-SPECIFIC PROTEIN HOMOLOGS
FILE REFERENCE: 97-30
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CURRENT FILING DATE: 2000-02-17
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TRSLVGSDAGPGPRH-----QPLAFDTEFVNIGGDFDAAAGVFRCRLPGAYFFSFTLGKL
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                                              GKTGSAGARGHTGPKGQKGSMGAPGERCKSH--YA--
                                                                                     GDT---VWLRLHGAP----HYALGAPGATFSGYLVYADADADAPARGPPAPPEPRSAFSAAR 183
                                                                                                                                   RCCDPGTSMYPATA--VPQINITILKGEKGDR------
                                                                                                                                                                          RCRVPGAYFFSFTAGKAPHKSLSVMLVRNRDEVQALAFDEQRRPGARRAASQSAMLQLDY 128
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RESULT 9
US-09-911-176B-2
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                                                                                                                            GENERAL INFORMATION:
APPLICANT: Sheppard, Paul O.
TITLE OF INVENTION: ANTIBODIES THAT BIND AN
TITLE OF INVENTION: ADIPOCYTE-SPECIFIC PROTEIN HOMOLOG
FILE REFERENCE: 97-30D1
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CURRENT APPLICATION NUMBER: US/09/911,176B
CURRENT FILING DATE: 2001-07-23
PRIOR APPLICATION NUMBER: 09/118,408
PRIOR FILING DATE: 1998-07-17
PRIOR APPLICATION NUMBER: 60/053,154
PRIOR FILING DATE: 1997-07-18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Lasser, Gerald W.
APPLICANT: Bishop, Paul D.
TITLE OF INVENTION: INHIBITORS FOR USE IN HEMOSTASIS
TITLE OF INVENTION: IMMUNE FUNCTION
FILE REFERENCE: 99-12
CURRENT EPPLICATION NUMBER: US/09/506,855
CURRENT FILING DATE: 2000-02-17
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ORGANISM: Homo sapien
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Pred. No. 7.6e-14;
6; Mismatches 86
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REPLICANT: Sheppard, Paul O.
APPLICANT: Lasser, Gerald W.
APPLICANT: Lasser, Gerald W.
APPLICANT: Lasser, Gerald W.
APPLICANT: Lasser, Faul D.
TITLE OF INVENTION: INHIBITORS FOR USE IN H
FILLS REFERENCE: 99-12C3
CURRENT APPLICATION NUMBER: US/09/619,740
CURRENT FILING DATE: 2000-07-19
PRIOR APPLICATION NUMBER: 09/253,604
PRIOR FILING DATE: 1999-02-19
PRIOR APPLICATION NUMBER: 09/444,794
PRIOR FILING DATE: 1999-11-22
PRIOR APPLICATION NUMBER: 09/506,855
PRIOR FILING DATE: 2000-02-17
NUMBER OF SEQ ID NOS: 55
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US-09-619-740-2
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; ORGANISM: Homo sapien
US-09-911-176B-2
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SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 2
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Best Local :
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TRSLVGSDAGPGPRH-----QPLAFDTEFVNIGGDFDAAAGVFRCRLPGAYFFSFTLGKL 238
                                                                                                                                                                                                                                                                                                                                 FastSEQ for Windows Version 3.0
                                                                                                                                                  RCRVPGAYFFSFTAGKAPHKSLSVMLVRNRDEVQALAFDEQRRPGARRAASQSAMLQLDY 128
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                                                  GKTGSAGARGHTGPKGQKGSMGAPGERCKSH--YA-----
                                                                                 GDT--VWLRLHGAP---HYALGAPGATFSGYLVYADADADAPARGPPAPPEPRSAFSAAR 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEELDTYITESGYLV 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NH--GKYITFSGFLV 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NOKETYLHIMKNEEEVVILFAQVG--DRSIMQSQSLMLELREQDQVWVRLYKGERENAIF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KK-----PMHSNHYYQTVIFDTEFVNLYDHFNMFTGKFYCYVPGLYFFSLNVHTW
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                                                                                                                   RCCDPGTSMYPATA--VPQINITILKGEKGDR------
                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                               12.5%; Score 215; DB 4; Length 281; 30.2%; Pred. No. 7.6e-14;
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Pred. No. 7.6e-14;
                                                                                                                                                                                  Mismatches
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                                                  -----AFSVGR
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; SEQ ID NO 2
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-506-852-2
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US-09-336-536-4
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US-09-506-852-2
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                                                                   APPLICANT: Leiby, K.
APPLICANT: McKay, C.
APPLICANT: McScore, S.
TITLE OF INVENTION: SECRETED PROTEINS AND US
FILE REFERENCE: 7853-144
CURRENT APPLICATION NUMBER: US/09/336,536
CURRENT FILING DATE: 1999-06-18
NUMBER OF SEQ ID NOS: 75
                                                                                                                                                                                                                   Sequence 4, Application US/09336536 Patent No. 6406884 GENERAL INFORMATION:
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SOFTWARE: PatentIn Ver.
SEQ ID NO 4
LENGTH: 228
TYPE: PRT
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EARLIER FILING DATE: 1997-07-18
NUMBER OF SEQ ID NOS: 44
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CURRENT APPLICATION NUMBER: US/09/506,852
CURRENT FILING DATE: 2000-02-17
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SOFTWARE: FastSEQ for Windows Version 3.0
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TITLE OF INVENTION: ADIPOCYTE-SPECIFIC PROTEIN HOMOLOGS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                184 TRSLVGSDAGPGPRH-----OPLAFDTEFVNIGGDFDAAAGVFRCRLPGAYFFSFTLGKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        129 GDT--VWLRLHGAP---HYALGAPGATFSGYLVYADADADAPARGPPAPPEPRSAFSAAR 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12.5%;
al Similarity 30.2%;
77; Conservation
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                                                                                                                                                                                                                                                                                                                                                   SEELDTYITFSGYLV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRKTLSVKLMKURDEVQAMIYDDGASRRREMQSQSVMLALRRGDAVWLLSHDHDGYGAYS
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Pred. No. 7.6e-14;
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RESULT 14
US-09-336-536-3
; Sequence 3, Application US/09336536
; Patent No. 6406884
; GENERAL INFORMATION:
; APPLICANT: Leiby, K.
; APPLICANT: MCKAY, C.
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US-09-140-804-2
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SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                            12.3%;
Best Local Similarity 34.9%;
Matches 66; Conservative
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: ADIPOCYTE-SPECIFIC PROTEIN HOMOLOGS FILE REFERENCE: 97-49 CURRENT APPLICATION NUMBER: US/09/140,804 CURRENT FILING DATE: 1998-08-26 CURRENT FILING CHARLES 1998-08-26 EARLIER APPLICATION NUMBER: 60/056,983 EARLIER FILING DATE: 1997-08-26 NUMBER OF SEQ ID NOS: 47
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ORGANISM: Homo
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                                                                                                                                                                                                                                                                                                                                                                                                          138 GAPHYALGAPGATFSG---YLVYADAD----ADAPARGPPAPP----EPRSAFSAARTR 185
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                                                                                                                                                                                    FSGFLVYPD
                                                                                                                                                                                                                                   DLVKNGESIASFFQFFGGWPKPASLSGGAMVRLEPEDQVWVQVGVGDYIGIYASIKTDST
                                                                                                                                                                                                                                                                     KLMKNRDEVQAMIYDDGASRRREMQSQSVMLALRRGDAVWLLSHDHDGYGAYSNHGKYIT 305
                                                                                                                                                                                                                                                                                                   SRV----PPPSDAPLPFDRVLVNEQGHYDAVTGKFTCQVPGVYYFA-VHATVYRASLQF 166
                                                                                                                                                                                                                                                                                                                                    SLVGSDAGPGPRHQPLAFDTEFVNIGGDFDAAAGVFRCRLPGAYFFSFTLGKLPRKTLSV 245
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                                                                                                                                                                FSGFLVYSD
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Pred. No. 9
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Pred. No. 9.9e-14;
8; Mismatches 83
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US-09-686-838B-2
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                                                                                                                                                                                                                                                                                                                                                                                                  SEQ ID NO 2
LENGTH: 243
TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                  Query Match 12.3%; Score 213; DB 4; Length 243; Best Local Similarity 34.9%; Pred. No. 9.9e-14; Matches 66; Conservative 18; Mismatches 83; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2, Application US/09686838B Patent No. 6482612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Sheppard, Paul O.
APPLICANT: Humes, Jacqueline M.
TITLE OF INVENTION: Adipocyte-Specific Protein
FILE REFERENCE: 97.49D1
CURRENT APPLICATION NUMBER: US/09/686,838B
CURRENT FILING DATE: 2000-10-10
PRIOR APPLICATION NUMBER: US 09/140,804
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/336,536
CURRENT FILING DATE: 1999-06-18
NUMBER OF SEQ ID NOS: 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: BOSSONE, S. TITLE OF INVENTION: SECRETED PROTEINS AND USES THEREOF FILE REFERENCE: 7853-144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 50
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: US 60/056,983 PRIOR FILING DATE: 1997-08-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR FILING DATE: 1998-08-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 2.
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          138 GAPHYALGAPGATFSG---YLVYADAD----ADAPARGPPAPP-----EPRSAFSAARTR 185
                                          246 KLMKNRDEVQAMIYDDGASRRREMQSQSVMLALRRGDAVWLLSHDHDGYGAYSNHGKYIT 305
                                                                                                                                                                                                                                     138 GAPHYALGAPGATFSG---YLVYADAD----ADAPARGPPAPP----EPRSAFSAARTR 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               246 KLMKNRDEVQAMIYDDGASRRREMQSQSVMLALRRGDAVWLLSHDHDGYGAYSNHGKYIT 305
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DLVKNGESIASFFQFFGGWPKPASLSGGAMVRLEPEDQVWVQVGVGDYIGIYASIKTDST
                                                                                                                                                                                        GAP----GAPGEKGEGGRPGLPGPRGDPGPRGEAGPAGPTGPAGECSVPPRSAFSAKRSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GAP----GAPGEKGEGGRPGLPGPRGDPGPRGEAGPAGPTGPAGECSVPPRSAFSAKRSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FSGFLVYSD 235
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                                                                                         PPPSDAPLPFDRVLVNEQGHYDAVTGKFTCQVPGVYYFA-VHATVYRASLQF 166
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306 FSGFLVYPD 314           227 FSGFLVYSD 235 completed: January 12, 2004, 08:20:03 completed: secs	Search c	Вb	γ
	ompleted: January : 17.7455 secs	27 FSGFLVYSD	FSGFLVYPD

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                                                                         derived by analysis
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Gapop 10.0 ,
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87
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(c) 1993 - 2004
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protein

A;Residues: 1-115 <ALM>
A;Cross-references: EMBL:L76605; NID:g1246298; PIDN:AAA93503.1; PID:g1246303
A;Cross-references: EMBL:L76605; NID:g12466303
A;Experimental source: strain PAO1
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, April 1996
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, April 1996
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, April 1996
A;Stover, C.K.; Pham, X.O.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Bri adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, LOTY, S.; Olson, M.V.
Nature 406, 959-964, 2000

type 4 fimbrial biogenesis protein Pily2 PA4555 [imported] - Pseudomonas aeruginosa C;Species: Pseudomonas aeruginosa C;Species: Pseudomonas aeruginosa C;Cate: 24-Jul-1998 #text\_change 31-Dec-2000 C;Date: 24-Jul-1998 #text\_change 31-Dec-2000 C;Accession: S72634; E83076 C;Accession: S72634; E83076 R;Alm, R.A.; Hallinan, J.P.; Watson, A.A.; Mattick, J.S. Mol. Microbiol. 22, 161-173, 1996 Mol. Microbiol. 22, 161-173, 1996 A;Title: Fimbrial biogenesis genes of Pseudomonas aerugenosa: pilW and pilX increase

S

A;Reference number: S72631; MUID:97055431; A;Accession: S72634
A;Status: nucleic acid sequence not shown;

translation not PMID:8899718

shown

pilX increase

the

A; Molecule type: DNA

ALIGNMENTS

## RESULT S72634 A;Cross-references: EMBL:Z49086; NID:g1089899; PIDN:CAA88910.1; PID:g1089900 C;Superfamily: protein-tyrosine kinase, receptor type eph; fibronectin type C;Keywords: ATP; transmembrane protein Oncogene 11, 2085-2095, 1995 A;Title: Cloning, characterization, and differential expression A;Reference number: I48652; MUID:96074837; PMID:7478528 A;Accession: I48653 밁 F;626-894/Domain: protein kinase homology <KIN>F;634-642/Region: protein kinase ATP-binding motif F;917-983/Domain: SAM homology <SAM> A; Molecule type: mRNA A; Residues: 1-993 < RES> C;Accession: I48653 R;Ciossek, T.; Lerci C;Species: Mus musculus (house mouse) C;Date: 02-Jul-1996 #sequence\_revision mouse developmental kinase 5 (MDK5) -A;Status: preliminary; translated from GB/EMBL/DDBJ I48653 RESULT 1 Matches Query Match Local ... ... 14 1 MLPLLLGLLGPAACWA 16 l Similarity 11; Conserva LAPLLLPLLLPAGCWA Lerch, M.M.; Ullrich, Conservative 68.8%; 29 Score 57; DB 2; Pred. No. 0.73; Þ Mismatches mouse 02-Jul-1996 #text\_change 18-Jun-1999 Length 993 Indels of. 0 MDK2 Gaps and III MDK5, 0 repeat t wo

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MLPLLLGLLGP

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C;Species: Mus musculus (house mouse)
C;Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 21-Jul-2000
C;Accession: T31066
R;Telo, P: Breviario, F:; Huber, P:; Panzeri, C:; Dejana, E.
J. Biol. Chem. 273, 17565-17572, 1998
A;Title: Identification of a novel cadherin (vascular endothelial cadherin-2) located at A;Reference number: Z20962; MUID:98316322; PMID:9651350
A;Accession: T31066
A;Accession: T31066
                                                                                                                                                                                                                                                               A;Description: The sequence of A;Reference number: Z18613 A;Accession: T16945
                                                                                                                                                                                                                                                                                                                                      C;Accession: R;Hallsworth,
                                                                                                                                                                                                                                                                                                                                                            hypothetical protein T27F7.3 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999 C;Accession: T16945
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A;Accession: E83076
A;Status: preliminary
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A;Reference number: A82950; MUID:20437337; PMID:10984043
                                                                                                                                                                                                            A;Residues: 1-283 <HAL>
                                                                                                                                                                                                                        A;Status: preliminary; translated from GB/EMBL/DDBJA;Molecule type: DNA
                                                                                                                                                                                                                                                                                                     submitted to the EMBL Data Library, May 1996
A;Description: The sequence of C. elegans cosmid T27F7
                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 4
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A;Cross-references: EMBL:Y08715; NID:g2764993; PIDN:CAA69965.1;
A;Experimental source: brain capillary
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A;Residues: 1-115 <STO>
A;Cross-references: GB:AE004869; GB:AE004091; NID:g9950793; PIDN:AAG07943.1;
A;Experimental source: strain PAO1
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Superfamily: Pseudomonas aeruginosa
                                                                                                                                                                     ;Cross-references: EMBL:U58762; NID:g1330398; PID:g1330400; PIDN:AAB00719.1; GSPDB:GNO:
Experimental source: strain Bristol N2; clone T27F7
                                                                                            Introns: 11/1; 45/1;
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                 Similarity 7; Conserv
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                     Conservative
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                                   52.9%;
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                                     Score 46;
Pred. No.
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                   4.
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Pred. No.
                     Mismatches
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                                                       Length 283;
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RESULT 7
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R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R., M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C. S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A;Reference number: A75250; MUID:20036896; PMID:10567266
A;Accession: E75382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Accession: AB3201
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Khen, L.; Wood, G.E.; Chen, Y.; Moclel erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClel; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
                                                                                                                                                                                                                                                         A;Molecule type: DNA
A;Molecule type: DNA
A;Rosiduse: 1-315 <WHI>
A;Cross-references: GB:AE001998; GB:AE000513; NID:g6459302; PIDN:AAF11113.1; PID:g645931;
                                                                                                                                                                                         A;Map position: 1
C;Superfamily: Deinococcus radiodurans hypothetical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hypothetical protein - Deinococcus radiodurans (strain R1)
C;Species: Deinococcus radiodurans
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 28-Jul-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Reference number: A; Accession: AE3201
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   conserved hypothetical protein Atu5339 [imported] - Agrobacterium tumefaciens
C;Species: Agrobacterium tumefaciens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C; Accession: E75382
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A;Experimental source: strain C58 (Dupont)
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A;Residues: 1-303 <KUR>
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Best Local
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8; Conserv
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LVPLLAPLLGYLVCW. 40
                                                                                              Conservative
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53.3%;
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Pred. No. 17;
                                                                                              Mismatches
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                                                                                                                                                                                            protein DR1541
                                                                                                                                            Length 315;
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precursor -

mouse

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R; Smith, M.
EMBO J. 8,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: protein
A; Residues: 18-41 <MA2>
A; Residues: 18-41 <MA2>
A; Residues: 18-41 <MA2>
Tanzer, M.L.

J. Biol. Chem. 270, 15926-15929, 1995
J. Biol. Chem. 270, 15926-15929, 1995
A; Title: Cell surface calreticulin is a putative mannoside lectin which triggers mouse
A; Reference number: A57498; MUID:95332280; PMID:7608143
A; Accession: A57498
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R;Murthy, K.K.; Banville, D.; Srikant, C.B.; Carrier, F.; Holmes, C.; Bell, A.; Patel, Nucleic Acids Res. 18, 4933, 1990
A;Tille: Structural homology between the rat calreticulin gene product and the Onchocerc A;Reference number: S11205; MUID:90370496; PMID:2395661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Date: 30-Sep-1993 #sequence_revision 20-Aug-1994 #text_change 20-Jun-2000 C;Accession: JH0819; A49176; S11205; PC1109; S45036; S04867; S39372; A34473; R;Nakamura, M.; Morilya, M.; Baba, T.; Michikawa, Y.; Yamanobe, T.; Arai, K.; Exp. Cell Res. 205, 101-110, 1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               calreticulin precursor - rat
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A;Accession: PC1233
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N;Alternate names: calcium-binding protein 3
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                                                                                                                         ;Cross-references: GB:D78308; NID:g1089798; PIDN:BAA11345.1; PID:g1845572;Experimental source: Sprague-Dawley, spermatogenic cells;Note: sequence_extracted_from_NCBI_backbone_(NCBIN:127639, NCBIP:127643)
                                                                                                                                                                                                                                                                                                                ;Cross-references: GB:D78308; NID:g1089798; PIDN:BAA11345.1; PID:g1845572;Accession: A49176
                                                                                                                                                                                                                                                  Molecule type: mRNA; protein
                                                                                                                                                                                                                                                                                      Status: preliminary;
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;Residues: 1-416 <NAK>
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;Residues: 74-80;142-151;186-193
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;Residues: 1-416 <MAZ>
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;Accession: $06763; JC1444; PC1233; A57498
.Smith, M.J.; Koch, G.L.E.
MBO J. 8, 3581-3586, 1989
                                                                                                                                                                                                                           Residues: 1-416 <NA2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Species: Rattus norvegicus (Norway rat)
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Best Local
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83.3%;
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Pred. No. 23;
1; Mismatches
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calreticulin precursor, skeletal muscle - rabbit
C;Species: Oryctolagus cuniculus (domestic rabbi
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-19
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A34154
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F;18-416/Product: calreticulin #status experimental <MAT-
F;204-212/Region: nuclear location signal
F;413-416/Region: endoplasmic reticulum retention signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R;Treves, S.; de Mattei, M.; Lanfredi, M.; Villa, A.; Green, N.M.; MacLennan, D.H.; Meldc Biochem. J. 271, 473-480, 1990
A;Title: Calreticulin is a candidate for a calsequestrin-like function in Ca(2+)-storage A;Reference number: S13045; MUID:91054414; PMID:2241926
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R;Van, P.N.; Peter, F.; Soeling, H.D.
J. Biol. Chem. 264, 17494-17501, 1989
A;Title: Four intracisternal calcium-binding glycoproteins itive calcium sequestering rat liver vesicles.
A;Reference number: A34473; MUID:90008920; PMID:2793869
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: mRNA
A; Residues: 'R',270-358,'AAG' <LON>
A; Residues: 'R',270-358,'AAG' <LON>
A; Residues: 'R',270-358,'AAG' <LON>
A; Cross-references: EMBL:X13702; NID:956055; PIDN:CAA31987.1; PID:9930260
A; Note: the authors designated the protein as D-beta-hydroxybutyrate dehydrogenase
A; Noto: T.; Nagayama, S.; Kajiwara, R.; Kawaguchi, Y.; Horiuchi, R.; Kamataki, T.
Biochim. Biophys. Acta 1158, 339-344, 1993
A; Title: Identification of protein disulfide isomerase and calreticulin as autoimmu
A; Reference number: 339371; MUID:94072621; PMID:8251535
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R;Scennichsen, B.; Fuellekrug, J.; van Nguyen, P.; Diekmann, W.; Robinson, D.G.; Mieskes,
submitted to the EMBL Data Library, May 1994
A;Description: Retention and retrieval: both mechanisms cooperate to maintain calreticuli
A;Reference number: S45036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R;Nakamura, M.; Michikawa, Y.; Baba, T.; Okinaga, S.; Arai, K. Biochem. Biophys. Res. Commun. 186, 668-673, 1992
A;Title: Calreticulin is present in the acrosome of spermatids of rat testis A;Reference number: PC1109; MUID:92360010; PMID:1497655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: protein A; Residues: 18-29 < TRE>
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A; Accession: S04867
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R;Nakamura, M.; Michikawa, Y.; Baba, T.; Okinaga, S.; Arai, K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     F;344/Binding site: carbohydrate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: protein
A; Residues: 18-36 < VAN>
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A;Residues: 18-23,'X',25-32 <YOK>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: protein
A; Residues: 18-32 < NAK2>
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A;Residues: 1-416 <SOE>
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83.3%;
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Pred. No. 23;
   10-Sep-1999
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#status predicted
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C;Accession: A34154; S13047
R;Filegel, L.; Burns, K.; MacLennan, D.H.; Reithmeier, R.A.F.; Michalak, M.
J. Biol. Chem. 264, 21522-21528, 1989
A;Title: Molecular cloning of the high affinity calcium-binding protein (calreticulin)
A;Reference number: A34154; MUID:90094320; PMID:2600080
A;Accession: A34154
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-418 <FLI>
A;Residues: 1-418 <FLI>
A;Cross-references: GB:J05138; NID:g164858; PIDN:AAA31188.1; PID:g164859
A;Cross-references: GB:J05138; NID:g164858; PIDN:AAA31188.1; M.; MacLennan, D.H.; Me
                                                                                                                               11-cis retinol dehydrogenase (EC 1.1.1.-) -
C;Species: Bos primigenius taurus (cattle)
C;Date: 10-Feb-1995 #sequence_revision 10-Fe
C;Accession: A55429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R;Treves, S.; de Mattei, M.; Lanfredi, M.; Villa, A.; Green, 1 Biochem. J. 271, 473-480, 1990
A;Title: Calreticulin a candidate for a calsequestrin-like A;Reference number: S13045; MUID:91054414; PMID:2241926
A;Accession: S13047
                      C;Accession: A55429

C;Accession: A55429

C;R;Simon, A.; Hellman, U.; Wernstedt, C.; Eriksson, U.

J. Biol. Chem. 270, 1107-1112, 1995

A;Title: The retinal pigment epithelial-specific 11-cis
A;Reference number: A55429; MUID:95138097; PMID:7836368

A;Accession: A55429
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C;Accession: D97073
    A;Status:
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A;Residues: 1-628 <KUR>
A;Cross-references: GB:AE001437; PIDN:AAK79375.1; PID:g15024346; GSPDB:GN00168
A;Experimental source: Clostridium acetobutylicum ATCC824
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Status: preliminary
A;Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TS system, beta-glucosides-specific IIABC component [imported] - Clostridi;Species: Clostridium acetobutylicum;Species: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 30-Sep-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Superfamily: calreticulin;
Keywords: skeletal muscle;
1-17/Domain: signal sequence #status predicted;
415-418/Region: endoplasmic reticulum retention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Superfamily: phosphotransferase system enzyme II
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83.3%;
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Pred. No.
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    conceptual translation
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                                                                     retinol dehydrogenase
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patched protein - zebra fish
C;Species: Brachydanio rerio (zebra fish)
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 20-Jun-2000
C;Accession: T18291
R;Concordet, J.P.; Lewis, K.E.; Moore, J.W.; Goodrich, L.V.; Johnson, R.L.;
Bevelopment 122, 2835-2846, 1996
A;Title: Spatial regulation of a zebrafish patched homologue reflects the roaps a zebrafish patched homologue reflects a zebrafish pat
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C;Accessio
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A; Residues: 1-318 <SIN's
A; Cross-references: GB:X82262; NID:g663170; PIDN:CAA57715.1; PID:g663171
A; Cross-references: GB:X82262; NID:g663170; PIDN:CAA57715.1; PID:g663171
C; Superfamily: retinol dehydrogenase; short-chain alcohol dehydrogenase |
C; Keywords: membrane protein; NAD; oxidoreductase
F;29-206/Domain: short-chain alcohol dehydrogenase homology <SADH>
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                                                                                                                                                                                                                                                                   C; Superfamily:
                                                                                                                                                                                                                                                                                                       A;Gene: ptcl
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A; Residues: 1-1220 <CON>
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Matches
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8; Conserv
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ce: strain R1
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                                                                                                                             50.6%;
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Pred. No. 25;
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Pred. No.
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Pred. No. 86;
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T.; Zalewski,
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LLPVLLSLMGPPA 1171

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A;Molecule type: DNA
A;Residues: 1-119 <TET>
A;Cross-references: GB:AE002413; GB:AE002098; NID:g7225797; PIDN:AAF40999.1; PID:g722579
A;Experimental source: serogroup B, strain MC58
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R;Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.P. Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.; ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Masignani, V.; Pizza, M. Science 287, 1809-1815, 2000

A;Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Ve A;Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.

A;Reference number: A81000; MUID:20175755; PMID:10710307

A;Accession: F81182
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A;Title: Complete DNA sequence of a serogroup A strain of Neisseria menigitidis Z2491.

A;Reference number: A81775; MUID:20222556; PMID:10761919

A;Accession: C81919
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C;Species: Neisseria meningitidis
C;Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 02-Feb-2001
C;Accession: C81919
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           conserved hypothetical protein NMB0571 [imported] - Neisseria meningitidis (strain MC58
C;Species: Neisseria meningitidis
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Search completed: January 12, 2004, 08:16:49 Job time : 3.92615 secs
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A;Residues: 1-119 <PAR>
A;Residues: 1-119 <PAR>
A;Cross-references: GB:AL162754; GB:AL157959; NID:g7379424; PIDN:CAB84037.1; PID:g737947
A;Experimental source: serogroup A, strain Z2491
                                                                                                                                                                                                                                                                                                                                                                           A;Gene: NMB0571
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Best Local S
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Best Local Similarity 34.5%;
Matches 10; Conservative
                                                                                                                                                                                                                                                   Matches
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                                                                                                                                                                                                                                                                             Local Similarity
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12 ISLLLGIIGIFLPLLPTTPFVLLSAACWA 40
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Copyright (c) 1993 - 2004 Compugen Ltd.
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CRT1 GNGIN
CRT1 GNGIN
CRTC_RABIT
ENV_SRV2
RDH1 BOVIN
PC12 HUMAN
PC12 HUMAN
PC13 BRARE
TAM_FSUBB
MIAA BUCBB
MIAA BUCBB
COA2_POVMK
COA2_POVBA
COA2_POVBA
COA2_FOVBA
MERK RAT
UCK CAEEL
TURA HUMAN
COA2 POVHA
COA2 POVLY
CRTC HUMAN
ACHA BRARE
ENV_SRV1
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EPB3 MOUSE
PC12 MOUSE
CRTC MOUSE
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      P18418
P521913
O8k3h7
P15253
P15253
P215250
Q27979
Q98864
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Q91081
P24596
P03094
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P03097
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P04027
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P54754 mus musculu
O55134 mus musculu
P14211 mus musculu
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8 rattus norv
13 bos taurus
13 cricetulus
17 cricetulus
28 oryctolagus
29 bos taurus
29 bos taurus
4 homo sapien
4 brachydanio
                       1 pseudomonas
7 buchnera ap
6 mouse polyo
6 mouse polyomaviru
7 polyomaviru
1 padus morhu
1 gadus morhu
7 mouse polyo
6 mouse polyo
6 mouse polyo
6 mouse polyo
7 rattus nory
7 rattus nory
8 creponema p
7 rattus nory
8 creponema p
7 rattus nory
8 creponema p
1 hamster pol
1 lymphotropi
1 homo sapien
0 brachydanio
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45	44	43	42	41	40	39	38	37	36	35	34
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46.0	46.0	46.0	46.0	47.1	47.1	47.1	47.1	47.1	47.1	47.1	47.1
353	336	333	315	1203	1182	1112	1108	994	830	705	631
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COA2_POVBO	PTHB_CLOBE	OTC2_ECOLI	MIAA_BUCAI	PTC2_HUMAN	PTC2_MOUSE	CN3B_HUMAN	CYGF_HUMAN	MERK_MOUSE	SREC_HUMAN	MMLD_STRCO	PTBA_ERWCH
	032333 clostridium			Q9y6c5 homo sapien	035595 mus musculu	Q13370 homo sapien	P51841 homo sapien	Q60805 mus musculu	Q14162 homo sapien	Q9xa86 streptomyce	P26207 erwinia chr

## ALIGNMENTS

RESULT EPB3_M ID E AC P DT 0	문왕	M B Q	STITI	DR DR DR	ននននននន	CCRARR	80000	2 E 5 5 5 5	TD COT4_H
TT 2 MOUSE EPB3 MOUSE STANDARD; PRT; 993 AA. PS4754; Q62214; PS4754; Q62214; PS4754; Q62214;	1 MLPLLLGLLGPAACWA 16               1 MLPLLLGLLGPAACWA 16	Query Match 100.0%; Score 87; DB 1; Length 329; Best Local Similarity 100.0%; Pred. No. 4.6e-06; Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	pi	EMBL; AF329838; AAK17962.1; Genew; HGNC:14346; C1QTNF4. InterPro; IPR001073; C1q. Pfam; PF00386; C1q; 2. SMART; SM00110; C1Q; 2. PROSITE; PS01113; C1Q; 2. Repeat; Signal.	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).	necrosis factor-related pi nBank/DDBJ databases. ins.	Homo sapiens (Human).  Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.  NCBI_TaxID=9606;  1)	28-FEB-2003 (Rel. 41, Created) 28-FEB-2003 (Rel. 41, Last sequence update) 28-FEB-2003 (Rel. 41, Last annotation update) 28-FEB-2003 (Rel. 41, Last annotation update) Complement-clq tumor necrosis factor-related protein 4 precursor. CloTNF4 OR CTRP4.	HUMAN CQT4 HUMAN STANDAR Q9BXJ3;

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GO; GO:0008046; Fraxon guidance receptor ac GO; GO:0007411; Fraxon guidance; IDA.
InterPro; IPR001090; Ephrin receptor.
InterPro; IPR003961; FN III.
InterPro; IPR003962; FnIII subd.
InterPro; IPR003719; Prot kinase.
InterPro; IPR000719; Prot kinase.
InterPro; IPR001245; Tyr_pkinase.
InterPro; IPR001245; Tyr_pkinase.
InterPro; IPR001245; YKase_receptorV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Imondi R., wideman C., Kaprielian 2.;
"Complementary expression of transmembrane ephrins and their receptors in the mouse spinal cord: a possible role in constraining the orientation of longitudinally projecting axons.";
Development 127:11397-1410(2000)
-I- FUNCTION: RECEPTOR FOR MEMBERS OF THE EPHRIN-B FAMILY.
-I- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-BALB/c; TISSUE=Embryo; MEDLINE-96074837; PubMedc7478528; Ciossek T., Lerch M.M., Ullrich A.; Clossek T., Lerch M.M., ullrich A.; "Cloning, characterization, and differential expression of MDK2 and MDK5, two novel receptor tyrosine kinases of the eck/eph family."; Oncogene 11:2085-2095(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=BALB/c; TISSUE=Brain;
MEDLINE=95034306; PubMed=7947319;
Becker N., Seitanidou T., Murphy P., Mattei M.-G., Topilko Nieto A., Wilkinson D.G., Charnay P., Gilardi P.;
"Several receptor tyrosine kinase genes of the Eph family a segmentally expressed in the developing hindbrain.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-OCT-1996 (Rel. 34, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Ephrin type-B receptor 3 precursor (EC 2.7.1.11;
kinase receptor MDK-5) (Developmental kinase 5)
EPHB3 OR ETK2 OR MDK5 OR SEK4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 + +
                         Pfam; PF01404; EPH lbd; 1. Pfam; PF00041; fn3; 2. Pfam; PF00069; pkinase; 1. Pfam; PF00536; SAM; 1.
                                                                                                                                                                                                                                                                                                                                                                             or send an
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=20171264; PubMed=10704386;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE SPECIFICITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 719-993 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUBCELLULAR LOCATION: Type I membrane protein.
SUBCELLULAR LOCATION: Type I membrane protein.
TISSUE SPECIFICITY: EXPRESSED IN CELLS OF THE RETINAL GANG
CELL LAYER DURING RETINAL AXON GUIDANCE TO THE OPTIC DISK.
SIMILARITY: Contains 1 sterile alpha motif (SAM) domain.
SIMILARITY: Contains 2 fibronectin type III domains.
SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                            s SWISS-PROT entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the EN European Bioinformatics Institute. There are no resti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RECEPTOR SUBFAMILY.
                                                                                                                                                                                                                                                                                      I48653; I48653.
I48761; I48761.
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X76012; CAA53599.1;
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                                                                                                                                                                                                                                                                                                                                                                           requires a license agreement (See http://www.isb-sib.ch/announce/
an email to license@isb-sib.ch).
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                          pkinase; 1.
SAM; 1.
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                                                                                                                                                                                                                                        activity;
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Loutstation -
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Matches 11
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ProDom; PD000001; Prot Kinase; 1.
SMART; SM00615; EPH 1Dd; 1.
SMART; SM00615; EPH 1Dd; 1.
SMART; SM000160; FN3; 2.
SMART; SM00216; TyrKc; 1.
SMART; SM00216; TyrKc; 1.
SMART; SM00216; PXOTEIN KINASE ATP; 1.
PROSITE; PS00107; PROTEIN KINASE TYR; 1.
PROSITE; PS00109; PROTEIN KINASE TYR; 1.
PROSITE; PS001790; RECEPTOR_TYR_KIN_V_1;
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NP BIND
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DOMAIN
DOMAIN
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SIGNAL
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                             TISSUE=Brain capillary;

MEDLINE=98316322; PubMed=9651350;

Telo P. Breviario F. Huber P., Panzeri C., Dejana E.;

Telo P. breviario F. Huber P., Panzeri C., Dejana E.;

"Identification of a novel cadherin (vascular endothelial cadherin-2 located at intercellular junctions in endothelial cells.";

J. Biol. Chem. 273:17565-71572(1998).

-i- FUNCTION: Cellular adhesion molecule that may play an important role in cell-cell interactions at interendothelial junctions.
                                                                                                                                                                                                                                                                                                                                               28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Protocadherin 12 precursor (Vascular cadherin-2) (Vascular endothelial cadherin-2) (VE-cadherin-2) (VE-cad-2).
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DOMAIN
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Mammalia; Eutheria;
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                                                                                                                                                                                                       SEQUENCE FROM N.A
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                                                                                                                                                                                                                                                                                                            musculus (Mouse)
Promotes homotypic calcium dependent clusters at intercellular junctions.
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1 29 POTENTIAL
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RECEPTOR TYR KIN V 2; 1.
SAM DOMAIN; 1.
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Rodentia;
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PHOSPHORYLATION (AUTO-)

PHOSPHORYLATION (AUTO-)

PHOSPHORYLATION (AUTO-)

PHOSPHORYLATION (AUTO-)
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Pred. No. 0.42;
1; Mismatches
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N-LINKED (GLCNAC. . .)
R -> Q (IN REF. 2).
R -> Q OB66A4D391266C79 CR
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CYS-RICH.
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| (vascular endothelial cadherin-2)
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Unable to bind t
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STRAIN=BALB/C; TISSUE=Liv
STRAIN=BALB/C; TISSUE=Liv
MEDLINE=90059955; PubMed=
"mith M.J., Koch G.L.E.;
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                                                                                                                                       Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                Calreticulin
                                                                                                                                                                                                                                                                                        P14211;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                               Mus musculus
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InterPro; IPR002126; Cadherin.
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SUBCELLULAR LOCATION: Type I membrane protein.
TISSUE SPECIFICITY: Expressed in endothelial cells.
SIMILARITY: Contains 6 cadherin domains.
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GO:0008014; F:calcium-dependent cell adhesion molecule ac. .
n M.J., no
nle zones
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Sciurognathi; Muridae;
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               calreticulin (CRP55, calregulin,
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(POTENTIAL).
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PRINTS; PR00626; CALRETICULIN.

PRODOM; PD001866; CALRETICULIN; 1.

PROSITE; PS000014; ER_TARGET; 1.

PROSITE; PS00803; CALRETICULIN_2; 1.

PROSITE; PS00804; CALRETICULIN_REPEAT; 3.

PROSITE; PS00805; CALRETICULIN_ENDEAT; 3.
                                                                                                                                                                                          DISULFID
SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Merrick B.A., Patterson R.M., Wichter L.L., He C., Selkirk J.K.;
Merrick B.A., Patterson R.M., Wichter L.L., He C., Selkirk J.K.;
"Separation and sequencing of familiar and novel murine proteins
using preparative two-dimensional gel electrophoresis.";
Electrophoresis 15:735-745(1994).
-!- FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND
LOW AFFINITY CALCIUM-BINDING SITES.
-!- SUBUNIT: Monomer (By similarity).
-!- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen.
-!- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mazzarella R.A., Gold P., Cunningham M., Green M.; Determination of the sequence of an expressible of ERp60/calregulin by the use of a novel nested set renewed to the control of the cont
                                                                                                                                                                                                                                                        REPEAT
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EMBL; M92988; AAA37569.1;
PIR; S06763; S06763.
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TISSUE=Fibroblast;
MEDLINE=95009907;
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Mazzarella R.A., Gold
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InterPro; IPR000886; ER_target.
Pfam; PF00262; calreticulin; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     entities requires a license agreement (Some send an email to license@isb-sib.ch).
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8:3581-3586(1989).
                                                                                                     Similarity
                                          LPLLLGLLGPAA
VPLLLGLLGLAA
                                                                                                                                                                      416 AA;
                                                                                    Conservative
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P-DOMAIN.
C-DOMAIN.
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Pred. No. 13;
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                                                                                    Mismatches
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RESULT 5
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P18418; P10452;
01-MAR-1989 (Rel. 10, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Calreticulin precursor (CRP55) (Calregulin) (
                                                         [7]
SEQUENCE OF 18-32.
STRAIN=LEC; TISSUE=Liver;
MEDLINE=94072621; PubMed=8251535;
MEDLINE=94072621; PubMed=8251535;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE .....
STRAIN-Sprague-Dawley;
STRAIN-Sprague-Dawley;
MEDLINE-93202172; PubMed-8453984;
MEDLINE-93202172; PubMed-8453984;
Moriya M., Baba T., Michikawa Y., Yamanobe T., Arai K.,
                                                                                                                                                                                                                                                            MEDLINE-91054414; PubMed-2241926;
Treves S., de Mattei M., Lanfredi M., Villa A., Green N.M.,
Maclennan D.H., Meldolesi J., Pozzan T.;
"Calreticulin is a candidate for a calsequestrin-like function
Ca2(+) storage compartments (calciosomes) of liver and brain.",
Eiochem. J. 271:473-480(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Soennichsen B., Fuellekrug J., van Nguyen P., Diekmann W., Robinson D.G., Mieskes G., "Retention and retrieval: both mechanisms cooperate to maintain calreticulin in the endoplasmic reticulum."; J. Cell Sci. 107:2705-2717(1994).
   "Identification of protein disulfide isomerase and calreticuli autoimmune antigens in LEC strain of rats."; Biochim. Biophys. Acta 1158:339-344(1993).

-!- FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH
                                                                                                                                                                                         STRAIN-Sprague-Dawley; TISSUE-Testis; MEDLINE-92360010; PubMed-1497655; Nakamura M., Michikawa Y., Baba T., O
                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 270-358 FROM N.A.
STRAIN-Sprague-Dawley;
Lone Y.C., Bailly A., Latruffe N.;
Submitted (DEC-1988) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-Sprague-Dawley; TISSUE-Liver; MEDLINE-95181573; PubMed-7876339;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nakamura M., Moriya M., Baba T., M. Okinaga S., Kobayashi T.;
"An endoplasmic reticulum protein,
the acrosome of rat sperm.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Structural homology between the rat calreticulin gene product the Onchocerca volvulus antigen Ral-1."; Nucleic Acids Res. 18:4933-4933(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=Sprague-Dawley; TISSUB=Brain cortex; MEDLINE=90370496; PubMed=2395661; Murthy K.K., Banville D., Srikant C.B., Car Holmes C., Patel Y.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rattus norvegicus
                                                                                                                                                Biochem.
                                                                                                                                                                                                                                    SEQUENCE OF 18-32.
                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 18-29.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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                                                                                                                                                                          'Calreticulin is present in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cell Res.
                                                                                                                                               Biophys.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      205:101-110(1993).
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                                                                                                                                               Res.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (Rat).
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Rodentia;
                                                                                                                                               Commun.
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                                                                                                                                               186:668-673 (1992)
                                                                                                                                                                           T., Okinaga
acrosome of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 calreticulin,
                                                                        Kawaguchi
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                                                                                                                                                                                                                                                                               of liver and brain.";
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RESULT 6
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EMBL; X53363; CAA37446.1; -.
EMBL; X13702; CAA31987.1; ALT_SEQ.
EMBL; X79327; CAA55890.1; -.
PIR; JH0819; JH0819.
PDB; 1HHN; 26-PEB-02.
PDB; 1K91; 12-OCT-02.
InterPro; IPR00180; Calreticulin.
InterPro; IPR000806; Extraget.
Pfam; PF00262; calreticulin; 1.
PRINTS; PR00626; CALRETICULIN.
PRODOM; PD001866; GALRETICULIN.
PRODOM; PD001866; CALRETICULIN.
PROSITE; PS00004; ExTARGET; 1.
PROSITE; PS00004; CALRETICULIN 2; 1.
PROSITE; PS000805; CALRETICULIN 2; 1.
PROSITE; PS000805; CALRETICULIN 2; 1.
PROSITE; PS00805; CALRETICULIN 2; 1.
PROSITE; PS00805; CALRETICULIN 2; 1.
PROSITE; PS00805; CALRETICULIN REPEAT; 3.
Endoplasmic reticulum; Calcium-binding; Repe
                                                                   TCRT1 BOVIN
P52133; Q88Q53;
01-OCT-1996 (Rel. 34, Created)
28-FBB-2003 (Rel. 41, Last sec
28-FBB-2003 (Rel. 41, Last and
Calreticulin, brain isoform 1
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Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniat
Mammalia; Eutheria; Cetartiodactyla;
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the European Bioinformatics Institute. There are no rest
use by non-profit institutions as long as its content
modified and this statement is not removed. Usage by a
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                                                                 CALR OR CRT.
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SUBCELLULAR LOCATION: Endoplasmic reticulum lumen.
SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.
CAUTION: WAS ORIGINALLY (REF.2) THOUGHT TO BE D-BE
HYDROXYBUTYRATE DEHYDROGENASE.
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P-DOMAIN.
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Pred. No. 13;
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BY SIMILARITY.
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4 X APPROXIMATE
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  Craniata; Vertebrata; Eutel
actyla; Ruminantia; Pecora;
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InterPro; IPR000886; ER target.
Pfam; PF00262; calreticulin; 1.
PRINTS; PR00626; CALRETICULIN.
ProDom; PD001866; Calreticulin; 1.
PROSTITE; PS00014; ER TARGET; 1.
PROSITE; PS00803; CALRETICULIN 1; 1.
PROSITE; PS00804; CALRETICULIN 2; 1.
PROSITE; PS00805; CALRETICULIN 2; 1.
PROSITE; PS00805; CALRETICULIN 2; 3.
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Hossain M.A., Takuwa K., Minakata H., Nakajima T.;
"Bovine brain calreticulin.";
"Bovine brain calreticulin.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      modified and this statement is not removed. entities requires a license agreement (See or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Covalent structure of bovine brain Biochem. J. 298:435-442(1994).
                                                                                                                                                                                                                                                                              REPEAT
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                                                                                                                                                                                                                                                                                                                                                                     Endoplasmic
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NCBI_TaxID=9913;
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                                                                                                                                                       Å,
           STANDARD;
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K., Yamakkawa Y., Okuyama T., Shinoda T.,
of bovine brain calreticulin.";
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PREVENT SECRETION I
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           PRT;
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(Rel. 14, Creat (Rel. 14, Last

sequence update)

STANDARD;

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DISULFID
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PRODOM; PD001866; CALRETICULIN; 1.
PROSITE; PS00803; CALRETICULIN_2; 1.
PROSITE; PS00804; CALRETICULIN_2; 1.
PROSITE; PS00805; CALRETICULIN_REPEAT;
PROSITE; PS00014; ER_TARGET; 1.
                                                                                                                                                                                                      REPEAT
REPEAT
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CHAIN
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InterPro; IPR001580; Calreticulin.
InterPro; IPR000886; ER target.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chung J.Y., Lee G.M. Submitted (APR-2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cricetulus griseus (Chinese hamster).
Eukaryota; Metazoa; Chordata; Craniat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Calreticulin precursor CALR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00262; calreticulin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cricetulus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28-FEB-2003
28-FEB-2003
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                                                                                                                                                                                           REPEAT
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                                                                                                                                                                                                                                            REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          mitted (APR-2002) to the EMBL/GenBank/DDBJ databases. FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH LOW AFFINITY CALCIUM-BINDING SITES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIMILARITY: BELONGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUBCELLULAR
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                                                                                             . Similarity
                                                           LPLLLGLLGPAA 13
                                               VPLLLGLLGLAA 16
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3 (Rel. 41,
3 (Rel. 41,
                                                                                                                                           417 AA;
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                                                                                              Conservative
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                                                                                                                                             48242
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Rodentia; Sciurognathi; Muridae;
                                                                                                        51.7%;
83.3%;
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Last
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                                                                                                                                                                                                                                                                                                                            Calcium-binding; Repeat; Glycoprotein; Signal.
BY SIMILARITY.
CALRETICULIN.
N-DOMAIN.
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TO THE CALRETICULIN FAMILY.
                                                                                                                                              MW.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sequence update)
annotation update)
                                                                                             Score 45; DB
Pred. No. 13;
1; Mismatches
                                                                                              <u>,,</u>
                                                                                                                                           ASP/GLU/LYS-RICH.
BY SIMILARITY.
PREVENT SECRETION FROM ER
D617DA37D14F2D45 CRC64;
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; Cricetinae;
                                                                                                                                                         (POTENTIAL)
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-- FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BO-
-- LOW AFFINITY CALCIUM-BINDING SITES.
-- SUBUNIT: Monomer (By similarity).
-- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=91054414; PubMed=2241926; Treves S., de Mattei M., Lanfredi M., Villa A., Green N.M., Treves S., de Mattei M., Pozzan T.; Meldolesi J., Pozzan T.; Meldolesi J., Pozzan T.; Calreticulin is a candidate for a calsequestrin-like function Ca2(+)-storage compartments (calciosomes) of liver and brain."; Biochem. J. 271:473-480(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=90094320; PubMed=2600080; Fliegel L., Burns K., Maclennan D.H., Reithmeier R.A.F., Michalak M.; "Molecular cloning of the high affinity calcium-binding protein (calreticulin) of skeletal muscle sarcoplasmic reticulum."; J. Biol. Chem. 264:21522-21528(1989).
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Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Oryctolagus cuniculus (Rabbit)
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Calreticulin precursor (CRP55) (Calregulin) (HACBP)
   PRINTS; PR00626; CALRETICULIN.
PRODOM; PD001866; CALRETICULIN; 1.
PROSITE; PS008014; ER_TARGET; 1.
PROSITE; PS00803; CALRETICULIN_1; 1.
PROSITE; PS00804; CALRETICULIN_REPEAT;
PROSITE; PS00805; CALRETICULIN_REPEAT;
                                                                                                                                                                                                                                                                                                 EMBL; J05138; AAA31188.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- SUBCELLULAR LOCATION: Endoplasmic reticulum lum -!- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=92002038; PubMedd1911780; Guan S., Fallck A.M., Williams D.E., Cas "Evidence for complex formation between monooxygenase and calreticulin.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Milner R.E., Baksh S., Shemanko C., Co
Vance J.E., Opas M., Michalak M.;
"Calreticulin, and not calsequestrin,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=91201375; PubMed=2016321; Milner R.E., Baksh S., Shemanko C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 18-36.
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MEDLINE-91282795; PubMed-2059224;
Filegel L., Michalak M.;
"Fast-twitch and slow-twitch skeletal muscles express
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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InterPro; IPRO01580; Calreticulin.
InterPro; IPRO00886; ER target.
Pfam; PF00262; calreticulin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the European Bioinformatics Institute.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SWISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the EN European Bioinformatics Institute. There are no rest
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chem.
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een rabbit lung flavin-containing
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Viruses; Retroviridae; Betaretrovirus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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HSSP; P03385; 1MOF.
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-!- PTM: SPECIFIC ENZYMATIC CLEAVAGES IN VIVO YIELD MATURE PROTEINS.
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Pfam; PF00429; ENV_polyprotein; 1.
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                                                                        Polyprotein; Transmembrane COAT PROTEIN GP70. COAT PROTEIN GP20.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gardner M.B.,
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Simon A., Hellman U., Wernstedt C., Eriksson U.;

"The retinal pigment epithelial-specific 11-cis retinal dehydrogenase belongs to the family of short chain alcohol dehydrogenases.";

J. Biol. Chem. 270:1107-1112(1995).

-i- FUNCTION: STEREOSPECIFIC 11-CIS RETINOL DEHYDROGENASE, WHICH CATALYZES THE FINAL STEP IN THE BIOSYNTHESIS OF 11-CIS RETINALDEHYDE, THE UNIVERSAL CHROWOPHORE OF VISUAL PIGMENTS. ACTIVE IN THE PRESENCE OF NAD AS COFACTOR BUT NOT IN THE PRESENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CARBOHYD
SEQUENCE
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InterPro, adh BILLE.,
PEAM; PF00106; adh BILLE.,
PRINTS; PR00080; SDRFAMILY.
PRINTS; PR00081; ADH SHORT; FALSE NEG.
PROSITE; PS00061; ADH SHORT; FALSE NEG.
Oxidoreductase; NAD; Membrane; Vision.
Oxidoreductase; NAD; Membrane; Vision.
Oxidoreductase; NAD; Membrane; Vision.
Oxidoreductase; NAD; Membrane; PASTANILARITY.

Oxidoreductase; PASTANILARITY.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea
                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a observeen the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RDH1_BOVIN
Q27979;
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                                                                                                                                                                                                                                                                                                                                          entities requires a license agreement (See or send an email to license@isb-sib.ch).
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01-NOV-1997
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                                                                                                                                                                             InterPro; IPR002198; ADH short. Pfam; PF00106; adh short; 1.
                                                                                                                                                                                                                                                             EMBL; X82262; CAA57715.1; -. PIR; A55429; A55429.
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01-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
11-cis retinol dehydrogenase (EC 1.1.1.105) (
                                                                                                                                                                                                                                    HSSP; P14061;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CATALYTIC ACTIVITY: Retinol + NAD(+) = retinal + NADH.
PATHMAY: Retinoic acid biosynthesis; first (rate-limiting) step.
SUBCELLULAR IOCATION: Membrane-associated.
SIMILARITY: Belongs to the short-chain dehydrogenases/reductases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (SDR) family.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                        78B4A1E43E5FB351 CRC64;
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17;
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                                                                                                                                                                                                                                                                                                                                                                   http://www.isb-sib.ch/announce/
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무나원
                                                                                                  RC TISSUE=Embryo, and Placenta;
RA Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
RA Isogai T., Ota T., Hayashi K., Sugano S., Shiratori A., Sudo H.,
RA Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H.,
RA Nishikawa T., Nagai K., Sugano S., Murakawa K., Ono Y., Takiguchi S.,
RA Takahashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi S.,
RA Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K.,
RA Ninomiya K., Iwayanagi T.;
RA Ninomiya K., Iwayanagi T.;
RY "WEDO human CDNA sequencing project.";
RT "WEDO human CDNA sequencing project.";
RT "WEDO human CDNA sequencing project.";
RT "WEDO human CDNA sequencing project.";
CC -: FUNCTION: Cellular adhesion molecule that may play an important coll in cell-cell interactions at interandothelial junctions.
CC -: FUNCTION: Cellular junctions. Unable to bind to catenins, CC useakly associates with the cytoskeleton (By similarity).
CC -:- SUBCELLULAR LOCATION: Type I membrane protein.
CC -:- SUBCELLULAR EDCATION: Type I membrane protein.
CC -:- SUBCELLULAR SPECIFICITY: Expressed in highly vascularized tissues contain a low cc level of expression. Prominent expression in the spleen.
-- SIMILARITY: Contains 6 cadherin domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
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Best Local
             use by modified
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PC19FG4; Q96KB8; Q9H7Y6; Q9H8E0;

28-FEB-2003 (Rel. 41, Created)

28-FEB-2003 (Rel. 41, Last sequence update)

28-FEB-2003 (Rel. 41, Last annotation update)

Protocodherin 12 precursor (Vascular cadherin-2) (VB-cadherin-2) (VB-cadherin-2) (VB-cadherin-2)
                                             the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. Seki N., Hattori A., Hayashi "Human vascular cadherin-2.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=Fetal kidney;
MEDLINE=20515266; Pu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HUMAN
                                                           between
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mamm.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "cDNA cloning,
VE-cadherin-2."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pytowski B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 feature of protocadherin genes
Proc. Natl. Acad. Sci. U.S.A. S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Large exons encoding multiple ectodomains are a characteristic feature of protocadherin genes.";
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MEDLINE=20202599;
Wu Q., Maniatis T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PCDH12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM
           s SWISS-PROT entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the Ew European Bioinformatics Institute. There are no restr by non-profit institutions as long as its content ified and this statement is not removed. Usage by and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genome 11:1030-1033(2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           (APR-1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                515266; PubMed=11063261;
Lorenz J., Dejana E., B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      chromosomal mapping,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PubMed=10716726;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hayashi A.,
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Q98864;
30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Patched protein homolog 1 (Patched 1) (PTC1).
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EMBL; AF240635; AAF73962.1;
EMBL; AB026893; BAA95162.1;
EMBL; AK024140; BAB14837.1;
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                      Actinopterygii; Neopterygii; Cyprinidae; Danio. NCBI TaxID=7955;
                                                            Brachydanio rerio (Zebrafish) (Danio rerio).
Eukaryota; Metazoa; Chordata; Craniata; Vert
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CADHERIN 2.
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                                                 ; Craniata; Vertebrata; Euteleostomi; Teleostei; Ostariophysi; Cypriniformes;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
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-!- FUNCTION: ACTS AS A RECEPTOR FOR SONIC HEDGEHOG (SHH), INDIAN HEDGEHOG (IHH) AND DESERT HEDGEHOG (DHH). ASSOCIATES WITH THE SMOOTHENED PROTEIN (SMO) TO TRANSDUCE THE HEDGEHOG'S PROTEINS SIGNAL (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=96379744; PubMed=8787757; Concordet J.P., Lewis K.E., Moore J.W., Goodrich L.V., Johnson R.L. Scott M.P., Ingham P.W.; Ingham P.W.; "Spatial regulation of the zebrafish patched homologue reflects the roles of sonic hedgehog and protein kinase A in neural tube and somi patterning.";
                                                                        use by non-profit institutions as long modified and this statement is not removed.
or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                        INDUCTION: ACTIVATED BY SONIC HEDGEHOG. PTM: GLYCOSYLATION IS NECESSARY FOR SHH BINDING (BY SIMILARITY). SIMILARITY: BELONGS TO THE PATCHED FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         DEVELOPMENTAL STAGE: AT ALL STAGES, EXPRESSION CORRESPONDS TO LOCALIZATION OF SHH. FIRST DETECTED DURING GASTRULATION. BY 36 HOURS, PTC1 APPEARS IN THE FIRST BRANCHIAL ARCH AND THE POSTER MESSENCHYME OF THE FIN BUD; BY 48 HOURS, IN THE HINDBRAIN AND
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                                    license agreement
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                                    noved. Usage by and for commercial
(See http://www.isb-sib.ch/announce/
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InterPro; IPR004766; Patched\_
InterPro; IPR000731; SSD\_5TM. TRANSMEM TRANSMEM Transmembrane; TIGR00918; 2A060602; 1. 1017 1038 1045 1066 1066 1073 1094 1111 11132 11144 11144 1165 1165 865 506 529 550 580 740 106 420 441 450 Ā 484 505 549 549 579 579 7739 7760 1016 1016 1005 1006 1006 1009 1109 1113 1113 11143 135544 Glycoprotein POTENTIAL.

CYTOPIASMIC (POTENTIAL).

CYTOPIASMIC (SICNAC. . .) (F

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RESULT 14
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DT 15-SEP-2003
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28-FEB-2003 (Rel. 41, Last sequence
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Trans-aconitate 2-methyltransferase
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MEDLINE=20437337; PubMed=10984043;

Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P.

Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou

Garber R.L., Goltry L., Tolentino E., Westbrock-Waddman S., Yuan Y.

Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.

Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,

Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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Q910S1;
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PIR; H83325; H83325.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Complete genome sequence of Pseudomonas aeruginosa PAO1, opportunistic pathogen.";
Nature 406:959-964(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                    Transferase; Me
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -:- FUNCTION: Catalyzes the S-adenosylmethionine monomethyl
esterification of trans-aconitate (By similarity).
-:- CATALYTIC ACTIVITY: S-adenosyl-L-methionine + trans-aconitate = S-
adenosyl-L-homocysteine + (E)-3-(methoxycarbonyl)pent-2-enedicate.
-:- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
-:- SIMILARITY: BELONGS TO THE METHYLTRANSFERASE SUPERFAMILY. TAM
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InterPro; IPR000051; SAM_bind.
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RESULT 15
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Best Local S
Matches 7
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Tamames J., Viguera E., Latorre A., Valencia A., Moran F., Moya A.;
"Reductive genome evolution in Buchnera aphidicola.";
Proc. Natl. Acad. Sci. U.S.A. 100:581-586(2003).
-I- FUNCTION: Catalyzes the first step in the biosynthesis of 2-
methylthio-N6 (delta(2)-isopentemyl)-adenosine (MS[2]I[6]A])
adjacent to the anticodon of several tRNA species (By similarity).
-I- CATALYTIC ACTIVITY: Isopentenyl diphosphate + tRNA containing 6-isopentenyladenosine.
-I- SIMILARITY: BELONGS TO THE IPP TRANSFERASE FAMILY.
                                                                                                                                                                                                                                  01-MAR-1992 (Rel. 21, Created)
01-FEB-1996 (Rel. 33, Last sequence updat
15-SEP-2003 (Rel. 42, Last annotation upo
Coat protein VP2 (Contains: Coat protein
Mouse polyomavirus (strain Kilham).
Viruses; dsDNA viruses, no RNA stage; Pol
                                                                                                                                                                                                                                                                                                                                 COA2_POVMK
P24596;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AE014017; AA027217.1; -. HAMAP; MF_00185; -; 1. Transferase; Nucleotidyltransf
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Buchnera aphidicola (subsp. Baizongia pistaciae)
Bacteria; Proteobacteria; Gammaproteobacteria; E
Enterobacteriaceae; Buchnera.
                                             Mayer M., Doerries K.;
Submitted (APR-1992) to the
                                                                                                          "Nucleotide sequence and genome polyomavirus, Kilham strain."; Virology 181:469-480(1991).
                                                                                                                                                      MEDLINE=91196237; PubMed=1849675
Mayer M., Doerries K.;
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NP_BIND 21
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Van Ham R.C.H.J., Kamerbeek J., Pa
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                                                                             REVISIONS TO 58
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ALTERNATIVE PRODUCTS:
Event=Alternative initiation;
Comment=2 isoforms, VP2 (shown
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menez L., Postigo M., Silva F.
A., Valencia A., Moran F., Mc
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Best Local Similarity 90.0%;
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EMBL; M55904; AAA46555.1; -.
InterPro; IPR001070; Polyoma_coat2.
Pfam; pF00761; Polyoma_coat2; 1.
Late protein; Coat protein; Alternative initiation.
Late protein; Coat protein; Alternative initiation.
CHAIN
COAT PROTEIN VP2, ISOFORM VP2.
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                                                                                                                                                                                                                                                                                                   283 MLPLLLGLYG 292
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Q8C883
                                                                                                                                                                                                                                                                                                          Q8R066
Q91YS9
Q51537
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1873.686 Million cell updates
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Q8iv25 homo sapien
Q8r066 mus musculu
Q91ys9 mus musculu
Q91ys9 mus musculu
Q51537 pseudomonas
Q8c833 mus musculu
Q9v914 drosophila
Q9dcw1 mus musculu
Q9v14 drosophila
Q9dre8 lithobius f
Q8p3b9 xanthomonas
Q9ak63 streptomyce
Q967f2 caenorhabdi
Q8chq8 mus musculu
Q8uvm5 coppinus ci
Q8vpz9 simian retr
                                                                                                                                                                                                                                                                                                                                                                                                                                    Description
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49.4	4 4 0 4	4 4 0 4 4 4	9	49.4	49.4	49.4	49.4	49.4	49.4	49.4	50.6	50.6	50.6	50.6	50.6	•	•	50.6	•	•	51.1	51.7	•	•	51.7	•	•	51.7
225	3 6	2 0	225	225	213	159	119	119	100	74	1413	1187	553	521	517	297	177	175	101	253	232	628	602	488	395	347	315	309
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F90328	180167	עמיים אי	Q91NN7	Q91NM4	Q8NMT4	Q9RY14	Q9JVP6	Q9K0M1	Q9UGS8	Q84349	Q9DEF3	QBIUPB	Q9RUP7	Q8ETN6	Q9ZGB6	Q8H527	Q9RKE7	Q8GSU7	Q8IF11	Q8R9M1	Q89737	Q97J79	Q9VUJ3	Q9NI45	Q8PFI3	Q9Y6U7	Q9RU53	Q8UJY5
P90328 polyomaviru		Q8Jub/ polyomaviru		4.		Q9ry14 deinococcus		1 neis	5	simian v	Q9def3 xenopus lae	Q8iup8 homo sapien	Q9rup7 deinococcus	σ	ω	oryza sati	Q9rke7 streptomyce	7	rt	بر		Q97j79 clostridium	Q9vuj3 drosophila		3 xan	~	Q9ru53 deinococcus	Q8ujy5 agrobacteri

## ALIGNMENTS

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RESULT
QBR066
QBR066
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Best Local S
Matches 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE=Brain;
Strausberg R.;
Strausberg R.;
Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC035628; AAH35628:1; -.
EMBL; BC035628; AAH35628:1; -.
SEQUENCE 329 AA; 35256 MW; 16064DA8182A6732 CRC64;
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Similar to C1q and tumor necrosis factor related protein 4.
Homo sapiens (Human).
Eukarvors - Motosis - Mot
                                             QBR066, PRELIMINARY; PRT; 326 AA.
QBR066, QBR066; QBR0
Mus
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Q8IV25;
Q1-MAR-2003 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   _
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16; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; 1
tive 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 87; DB 4;
Pred. No. 2.4e-05;
Mismatches 0;
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Chordata;

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SORRE DE RESERVA
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Best Local S
Matches 14
          InterPro; IPR001090; Ephrin_receptor.
InterPro; IPR003962; FNIII subd.
InterPro; IPR003961; FN_III.
InterPro; IPR003961; FN_III.
InterPro; IPR001660; SAM_
InterPro; IPR001245; Tyr_pkinase.
InterPro; IPR001245; Tyr_pkinase.
InterPro; IPR001246; YKase_receptorv.
Pfam; PP00041; fn3; 2.
Pfam; PP00041; fn3; 2.
Pfam; PP00056; SAM; 1.
Pfam; PP00056; SAM; 1.
PRINTS; PR00014; FNTYPEIII.
PRINTS; PR000149; PYRKINASE.
ProDom; PD001495; Ephrin_receptor; 1.
PRINTS; PR00019; TyrKINASE.
ProDom; PD00109; TyrKINASE.
ProDom; PD000001; Prot kinase; 1.
SMART; SM00615; EPH 156; 1.
SMART; SM00619; EPH 156; 1.
SMART; SM00454; SAM; 1.
SMART; SM00454; SAM; 1.
PROSITE; PS00107; PROTEIN_KINASE_DOM; 1.
PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
PROSITE; PS00790; RECEPTOR_TYR_KIN_V_1;
PROSITE; PS00791; RECEPTOR_TYR_KIN_V_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q91YS9 PRELIMINARY; FKI; 737 AAA.
Q91YS9,
Q119B9,
Q1-DEC-2001 (TrEMBLrel. 19, Created)
Q1-DEC-2001 (TrEMBLrel. 19, Last sequence update)
Q1-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Similar to EphB3 (EC 2.7.1.112) (Ephrin receptor) (Tyrosine-protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (APR-2002) to the EMBI EMBL; BC027315; AAH27315.1; -. MGD; MGI:1914695; 0710001E10Rik. InterPro; IPR001073; C1q.
                                                                                                                                                                                                                                                                                                                                                                           -!- SUBCELLULAR LOCATION: TO RECEPTOR SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00386; Clq; 2.
SMART; SM00110; ClQ; 2.
PROSSITE; PS00113; ClQ; 2.
SEQUENCE 326 AA; 35057 MW;
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NCBI_TaxID=10090;
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Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EPHB3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                 EMBL; BC014822; AAH14822.1; -. MGD; MGI:104770; Ephb3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Strausberg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     w
                                                                                                                                                                                                                                                                                                                                                                                                                     mitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE = ADP +
TYROSINE PHOSPHATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14;
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RECEPTOR_TYR_KIN_V_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chordata;
Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rodentia;
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87.5%;
                                                                                                                                                                                                                                                                                                                                                                                          TYPE
O THE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 73;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
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TYR FAMILY
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                                                                                                                                                                                                                                                                                                                                                                                                         PROTEIN (BY SIMILARITY)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Murinae; Mus
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Best Local S
Matches 11
                                                                                                P SEQUENCE FROM N.A.

C STRAIN=ATCC 15692 / PAO1;
C STRAIN=ATCC 15692 / PubMed=10984043;
X MEDLINE=20437337; PubMed=10984043;
A Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener A. Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagro A. Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan B. Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R. A. Brody L.L., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T., Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T., A. Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.;
T' "Complete genome sequence of Pseudomonas aeruginosa PAO1, an Opportunistic pathogen.";
Li Nature 406:959-964(2000).
R EMBL; L76605; AAA93503.1; -.
 Matches
            Query Match
Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q51537 PRELIMINARY;
Q51537;
Q51537;
Q1-NOV-1996 (TrEMBLrel. 01, C
Q1-NOV-1996 (TrEMBLrel. 01, L
Q1-DEC-2001 (TrEMBLrel. 19, L
Type 4 fimbrial biogenesis pr
                                                                                                                                                                                                                                                                                                             Alm R.A.,
Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATP-binding; Glycoprotein; Kinase; Phosphorylation; Receptor; Repeat; Transferase; Transmembrane; Tyrosine-protein kinase.
SEQUENCE 993 AA; 109661 MW; 07C6EF2AC98AE1B4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                 "Identification of a gene, pily, required for type 4 fimbrial biogenesis in Pseudomonas aeruginosa, whose product possesses pilin-like leader sequence.";
                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN-ATCC 15692 / PAO1;
MEDILINE=96037793; PubMed=7565109;
Alm R.A., Mattick J.S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN-ATCC 15692 / PAO1;
MEDLINE-95157261; PubMede7854130;
RUSSell M.A., Darzins A.;
                                                           Complete proteome. SEQUENCE 115 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "The pilE gene product of Pseudomonas aeruginosa, required biogenesis, shares amino acid sequence identity with the N-type 4 prepilin proteins.";
Mol. Microbiol. 13:973-985(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        type 4 prepilin Mol. Microbiol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Proteoar{b}acteria; Gammaproteobacteria; Pseudomonadales; Pseudomonadaceae; Pseudomonas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pseudomonas aeruginosa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PILY2 OR PA4555.
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                                                                                                                                                                                                                                                                                                                                            STRAIN-ATCC
                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                     Mol. Microbiol. 16:485-496(1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4
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                                                                                       AE004869; AAG07943.1; -.
Similarity
9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
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                                                                                                                                                                                                                                                                                                             CC 15692 / PAO1;
Hallinan J.P., Watson A.A., Mattick J.S.;
(APR-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      65.5%;
68.8%;
                                                           12986 MW;
            59.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             , Last sequence update), Last annotation updat protein PILY2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Created)
Score 52; DB
Pred. No. 1.9;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 57; Pred. No.
2
                                                           AC19C31640473181 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          115
             DB
1.9;
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2.4;
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                              16;
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                             Length 115;
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   Indels
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1 S., Yuan Y.,
K., Lim R.M.,
                                                                                                                                                                                                                                        Warrener P.
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RA Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,
RA Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,
RA Alves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.E.A.,
RA Camarotte G., Cannavan F., Cardozo J., Chambergo F., Ciapina L.P.,
RA Camarotte G., Cannavan F., Cardozo J., Chambergo F., Ciapina L.P.,
RA Ciarelli R.M.B., Coutinho L.L., Cursino-Santos J.R., El Dorry H.,
RA Faria J.B., Ferreira A.J.S., Ferreira R.C.C., Ferro M.I.T.,
RA Formighieri E.F., Franco M.C., Greggio C.C., Gruber A.,
RA Katsuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,
RA Katsuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,
RA Martins E.C., Machado M.A., Madeira R.P., Lemos E.G.M., Lemos M.V.F.,
RA Martins E.C., Meidanis J., Menck C.F.M., Miyaki C.Y., Moon D.H.,
RA Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,
RA Moreira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.F.,
RA Spinola L.A.F., Takita M.A., Tamura R.E., Teixeira B.C., Tezza R.I.D.,
RA Spinola L.A.F., Takita M.A., Tamura R.E., Teixeira B.C., Tezza R.I.D.,
RA Setubal J.C., Kitajima J.P.;
Nasura S. M., White F.F.,
Nasura S. M., Sana S. M., White F.F.,
Nasura S. M., Sana S. M., White F.F.,
Nasura S. M. S. M., White F.F
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Q8C883;
01-MAR-2003
01-MAR-2003
01-MAR-2003
                                                                                                                                                                                                                                                                                                   )l-Mus
Protocadherin ...
Mus musculus (Mouse).
Mus musculus (Mouse).
Metazoa; Chordata;
Metazoa; Rodentia;
the RIKEN Genome Exploration Research Group Phase I & II Team; "Analysis of the mouse transcriptome based on functional annotation 60,770 full-length cDNAs."; Nature 420:563-573(2002).
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                                                                                                                                SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Head;
MEDLINE=22354683; PubMed=12466851;
The FANTOM Consortium,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL;
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STRAIN=ATCC 33913 / NCPPB
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Bacteria; Proteobacteria; Gamm
Xanthomonadaceae; Xanthomonas.
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XCC0653.
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01-OCT-2002
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AE012163; AAM39969.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ll protein; Complete
155 AA; 17448 MW;
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(TrEMBLrel. 22, Last sequence update)
(TREMBLrel. 22, Last annotation update)
protein XCC0653.
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Last
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
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RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.M., Ra George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.M., Ra Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Ra Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D., Ra Brandon R.C., Moyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G., RA Abril J.F., Agbayani A., An H.-J., Andrews Pfannkoch C., Baddwin D., Ra Ballew R.M., Basun A., Baxendale J., Bayraktaroglu L., Beasley E.M., Ra Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P., Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I., RA Borkova D., Botchar A., Dan, Burler H., Cadieu E., Center A., Chandra I., Ra Gebrer G., Bouck J., Brokstein P., Brottier P., Ra Dodson K., Doup L.E., Downes M., Duyan-Rocha S., Dunkoy B.C., Dunn P., RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., Ra Gebric C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K., Cholon K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W., Ra Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M., Ra Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J., Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibeywam C., Jalai M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A., Alion M., Kalush F., Karpen G.H., Ke Z., Kunison J.A., Ketchum K.A., Alion N., Murphy B., Mur
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Best Local (
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01-MAY-2000
01-MAY-2000
01-MAR-2003
                                                                               Zneng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.; "The genome sequence of Drosophila melanogaster."; Science 287:2185-2195(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygo
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AK048100; BAC33242.1; -. SEQUENCE 998 AA; 109373 MW;
                                                                       EMBL; AE003784; AAF57274.1;
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Amanatides P.G.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Drosophila melanogaster
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                                   FBgn0033068; CG11212; IPR003392; Patched.
                   IPR006162;
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P.G., Scherer S.E., Li P.W.,
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Ppantne_attach.
SSD_5TM.
                                                      CG11212.
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..A., Galle
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Smith H.O.,
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RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Pukuda S.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Pukuda S.,
RA Arakawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaio I., Pesole G., Quackenbush J.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaio I., Fosole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Havashizaki Y.;
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                                                                                                                                                                                                                                                                                                                                                                                                                              Nature 409:685-690(2001).
-!- SIMILARITY: CONTAINS 1 RING-TYPE
EMBL; AK002414; BAB22082.1; -.
HSSP; P28990; 1CHC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9DCW1;
01-JUN-2001
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PROSITE; PS001012; PHOSPHOPANTETHEINE; 1.
PROSITE; PS59156; SSD; 1.
SEQUENCE 1061 AA; 120880 MW; DC6F322
                                                                                                                                                                                                                           SMART; SM00184; RING; 1.
PROSITE; PSS0089; ZF RING; 2; 1.
Metal-binding; Zinc; Zinc-finger.
SEQUENCE 379 AA; 41577 MW; DA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JUN-2001
01-MAR-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus (Mouse)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                      MGD; MGI:1918923; 0610009J22Rik.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Functional annotation of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hayashizaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8
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                                                                                                            Similarity
9; Conserv
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LLPLWLGLMGPGA 43
                                                      MLPLLLGLLGPAA 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (TrEMBLrel. 17, (TrEMBLrel. 23,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (TrEMBLrel. 17,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=Kidney;
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Rodentia;
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57.1%;
                                                                                                                                          55.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Created)
Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                full-length mouse cDNA
                                                                                                                                          Score 48; DB
Pred. No. 23;
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                                                                                                                                                                                                                                 DA36AA22623E3901 CRC64;
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                                                                                                                                                                     Length 379;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      collection.";
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RESULT 9 Q94RE8

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RESULT 10
Q8P3B9
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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

CONTRAINATICC 33913 / NCDPB 528;

REDLINE=22022145; PubMed=12024217;

REDLINE=22022145; PubMed=120
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Best Local
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InterPro; IPR001750; Oxidored_q1.
InterPro; IPR001516; Oxidored_q1.
InterPro; IPR006162; Ppantne_attach.
Pfam; PF00361; oxidored_q1; 1.
Pfam; PF000662; oxidored_q1, 1.
PRINTS; PR01434; NADHDHGNASE5.
PROSITE; PS00012; PHOSPHOPANTETHEINE; 1.
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Q94RE8;
01-DEC-2001
01-DEC-2001
01-MAR-2003
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01-OCT-2002
01-OCT-2002
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NON TER
SEQUENCE
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EMBL; AJ270997; CAC69943.1; -.
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Pleurostigmophora; L
NCBI_TaxID=7552;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Xanthomonas campestris (pv. campestris).
Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mitochondrion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NADH dehydrogenase
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XCC4157.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=340;
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(TrEMBLrel. 19, Last sequence update)
(TrEMBLrel. 23, Last annotation update)
ogenase subunit 5 (Fragment).
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ch M., Choe C., Kim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Xanthomonas.
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Last annotation update)
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RESULT 12
Q967F2
ID Q967F
AC Q967F
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DT 01-JU
DT 01-MA
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DE manno
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Best Local S
Matches 11
                                                                     Q967F2;
Q967F2;
01-DEC-2001
01-JUN-2002
01-MAR-2003
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SEQUENCE
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Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Kieser H.,
Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neil S.,
Rabbinowitsch E., Rajandream M.A., Rutherford K., Rutter S.,
Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.
Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Putative integral membrane protein.
SCO4054 OR 2SCD60.20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q9AK63
Q9AK63;
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Trindade dos Santos M., Truir
J.C., Kitajima J.P.;
                                       01-DEC-2001 (TrEMBLrel. 19, Created)
01-JUN 2002 (TrEMBLrel. 21, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation updat
Hypothetical 57.2 kDa protein (Putative alpha 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Complete genome sequence of the coelicolor A3(2).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Streptomyces coelicolor.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
mannosyltransferase).
T27F7.3 OR PIG-B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nature 417:141-147(2002).
EMBL; AL939118; CAC32325.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=A3(2) / M145;
MEDLINE=21996410; PubMed=12000953;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Streptomycineae; Streptomycetaceae; Streptomycetaceae; NCBI_TaxID=1902;
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Nature 417:459-463 (2002).
EMBL; AE012541; AAM43373.1; ...
InterPro; IPR001823; Ald1_epimerase.
Pfam; PF01263; Aldose_epim; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hopwood D.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Complete proteome. SEQUENCE 719 AA;
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9; Conser
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Pred. No. 29;
1; Mismatches
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Pred. No. 70;
0; Mismatches
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Tsai S.M., White F.F.,
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Best Local S
Matches
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Best Local S
Matches 7
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QBCHQB;
Q1-MAR-2003 (TrEMBLrel. 23, Created)
Q1-MAR-2003 (TrEMBLrel. 23, Last sequence update)
Q1-MAR-2003 (TrEMBLrel. 23, Last sequence update)
Q1-MAR-2003 (TrEMBLrel. 23, Last sequence update)
Similar to N-acetylglucosamine-1-phosphodiester
alpha-N-acetylglucosaminidase.
Mus musculus (Mouse).
                                                                                                                                              Strausberg R.;
Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC039790; AAH39790.1; -.
SEQUENCE 517 AA; 56013 MW; 80F6E9AFB3873177 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Oriol R., Martinez-Duncker I., Chantret I., Mollicone R., ("Common origin and evolution of glycosyltransferases using monosaccharides as donor substrate.";
Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN=Bristol N2;
MEDLINE=99069613; PubMed=9851916;
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Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium."; Science 282:2012-2018(1998).
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                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=10090;
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Pro; IPR005599; PMP.
PF03901; PMP; 1.
hetical protein; Glycosyltransferase; Transferase.
hetical protein; Glycosyltransferase; Transferase.
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                                                Similarity 64.: 9; Conservative
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  MLPLLLGLLGPAAC
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Rodentia;
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EMBL/GenBank/DDBJ databases
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Pred. No.
                                                                       Score 46;
Pred. No.
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RESULT 14
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IDD Q8BJ4
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Q9UVM5
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Best Local Similarity
Thes 9; Conserve
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Query Match
Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                     PROSITE; PS5085
Transmembrane.
SEQUENCE 558
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Q9UVM5;
01-MAY-2000
01-MAY-2000
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MEDLINE=22354683; PubMed=12466851;

The FANTOM Consortium,

the RIKEN Genome Exploration Research Group Phase I & II Team;

"Analysis of the mouse transcriptome based on functional annotation
60,770 full-length cDNAs.";

Nature 420:533-573(2002)

NATURE 420:533-573(2002)
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Q8BJ48;
Q1-MAR-2003 (TrEMBLrel. 23, Created)
O1-MAR-2003 (TrEMBLrel. 23, Last sequence update)
O1-MAR-2003 (TrEMBLrel. 23, Last annotation update)
O1-MAR-2003 (TrEMBLrel. 23, Last annotation update)
N-acetylglucosamine-1-PHOSEHODIESTER
                                                                                                                                                                                                                                                                                   -- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
EMBL; AF186392; AAF01427.1; -.
InterPro; IPR007114; MFS.
InterPro; IPR005828; Sub_transporter.
InterPro; IPR001411; TCR TetB.
Pfam; PF00083; sugar_tr; 1.
Pfam; PF00083; TCRTETB.
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MFS1.2.
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Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;
Agaricales; Psathyrellaceae; Coprinopsis.
NCBI_TaxID=5346;
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Three Subfamilies of Pheromone and Receptor Genes Generate Multiple Mating Specificities in the Mushroom Coprinus cinereus."; Genetics 154:1115-1123(2000).
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Halsall J.R., Milner M.J., Casselton L.A.;
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                                                                                                                                                                     59446 MW;
    52.9%; Score 46; DB 3; Length 558; 53.3%; Pred. No. 66; tive 4; Mismatches 3; Indels
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  04-APR-2001
                                                                    Holtzman DA,
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TANGO; MANGO; colon; inflammation; tumor; renal; liver; lung;
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AABC 245 signal peptide #2.
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AABC 245 signal peptide #2.
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AABC 245 signal peptide #2.
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AABC 245 proteins, useful in the treatment of inflammatory diseases
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02-MAY-2001;
29-MAY-2001;
24-JUL-2001;
10-AUG-2001;
          Gangolli |
Stone DJ,
                                                                                                                                                                                                                                                                                                                                                    obesity; diabetes; infectious disease; neurodegenerative disorder; acne; Alzheimer's disease, Parkinson's disease; immune disorder; cancer; haematopoietic disorder; cirrhosis; pancreatitis; learning defect; memory defect; infertility; congenital heart defect; hair growth; pigmentation disorder; endocrine disorder; respiratory disease; health; gastro-intestinal disease; reproductive; neurological disease; health; bone marrow transplantation; endocrine disease; allergy; inflammation; nephrological disorder; urinary system disorder; age-related disorder; neuropsychiatric disorder; EGF-related, SCUBBI; TEN-M4; adipocyte complement-related City tumour necrosis factor; out at first; beta adrenergic receptor kinase; Ephh6/ehk-2; glucose transporter; type la membrane sushi-containing domain; butyrophilin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention relates to cDNAs encoding TANGO 244, TANGO 246, TANGO 275, TANGO 300 and MANGO 245 proteins.

The nucleic acids, proteins and protein modulators are useful for treating colonic disorders, inflammatory diseases, tumors, renal disorders, liver disorders, lung disorders, autoimmune diseases, allergic diseases, cardiovascular diseases, brain disorders, degenerative diseases placental, pancreatic, skeletal and muscle
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29-AUG-2001;
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          n M, Vernet CAM, Malyank
Shimkets RA, Burgess CE,
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          Zerhusen BD,
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XX Huma
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cell signal processing; metabolic pathway modulation; metabolic disorder; obesity; diabetes; infectious disease; neurodegenerative disorder; acne; Alzheimer's disease; Parkinson's disease; immune disorder; cancer; haematopoietic disorder; cirrhosis; pancreatitis; learning defect; memory defect; infertility; congenital heart defect; hair growth;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; NOVX; NOVX-associated disorder; cardiomyopathy; atherosclerosis;
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2.9e-06;
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Best Local S
Matches 16
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20-DEC-2000;
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Alzheimer's disease; Parkinson's disease; immune disorder; cancer; haematopoietic disorder; cirrhosis; pancreatitis; learning defect; haematopoietic disorder; cirrhosis; pancreatitis; learning defect;
                                              cell signal processing; metabolic pathway modulation; metabolic disobsity; diabetes; infectious disease; neurodegenerative disorder;
                                                                              Human; NOVX; NOVX-associated disorder;
                                                                                                            Adipocyte complement-related
                                                                                                                                            05-NOV-2002
                                                                                                                                                                                                         ABG70385 standard; Protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                     284 AA;
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2001US-311590P.
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Iderson D, Si
Basman SJ, B
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Shimkets RA, Burgess CE, Zerhusen
Boldog FL, Smithson G, Li L, Ji W
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                                                                                                            Clq Tumour Necrosis Factor-like protein #3.
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Pred. No. 6.7e-06;
                                                                            cardiomyopathy; atherosclerosis;
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sen BD, Liu
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MLPLLLGLLGPAACWA 16 MLPLLLGLLGPAACWA

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Query Match Best Local : Matches

Similarity

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Score 87; DB 23 Pred. No. 7e-06; Mismatches

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CC useful for treating or preventing a NOVX-associated disorder such as CC cardiomyopathy or atherosclerosis, where the disorder is related to cell company that the control of the disorder is related to cell company that the control of the disorder is related to cell company that the control of the disorder is related to cell company that the control of the contro
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10-AUG-2001;
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DB; ABS52097.
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Shimkets RA, Burgess CE, Zerh
Boldog FL, Smithson G, Li L,
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                                          Human; zacrp4; complement factor Clq domain; chromosome 11q11; energy balance; cellular metabolic reaction; autocrine factor; development; cell proliferation; differentiation; cell survival
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention relates to cDNAs encoding TANGO 244, TANGO 246, TANGO 275, TANGO 300 and MANGO 245 proteins. TANGO 275 proteins are useful for The nucleic acids, proteins and manual actors are useful for treating colonic disorders, inflammatory diseases, tumors, renal disorders, liver disorders, lung disorders, autoimmune diseases, allergic diseases, cardiovascular diseases, brain disorders, allergic diseases, cardiovascular diseases, brain disorders,
                                                                                                         Human ZACRP4
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                                                                                                                                                                                                  AAB61606 standard;
                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                         degenerative diseases placental, pancreatic, skeletal and muscle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; Fig 25; 262pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Isolated cDNAs encoding TANGO 244, TANGO 246, TANGO 275, TANGO 300 and MANGO 245 proteins, useful in the treatment of inflammatory diseases (e.g. idiopathic ulcerative colitis), tumors, renal disorders and liver disorders (e.g. jaundice) -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Catarrhini sp..
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               Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Monkey MANGO 245 protein.
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                                                                                                                                                                                                                                                                           MLPLLLGLLGPAACWA 16
                                                                                                                                                                                                                                                                                                       WIPLIEGLIGPAACWA 16
                                                                                                                                                                                                                                                                                                                                                                                               329 AA;
                                                                                                                                                                                                                                                                                                                                   100.0%; Score 87; ilarity 100.0%; Pred. No. Conservative 0; Mismatch
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                                                                                                                                                                                                 Protein; 329
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                                                                                                                                                                                                                                                                                                                                     7.8e-06;
hes 0;
                                                                                                                                                                                                                                                                                                                                                                   DB 22;
                                                                                                                                                                                                                                                                                                                                                               Length 329;
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ABG79643
ID ABG7
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AC ABG7
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DT 15-A
DX
Huma
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Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence is human ZACRP4 protein. ZACRP4 protein has two complement factor C1q domains. The ZACRP4 gene is located on human chromosome l1q11. The ZACRP4 coding sequence and protein have a number of uses described in the specification, including, modulatation of energy balance and cellular metabolic reactions in mammals. In addition, ZACRP4 protein is useful as an autocrine factor, particularly during development, in mediating the processes of an organism, in regulating cellular processes such as cell proliferation and/or differentiation, cell survival and energy balance.
                                                                                                                 hypertensive heart disease; neurological disorder; cerebral neoplasm, Alzheimer's disease; developmental disorder; renal tubular acidosis; Cushing's syndrome; Duchenne muscular dystrophy; hypothyroidism;
                                                                                                                                                                                                          Human; SECP; secreted protein; cell proliferative disorder; actinic keratosis; arteriosclerosis; bursitis; hepatitis; cancer; autoimmune disorder; inflammatory disorder; AIDS; asthma; allergy; acquired immunodeficiency syndrome; anaemia; atopic dermatitis; cardiovascular disorder; congestive heart failure; vascular tumour; ischaemic heart disease; myocardial infarction; epilepsy; stroke; schaemic heart disease; myocardial infarction; epilepsy; stroke;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Key
                                                                                           Becker muscular dystrophy
                                                                                                                                                                                                                                                                                                                                                                                                                             Human novel secreted protein SECP19, Incyte ID No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABG79643 standard; Protein; 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2001-138140/14.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
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17..159
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160..328
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Pred. No. 7.8e-06;
; Mismatches 0;
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Homo sapiens

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RESULT 8
AAB61423
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Best Local Similarity
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Xu Y, 1
Lee EA,
                                                                                                                                                                                                                                                                                                                                                                          useful in the diagnosis, treatment and prevention of cell proliferative (e.g. actinic keratosis, arteriosclerosis, bursitis, hepatitis or cancer), autoimmune/inflammatory (e.g. AIDS (acquired immunodeficiency syndrome), asthma, anaemia, allergies or atopic dermatitis), cardiovascular (e.g. congestive heart failure, ischaemic heart disease, myocardial infarction, hypertensive heart disease, or vascular tumours), neurological (e.g. epilepsy, stroke, cerebral neoplasms, or Alzheimer's disease), and developmental (e.g. renal tubular acidosis, Cushing's syndrome, Duchenne and Becker muscular dystrophy, or hypothyroidism) disorders. Many other diseases and disorders are listed in the specification. These may also be used in assessing the effects of exogenous compounds on the expression of nucleic acid and amino acid sequences of the secreted proteins. The present sequence represents a RECP protein of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to twenty four human secreted proteins (SECP1-24), proteins 90% identical to them and active fragments of them. Also included are nucleic acids encoding the SECP proteins, a recombinant polynucleotide comprising a promoter sequence operably linked to the nucleic acid, a cell transformed with the recombinant polynucleotide, a transgenic organism comprising the recombinant polynucleotide, an anti-SECP antibody, and screening for ant/agonists and modulators of SECP function or expression. The SECP proteins and mucleic acids are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New human secreted proteins and nucleic acids useful in diagnosing, treating and preventing cell proliferative, autoimmune/inflammatory, cardiovascular, neurological, and developmental disorders -
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07-SEP-2001;
                                                                                                                                                                                                                                                                                                                                  Sequence
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08-FEB-2001;
               Human MANGO 245 protein.
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                                                 04-APR-2001
                                                                                                              AAB61423 standard; protein; 348 AA
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Yang ,
                                                                                                                                                                                                                                                                                                                                                                   protein of the invention.
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ang J, Thangavelu
Richardson TW, Ba
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2001US-271639P.
2001US-317818P.
2001US-343553P.
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                                                 (first entry)
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2001US-267816P.
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elu K, Lal PG,
Baughn MR, E
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                                                                                                                                                                                                                                                                Score 87; DB 23;
Pred. No. 7.8e-06;
); Mismatches 0;
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Honchell CD,
Elliott VS;
                                                                                                                                                                                                                                                                                                 Length 329;
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D, Walia NK,
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RESULT 9
AAB61488
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Best Local S
Matches 16
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                                                                                                                                                                                         04-JAN-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Murine MANGO
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pancreatic; skeletal; muscle.
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                                                                                29-JUN-1999;
                                                                                                                                      29-JUN-2000; 2000WO-US18184
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                                                                                                                                                                                                                                                                                                      Mus musculus.
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16; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      245 protein.
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Pred. No. 8.3e-06;
; Mismatches 0;
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(MILL-) MILLENNIUM PHARM INC

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Best Local Similarity
Matches 14; Conserv
    The present invention relates to cDNAs encoding TANGO 244, TANGO 246, TANGO 275, TANGO 300 and MANGO 245 proteins.

The nucleic acids, proteins and protein modulators are useful for treating colonic disorders, inflammatory diseases, tumors, renal disorders, liver disorders, lung disorders, autoimmune diseases.
                                                                                                                                                    Isolated cDNAs encoding TANGO 244, TANGO 246, TANGO 275, TANGO 300 and MANGO 245 proteins, useful in the treatment of inflammatory diseases (e.g. idiopathic ulcerative colitis); tumors, renal disorders and liver disorders (e.g. jaundice) -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention relates to cDNAs encoding TANGO 244, TANGO 246, TANGO 275, TANGO 300 and MANGO 245 proteins.

The nucleic acids, proteins and protein modulators are useful for treating colonic disorders, inflammatory diseases, tumors, renal disorders, liver disorders, lung disorders, autoimmune diseases, allergic diseases, cardiovascular diseases, brain disorders, degenerative diseases placental, pancreatic, skeletal and muscle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TANGO; MANGO; colon; inflammation; tumor; renal; liver; lung; autoimmune; allergy; cardiovascular; brain; degenerative; placental; pancreatic; skeletal; muscle.
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                                                                                                                    Disclosure; Page 242; 262pp; English.
                                                                                                                                                                                                                                                          WPI; 2001-050127/06.
                                                                                                                                                                                                                                                                                                Holtzman
                                                                                                                                                                                                                                                                                                                                                                                                              29-JUN-2000; 2000WO-US18184
                                                                                                                                                                                                                                                                                                                                                                                                                                                    04-JAN-2001.
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                                                                                                                                                                                                                                                                                                                                  (MILL-) MILLENNIUM PHARM INC
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                                                                                                                                                                                                                                                                                            DA,
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87.5%;
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Pred. No.
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0.00082;
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      autoimmune diseases
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Sequences AAY52377-Y52385 are involved in pilus synthesis and motility and are required for biofilm formation by Pseudomonas aeruginosa. The CC formation of bacterial biofilms occurs when bacteria make the transition from a planktonic (free swimming) existence to a lifestyle in which the microorganisms are firmly attached to biotic or abiotic surfaces. This cransition is thought to be regulated in part by the mutritional status of the environment and is accompanied by a change in gene expression cc patterns, cellular physiology and higher resistance to antibiotics relative to planktonic bacterial counterparts. Pilus synthetic and contility genes, gene products, and transcriptional control regions may call be used for the control of biofilm formation in fields such as manufacturing, agriculture, and healthcare. The products may also be used to identify compounds which modulate biofilm formation. Compounds that stimulate biofilm formation can be used to improve colonisation of plant roots by beneficial bacteria (e.g., nitrogen fixing bacteria). Cc conversely, compounds that inhibit biofilm formation can be used to restrict the growth of bacteria on contact lenses, medical implants ce.g., artificial hips), the walls of catheters, fluid contacting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                pilus; motility; biofilm; biotic surface; abiotic surface;
nutritional status; environment; gene expression; cellular physiology;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Isolated surface attachment defective genes, useful for developing
products which modulate bacterial biofilm formation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         O'Toole
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02-OCT-1998;
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98US-0102870.
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3. 6.8e-05;
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                                                                                                                                                             The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL101840-ABL16175) and the encoded proteins (ABB7037-ABB72072).
                                                                                                                                                                                                                                                                                                                      New isolated nucleic acid genes from Drosophila and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Drosophila melanogaster polypeptide SEQ ID NO 23451.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            surfaces of industrial devices, water and sewerage pipes, and within the lungs of infected patients. The inhibitor compounds can also be applied to soil, seeds or plant roots to inhibit bacterial growth.
                                                                                                  Sequence
                                                                                                                                                                                                                                                                                 Disclosure; SEQ ID NO 23451; 21pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200171042-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Drosophila melanogaster.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABB65553 standard; Protein; 1061
                                                                                                                                       The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from
                                                                                                                                                                                                                                                                                                                                                                                                                                                     23-MAR-2000;
11-JUL-2000;
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                                                                                                                        scification, but was obtained in electronic ftp.wipo.int/pub/published_pct_sequences.
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                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity 9; Conserv
                                                 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VLPMLLALAVPGLCWA 18
                      MLPLLIGILGPAAC 14
                                                                                                                                                                                                                                                                                                                                                                                                                             CORP NY.
                                                                                                   1061 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    115 AA;
                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                    Adams M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                     2000US-191637P.
2000US-0614150.
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                                                            56.3%;
57.1%;
                                                                                                                                                                                                                                                                                                                                                                                                    PWD,
                                                                                                                                                                                                                                                                                                                    detection reagent for detecting 1000 or more for elucidating cell signalling and cell-cel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 52; I
Pred. No. 1
                                                             Score 49;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                    Myers
                                                 Mismatches
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                                                               36;
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                                                                         22;
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                                                                         Length 1061;
                                                                                                                                                                                                                                                                                                                       and cell-cell
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AAW61273
ID AAW61
XX AAW61
XX AAW61
XX DCAH-
XX PCCH-
XX 
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                                                                                                                                                                                                                                                                                                                                            The sequence is that of protocadherin-4 (pcdh-4), or as it may CC alternatively be known, VE-cadherin-2. As a vascular endothelial CC cadherin it promotes cell-to-cell homotypic adhesion and its CC expression is upregulated in proliferating endothelial cells in CC expression is upregulated in proliferating endothelial cells in CC anglogenesis and inhibiting pathological conditions such as tumours, CC anglogenesis and inhibiting pathological conditions such as tumours, CC encovascular glaucoma, proliferative retinopathy including proliferative CC diabetic retinopathy, macular degeneration, hemangiomas, angiofibromas, and psoriasis. It may also be used for the prevention or inhibition of leukocyte infiltration, tumour cell metastasis, or endothelial CC permeability, as a vaccine and for making endothelial junctions more permeable to antigens, thus indicating use of the modifiers for treatment or prevention of acute and chronic inflammatory diseases, corgan transplantation, myocardial ischaemia, atherosclerosis, rheumatoid architection, infection. It may also be used for detection,
                                                                                                                           Matches
                                                                                                                                                             Best
                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New isolated vascular endothelial cadherin-2 - used to develop products for modulating angiogenesis, e.g. for treating tumours, glaucoma, psoriasis, inflammatory diseases or organ transplantation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; Page 31-37; 54pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Dejana E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12-DEC-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          05-NOV-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18-JUN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO9825946-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      vascular endothelial; angiogenesis; modulation; glaucoma; psoriasis;
inflammatory disease; organ transplantation; treatment; inhibition;
tumour; metastasis; rheumatoid arthritis; diagnosis; detection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         pcdh-4 gene; VE-cadherin; protocadherin-4; VE-cadherin-2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           27-OCT-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (IMCL-) IMCLONE SYSTEMS INC
                                                                                                                                                      Local
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9; Conser
                                                   мірііцістіст
                                                                                                                                                                                                                                                                                                      and intestinal inre-
                                                                                                                                                                                                                                                         1180 AA;
                                                                                                                           Conservative
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                                                                                                                                                      56.3%;
16
                                                                                                                           2;
                                                                                                                           Score 49; DB
Pred. No. 41;
2; Mismatches
                                                                                                                                                                                     DB 19;
                                                                                                                                                                                     Length 1180;
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AAU52873 ID AAU! XX

AAU52873 standard; Protein;

RESULT 14

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ABG17123
ID ABG1
XX
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                                                                                                                                                                                                                                                             RESULT 15
                                                                                                                                                                                  Query Match
Best Local S
Matches 9
                                                                                                                                                                                                                                                                                                           presence or absence of P. acnes in a patient comprises contacting a sample with a binding agent that binds to the proteins of the invention and determining the amount of bound protein in the sample. The polypeptides may be used as antigens in the production of antibodies specific for P. acnes proteins. These antibodies can be used to downregulate expression and activity of P. acnes polypeptides and therefore treat P. acnes infections. The antibodies may also be used as diagnostic agents for determining P. acnes presence, for example, by enzyme linked immunosorbent assay (ELISA).

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic polypeptides. The proteins and their associated DNA sequences are used in the treatment, prevention and diagnosis of medical conditions caused by P. acnes. The disorders include SAPHO syndrome (synovitis, acne, pustulosis, hyperiosis and osteomyelitis), uveitis and endophthalmitis. P. acnes is also involved in infections of bone, joints and the central
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   uveitis; endophthalmitis; bone; joint; central nervous system; ELISA; inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay; dermatological; osteopathic; neuroprotectant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Propionibacterium acnes polypeptides and nucleic acids useful for vaccinating against and diagnosing infections, especially useful for treating acne vulgaris -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21-APR-2000; 2000US-199047P.
02-JUN-2000; 2000US-208841P.
07-JUL-2000; 2000US-216747P.
                   ABG17123 standard; Protein; 167
                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    nervous system, however it is particularly involved in the inflammatory lesions associated with acne vulgaris. A method for detecting the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 1; SEQ ID No 14068; 1069pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Skeiky YAW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200181581-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Propionibacterium acnes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis; uveitis; endophthalmitis; bone; joint; central nervous system; ELISA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Propionibacterium acnes immunogenic protein #13769
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        L'maisonneuve J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20-APR-2001; 2001WO-US12865.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                             ftp.wipo.int/pub/published_pct_sequences.
                                                                                                             373
                                                                                                                                                                                  l Similarity
9; Conserv
                                                                                                                                             LLLGLLGPAACWA 16
                                                                                                                                                                                                                                                             912
                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Persing DH, Mitcham JL, Wang SS, e J, Zhang Y, Jen S, Carter D;
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                                                                                                                                                                                                     55.2%;
                                                                                                                                                                                  Score 48; DB Pred. No. 45; 2; Mismatches
                     ξ
                                                                                                                                                                                                                        DB 22;
                                                                                                                                                                                    2
                                                                                                                                                                                                                        Length 912;
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                                                                                                                                                                                                                                                                                                                  part of the printed directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;
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                                                                                                                                                                                                                 The invention relates to isolated polynucleotide (I) and collypeptide (II) sequences. (I) is useful as hybridisation probes, (C polymerase chain reaction (PCR) primers, oligomers, and for chromosome (C polymerase chain reaction the primers, oligomers, and for chromosome (C polymucleotides are also used in diagnostics as expressed sequence tags (C for identifying expressed genes. (I) is useful in gene therapy techniques (C to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as (C a food supplement. (II) and its binding partners are useful in medical (II) imaging of sites expressing (II). (I) and (II) are useful for treating (II) disorders involving aberrant protein expression or biological activity. (II) and (II) are useful for treating (II) disorders involving aberrant protein expression or biological activity. (II) and (II) are useful for treating (III) are useful for treating (III) are useful for treating (III) and (III) are useful for treating (III) and (III) are useful for treating (III) and (III) are useful for treating (III) are useful for treating (III) and (III) are useful for treating (III) are useful for treating (III) and (III) are useful for treating (III) and (III) are useful for treating (II
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                                                                                                                                    Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.
                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 20; SEQ ID No 47482; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Drmanac RT, Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    31-MAR-2000; 2000US-0540217
23-AUG-2000; 2000US-0649167
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel human diagnostic protein #17114.
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                                                                                                                 Local
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DB; AAS81310.
83
                                            2 LPLLL--GLLGPAACWA 16
                                                                                         10;
                                                                                                                 Similarity
                                                                                                                                                                                   167
                                                                                         Conservative
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                                                                                                            54.0%;
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    84
                                                                                         Score 47; DB Pred. No. 10; 2; Mismatches
                                                                                                          DB
10;
                                                                                                                                      22;
                                                                                                                                    Length 167;
                                                                                         Gaps
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Search completed: January 12, Job time: 4.41118 secs

2004, 08:15:38

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Result
No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Database
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                     Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   January 12, 2004, 08:15:44; Search time 1.9481 Seconds (without alignments) 1655.023 Million cell updates/sec
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                                                                                                                                                                                                                                                                                100.0
                                                                                                                                                                                                                                                                                                                                                     Match
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11:
12:
13:
14:
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Copyright (c) 1993 - 2004 Compugen Ltd.
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/cgn2 6/ptodata/1/pubpaa/US09B PUBCOMB.pep: *
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_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
US-10-236-05A-14
US-10-085-167-2
US-10-236-05SA-16
US-09-759-130B-42
US-09-759-130B-42
US-09-554-000-8
US-09-554-000-56
US-09-554-000-56
US-10-120-801-41
US-10-120-801-4
US-10-1316-253-4
US-10-316-253-6
US-10-316-253-6
US-10-316-253-7
US-10-316-253-7
US-10-316-253-7
US-10-316-253-7
US-10-316-253-7
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    Sequence 14, Appl
Sequence 2, Appli
Sequence 16, Appl
Sequence 42, Appl
Sequence 40, Appl
Sequence 8, Appli
Sequence 56, Appli
Sequence 41, Appli
Sequence 4, Appli
Sequence 7540, Ap
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US-10-236-055A-14
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                                                                                                                                                                                                                                        Best
                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Mattson, Jeanine
APPLICANT: Moshrefi, Mehrdad
APPLICANT: Parham, Christi
TITLE OF INVENTION: WAMMALIAN GENES; RELATED REAGENTS
FILE REFERENCE: DX01343K
CURRENT APPLICATION NUMBER: US/10/236,055A
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/317,988
PRIOR FILING DATE: 2001-09-06
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45	44	43	42	41	40	39	38	37	36	35	4	<b>ω</b>	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18		16
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12	12	12	12	12	12	12	12	11	11	11	11	11	11	11	11	11	11	11	11	11	11	11	11	10	10	10	10	10	10
-10-140-471-3	0-140-274-3	-10-140-021-3	0-140-01	-10-137-870-3	9-978-2	-09-978-188A-42	-09-978-375A-42	78-643A-42	78-187B-42	9-978-757A-4	99-830A-42	-193A-42	78-423A-42	US-09-918-585A-425	78-824-42	-09-981-915A-42	-09-999-833A-42	-09-978-5	78-403A-42	78-191A-42	78-585A-42	-978-608A-42	78-18	99-832A-42	78-	78-697-42	-295A-4	08-193-2	08-193-
equence 39	equence 394,	nce 394,	equence 394,	e 394,	equence 425,	equence 425,	e 425,	equence 425,	equence 425,	e 425,	equence 425,	equence 425,	equence 425,	e 425,	equence 425,	equence 425,	e 425,	equence 425,	9 425,	տ	9 425,	equence 425,	e 425,	425,	•	9 425,	425,	e 27,	φ,

# ALIGNMENTS

Forsythe, Ian Gorman, Daniel M.

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; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 14
; SEQ ID NO 14
; LENGTH: 329
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-236-055A-14
RESULT 2
US-10-085-167-2
; Sequence 2, Application US/10085167
; Publication No. US20030170781A1
                                                                                                                                                                        Matches
                                                                                                                                                                                                     Query Match
                                                                                                                                                                                     Local
                                                                                                                                                                      l Similarity
16; Conserv
                                                                                                                                1 MLPLLLGLLGPAACWA 16
                                                                                                      MLPLLLGLLGPAACWA
                                                                                                                                                                    100.0%; Score 87; DB 12; ilarity 100.0%; Pred. No. 0.00012; Conservative 0; Mismatches 0;
                                                                                                          16
                                                                                                                                                                                                     Length 329;
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GENERAL INFORMATION:

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US-09-759-130B-42
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/10/236,055A
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/317,988
PRIOR FILING DATE: 2001-09-06
NUMBER OF SEQ ID NOS: 36
SOFTWARE: Patentin version 3.1
SEQ ID NO 16
                                                                                                                                                                      Sequence 42, Application US/09759130B Publication No. US20030022279A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 16, Application US/102 Publication No. US20030134328A1 GENERAL INFORMATION:
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Best Local Similarity
Matches 16; Conserv
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SEQ ID NO 2
LENGTH: 329
TYPE: PRT
                                                                                                                                                       GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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CURRENT APPLICATION NUMBER: US/10/085,167
CURRENT FILING DATE: 2002-02-27
PRIOR APPLICATION NUMBER: 60/141,928
PRIOR PILING DATE: 1999-07-01
NUMBER OF SEQ ID NOS: 9
                                                                                         APPLICANT: Millennium Pharmaceuticals, APPLICANT: McCarthy, Sean A APPLICANT: Fraser, Christopher C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Parham, Christi
TITLE OF INVENTION: MAMMALIAN GENES; RELATED REAGENTS
FILE REFERENCE: DX01343K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Holloway, James L. APPLICANT: Lok, Si
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Basham, Beth E. APPLICANT: Forsythe, Ian
                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ENGTH: 326
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TLE OF INVENTION: SECRETED PROTEIN ZACRP4
                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
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Barnes, Thomas S
Kirst, Susan J
Mackay, Charles R
Myers, Paul S
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Gorman, Daniel M.
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Moshrefi, Mehrdad
                                                                       McCarthy, Sean A
Fraser, Christopher C
Sharp, John D
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Pred. No. 0.011;
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; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 42
; LENGTH: 1135
; TYPE: PRT
; ORGANISM: Mus sp.
US-09-759-130B-42
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Best Local :
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               APPLICANT: Komuves, Laszlo
APPLICANT: Komuves, Laszlo
TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
FILE REFERENCE: 21402-340
CURRENT APPLICATION NUMBER: US/10/120,801
CURRENT FILING DATE: 2002-04-11
PRIOR APPLICATION NUMBER: 60/285748
PRIOR FILING DATE: 2001-04-23
                                                                                                                                                                                                                             APPLICANT:
                                                                                                                                                                                                                                                                                                                                              APPLICANT: Pena, Carol
APPLICANT: Guo, Xiaojia
APPLICANT: Shimkets, Richard
APPLICANT: Padigaru, Muralidhara
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PRIOR FILING DATE: 2000-01-07
PRIOR PPLICATION NUMBER: US 09/559,497
PRIOR FILING DATE: 2000-04-27
PRIOR APPLICATION NUMBER: US 09/578,063
PRIOR FILING DATE: 2000-05-24
PRIOR FILING DATE: 2000-05-24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: US 09/602,871
PRIOR FILING DATE: 2000-06-23
PRIOR APPLICATION NUMBER: US 09/420,707
PRIOR FILING DATE: 1999-10-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILE REFERENCE: MP100-535OMNIM
CURRENT APPLICATION NUMBER: US/09/759,130B
CURRENT FILING DATE: 2002-09-16
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TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING
TITLE OF INVENTION: PROGNOSTIC, DIAGNOSTIC, PREVENTIVE,
TITLE OF INVENTION: USES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS:
                                                                                                                                                                                     APPLICANT
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PRIOR FILING DATE: 1999-06-14
PRIOR APPLICATION NUMBER: US 09/596,194
PRIOR FILING DATE: 2000-07-14
                                                                                                                                                                                                                                                                                                                                      APPLICANT:
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FILING DATE: 1999-06-29
APPLICATION NUMBER: 60/286068
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9; Conserv
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Spytek, Kimberly
Mehraban, Fuad
Topper, James N.
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Wasserman, Scott
                                                                                                                                                                                 Smithson, Glennda
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Pred. No. 95;
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RESULT 6
US-09-554-000-8
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                                                                                                                                                                                                                                                                                  US-09-554-000-56
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PRIOR APPLICATION NUMBER: 60/288334
PRIOR PILING DATE: 2001-05-03
PRIOR APPLICATION NUMBER: 60/291241
PRIOR APPLICATION NUMBER: 60/291241
PRIOR FILING DATE: 2001-05-16
PRIOR PILING DATE: 2001-09-14
PRIOR FILING DATE: 2001-09-14
PRIOR APPLICATION NUMBER: 60/285609
PRIOR FILING DATE: 2001-04-20
NUMBER OF SEQ ID NOS: 155
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 8
LENGTH: 656
TYPE: PRT
                                                                                                                                                                                                                                    Sequence 56, Application US/09554000 Patent No. US20020165364A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 8, Application US/09554000 Patent No. US20020165364A1 GENERAL INFORMATION:
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LENGTH: 379
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APPLICANT: TSien, ROGET Y.
APPLICANT: TSien, ROGET Y.
APPLICANT: MYYAWAKI, ALSUSHI
TITLE OF INVENTION: FLUORESCENT PROTEIN SENSORS FOR
TITLE OF INVENTION: DETECTION OF ANALYTES
FILE REFERENCE: 07257/042001
CURRENT APPLICATION NUMBER: US/09/554,000
CURRENT FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: 08/818,252
PRIOR APPLICATION NUMBER: 08/818,252
PRIOR FILING DATE: 1997-03-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: FLUORESCENT PROTEIN SENSORS FOR TITLE OF INVENTION: DETECTION OF ANALYTES FILE REFERENCE: 07257/042001 CURRENT APPLICATION NUMBER: US/09/554,000 CURRENT FILING DATE: 2000-04-20 DETICE NUMBER: 1000-04-20 CURRENT FILING DATE: 2000-04-20 CURRENT FILING DATE: 2000-04-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Aequorea victoria
-09-554-000-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: 08/818,252
PRIOR FILING DATE: 1997-03-14
NUMBER OF SEQ ID NOS: 56
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                                                                                                                                                                                                                                                                                                                                                                                                                                              y match
Local Similarity 83.3%;
Local Similarity 83.3%;
tes 10; Conservative
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Pred. No. 1.1e+02;
1; Mismatches 1
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; TYPE: PRT ; ORGANISM: Rattus norvegicus US-09-554-000-56
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                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/10/120,801
CURRENT FILING DATE: 2002-04-11
PRIOR APPLICATION NUMBER: 60/285748
PRIOR FILING DATE: 2001-04-23
PRIOR PELICATION NUMBER: 60/286068
PRIOR PELICATION NUMBER: 60/286292
PRIOR PELICATION NUMBER: 60/286292
PRIOR PILING DATE: 2001-04-25
PRIOR PILING DATE: 2001-04-25
PRIOR PILING DATE: 2001-05-03
PRIOR APPLICATION NUMBER: 60/28134
PRIOR APPLICATION NUMBER: 60/291241
PRIOR PILING DATE: 2001-05-03
PRIOR PILING DATE: 2001-05-04
PRIOR PILING DATE: 2001-05-04
PRIOR PILING DATE: 2001-09-14
PRIOR APPLICATION NUMBER: 60/285609
PRIOR APPLICATION NUMBER: 60/285609
PRIOR APPLICATION NUMBER: 60/285609
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                                                                                                                                                   ; ORGANISM: human US-10-120-801-41
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 56
                                                                                                                                                                                                                            SEQ ID NO 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 41, Application US/10120801 Publication No. US20030203843A1
                                                                        Matches
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APPLICANT:
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Best Local Similarity 83.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Pena, Carol
APPLICANT: Guo, Xiaojia
APPLICANT: Shimkets, Ri
                                                                                                                                                                                                                                          PRIOR FILING PARENT IN NOS: 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Wasserman, Scott
APPLICANT: Edinger, Shlomit
APPLICANT: Smithson, Glennda
APPLICANT: Gunther, Erik
APPLICANT: Komuves, Laszlo
TITLE OF INVENTION: Proteins and Nucleic Acids Encoding
FILE REFERENCE: 21402-340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 18
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29 LLPLWLGLAGPGA 41
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                                   1 МІРІГІСТІСТИ
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Similarity 69.2%;
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Padigaru, Muralidhara
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Spytek, Kimberly
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                                                                          Conservative
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    Mismatches

                                                                                          Score 45; DB 12;
Pred. No. 1.1e+02;
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Pred. No. 7;
                                                                          Mismatches
                                                                                                              DB 12; Length 347;
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RESULT 9 US-10-120-801-4

Sequence 4, Application US/10120801 Publication No. US20030203843A1

Shimkets, Richard Padigaru, Muralidhara Kekuda, Ramesh Spytek, Kimberly

Carol Xiaojia

Mehraban, Fuad

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PRIOR FILING DATE: 2001-04-23
PRIOR APPLICATION NUMBER: 60/286068
PRIOR FILING DATE: 2001-04-24
PRIOR APPLICATION NUMBER: 60/286292
PRIOR APPLICATION NUMBER: 60/286394
PRIOR APPLICATION NUMBER: 60/28334
PRIOR APPLICATION NUMBER: 60/291241
PRIOR APPLICATION NUMBER: 60/291241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR FILING DATE: 2001-09-14
PRIOR APPLICATION NUMBER: 60/285609
PRIOR FILING DATE: 2001-04-20
NUMBER OF SEQ ID NOS: 155
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 4
            CURRENT APPLICATION NUMBER: US/10/316,253
CURRENT FILING DATE: 2002-12-10
PRIOR APPLICATION NUMBER: US 60/355,295
PRIOR FILING DATE: 2002-02-08
NUMBER OF SEQ ID NOS: 308
SOFTWARE: Patentin version 3.1
SEQ ID NO 2
LENGTH: 416
                                                                                                                                                                                                                                                                                                                                Sequence 2, Application US/10316253 Publication No. US20030162706A1 GENERAL INFORMATION:
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Homo sapiens -10-120-801-4
                                                                                                                                                                                    APPLICANT: Wang, Feng
APPLICANT: Greis, Kenneth
TITLE OF INVENTION: Angiogenesis Modulating Proteins
FILE REFERENCE: 8865M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 37
TYPE: PRT
                                                                                                                                                                                                                                                                                                           APPLICANT: The Procter & Gamble Company
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/10/120,801
TYPE: PRT
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T: Gunther, Erik
T: Komuves, Laszlo
INVENTION: Proteins and Nucleic Acids Encoding Same
ERENCE: 21402-340
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9; Conservative
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Wasserman, Scott
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Pred. No. 1
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; TYPE: PRT
ORGANISM: Rattus norvegicus
US-10-316-253-4
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                                                                  US-10-316-253-6
                                                                                                                                   SOFTWARE: PatentIn version 3.1 SEQ ID NO 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn version 3.1 SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Wang, Feng
APPLICANT: Greis, Kenneth
APPLICANT: Greis, Kenneth
TITLE OF INVENTION: Angiogenesis Modulating Proteins
FILE REFERENCE: 8865M
CURRENT APPLICATION NUMBER: US/10/316,253
CURRENT FILING DATE: 2002-12-10
PRIOR APPLICATION NUMBER: US 60/355,295
PRIOR FILING DATE: 2002-02-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
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Publication No. US20030162706A1
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Best Local Similarity 83.3 Matches 10; Conservative
                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                       Sequence 6, Application US/10316253
Publication No. US20030162706A1
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Best Local Similarity
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                                                                                                                                                                 PRIOR APPLICATION NUMBER: US 60/355,295
PRIOR FILING DATE: 2002-02-08
NUMBER OF SEQ ID NOS: 308
                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/10/316,253
CURRENT FILING DATE: 2002-12-10
                                                                                                                                                                                                                                                     APPLICANT: Greis, Kenneth
TITLE OF INVENTION: Angiogenesis Modulating Proteins
FILE REFERENCE: 8865M
                                                                                                                                                                                                                                                                                                                                        APPLICANT: The Procter & Gamble Company APPLICANT: Peters, Kevin
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                                                                             LENGTH: 416
TYPE: PRT
ORGANISM: Rattus norvegicus
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10; Conser
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Greis, Kenneth
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               51.7%;
83.3%;
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83.3%;
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Pred. No.
              Score 45; DB 12; Length 416; Pred. No. 1.4e+02;

    Mismatches

 1; Mismatches
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Pred. No. 1.4e+02
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CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 7540
LENGTH: 242
TYPE: PRT
ORGANISM: Burkholderia cepacia
US-10-369-493-7540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Sequence 4780, Application US/10369493
Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Green C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
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US-10-369-493-7540
RESULT 15
US-10-156-761-10413
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US-10-369-493-4780
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CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 4780
LENGTH: 242
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                                                                                                                                                                                                                                                 Query Match
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                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10 (52052) B
                                                                                                                                                                                             / Match 50.6%; Score 44; DB 12; Length 242; Local Similarity 64.3%; Pred. No. 1.1e+02; nes 9; Conservative 2; Mismatches 3; Indels
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                                                                                                3 PLLLGLLGPAACWA 16
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57 PLVVDLLDPAACSA 70
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APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-05-97
PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 10413
Search completed: January 12, 2004, 08:33:40 Job time: 4.9481 secs
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                                                                                                                                                                                                                                                                                                                ORGANISM: Streptomyces avermitilis US-10-156-761-10413
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                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                Query Match 50.6%; Score 44; DB 15; Best Local Similarity 55.0%; Pred. No. 1.8e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 10413, Application US/10156761
Publication No. US20030119018A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
APPLICANT: HORIKAWA, HIROSHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: OMURA, SATOSHI
                                                                                                                                                                                                                                                                                                                                                                LENGTH: 394
TYPE: PRT
                                                                                                        113 LPWLTGLLTVIGGVGPAAVW 132
                                                                                                                                                                                                          11;
                                                                                                                                                        2 LPLLLGLL----GPAACW 15
                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                             DB 15; Length 394;
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Gaps

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Minimum
Maximum
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Searched
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Scoring table:
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            Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Match
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Gapop 10.0 ,
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87
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GenCore version
Copyright (c) 1993 - 2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length
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      US-09-252-991A-2141
US-08-818-253-8
US-08-818-253-61
US-08-818-253-61
US-08-818-253-61
US-08-818-253-61
US-08-818-253-61
US-08-818-253-61
US-08-940-424-3
US-08-940-424-3
US-08-940-373-389
US-09-99-6373-389
US-09-197-984-2
US-09-197-986-12
US-09-297-987-2
US-09-297-987-2
US-09-297-987-2
US-09-297-987-2
US-09-297-857-2
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Compugen Ltd.
Sequence 56, Appl
Sequence 61, Appl
Sequence 14, Appl
Sequence 13, Appl
Sequence 11, Appl
Sequence 13, Appl
Sequence 2389, Appl
Sequence 2, Appli
Sequence 2, Appli
Sequence 12, Appli
Sequence 12, Appli
Sequence 2, Appli
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Sequence 2, Appli
Sequence 21, Appli
Sequence 31174, Appli
Sequence 3174, Appli
Sequence 3, Appli
Sequence 4, Appli
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Sequence 8, Appli
Sequence 8, Appli
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41 47.1 1311 4 US-08-918-658-4 41 47.1 1311 5 US-08-918-658-4 41 47.1 1311 5 US-08-918-631-4 41 47.1 1311 5 US-08-918-2631-4 40.5 46.6 176 4 US-09-252-991A-26925 Sequence 4 Appli 40.5 46.6 176 4 US-09-252-991A-26925 Sequence 26925, A 40 46.0 218 4 US-09-252-991A-25415 Sequence 25415, A 40 46.0 584 2 US-08-845-295A-2 Sequence 2, Appli 40 46.0 584 3 US-09-146-661-2 Sequence 2, Appli 40 46.0 584 3 US-09-146-661-2 Sequence 2, Appli 40 46.0 986 3 US-09-150-515-2 Sequence 2, Appli 40 46.0 986 3 US-09-150-515-2 Sequence 2, Appli 40 46.0 986 4 US-09-850-048A-4 Sequence 4, Appli 40 46.0 986 4 US-09-850-048A-4 Sequence 2, Appli 39 5 45.4 495 4 US-09-852-921A-19330 Sequence 2, Appli 39 44.8 182 4 US-09-134-001C-5022 Sequence 5022, Ap 39 44.8 192 3 US-08-486-099-107 Sequence 107, App 39 44.8 192 3 US-08-360-107A-117 Sequence 117, App 39 44.8 192 3 US-08-360-107 Sequence 107, App 39 44.8 192 3 US-08-919-597-107 Sequence 107, App	45	44	43	42	41	40	39	38	37	36	ω S	34	ω u	32	31	30	29	28
1311 4 US-08-918-658-4 1311 4 US-09-724-631-4 1311 5 PCT-US95-1323-4 176 4 US-09-7252-991A-26925 176 4 US-09-252-991A-25415 176 4 US-09-252-991A-25415 176 4 US-09-252-991A-25415 176 4 US-09-252-991A-25415 177 4 US-09-452-95A-2 178 2 US-09-140-933-2 178 3 US-09-157-4 178 2 Sequence 178 4 US-09-850-048A-4 178 2 Sequence 178 4 US-09-252-991A-19330 178 2 Sequence 179 3 US-08-140-001C-5022 179 3 US-08-1486-099-107 178 2 Sequence 179 3 US-08-486-099-107 178 2 Sequence 179 3 US-08-486-099-107 178 2 Sequence 179 3 US-08-484-2238-107 178 2 Sequence 179 3 US-08-484-2238-107 178 2 Sequence 179 3 US-08-919-597-107 189 2 Sequence 189 3 US-08-484-2238-107 189 2 Sequence 189 3 US-08-919-597-107	39	39	39	39	39	39.5	40	40	40	40	40	40	40	40	40.5	41	. 41	41
1 4 US-08-918-658-4 1 5 PCT-US95-1133-4 1 Sequence 2 US-09-724-631-4 3 Sequence 4 US-09-252-991A-26925 4 US-09-252-991A-26925 4 US-09-252-991A-26925 4 US-09-140-933-2 2 Sequence 4 US-09-140-933-2 3 US-09-140-661-2 4 US-09-150-515-2 5 Sequence 6 US-09-186-661-2 6 US-09-186-661-2 7 Sequence 7 US-08-872-757-4 8 Sequence 8 US-09-872-757-4 8 Sequence 9 US-08-872-757-4 9 US-08-252-991A-19330 9 Sequence 1 US-08-252-991A-19330 9 Sequence 2 US-08-134-001C-5022 2 US-08-134-001C-5022 3 US-08-486-099-107 2 US-08-486-099-107 2 US-08-486-099-107 2 Sequence 2 US-08-486-099-107 2 Sequence 2 US-08-486-099-107 3 US-08-484-01578-117 5 Sequence 2 US-08-484-01578-117 5 Sequence	44.8	44.8	44.8	44.8	44.8	45.4	46.0	46.0	46.0	46.0	46.0	46.0	46.0	46.0	46.6	47.1	47.1	47.1
Sequence  Sequence  26925  Sequence  25415  Sequence  26925  Sequence	192	192	192	192	182	495	999	986	986	584	584	584	584	218	176	1311	1311	1311
Sequence  Sequence  26925  Sequence  25415  Sequence  26925  Sequence	ω	ω	ω	w	4.	4	<b>_</b>	4	w	w	w	w	N	4	4	ហ	4.	4
	US-08-919-597-107	US-08-484-223B-107	US-08-360-107A-117	US-08-486-099-107	US-09-134-001C-5022	US-09-252-991A-19330	US-08-252-626A-2	US-09-850-048A-4	US-08-872-757-4	US-09-150-515-2	US-09-146-661-2	US-09-140-933-2	US-08-845-295A-2	US-09-252-991A-25415	US-09-252-991A-26925	PCT-US95-13233-4	US-09-724-631-4	US-08-918-658-4
	107,	107,	117,	107,	5022,		Sequence 2, Appli	4	4	2	2	2	Sequence 2, Appli			Sequence 4, Appli	4.	4

### ALIGNMENTS

US-09-252-991A-21441

Sequence 21441, Application US/09252991A Patent No. 6551795

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PSEUDOMONAS

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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: MATC J. RUBERFIELD ACID AND AMINO ACID SEQUENCES RELATING TO:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO:
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US/60/074,788
PRIOR APPLICATION NUMBER: US/60/074,788
PRIOR APPLICATION NUMBER: US/60/094,190
PRIOR APPLICATION NUMBER: US/60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 21441
LENGTH: 135
TYDE: PRT
ORGANISM: PBEUDOMONDAS AERUGINOSA
                                                                                                                                                                                                                                                                                                                                                       RESULT 2
US-08-818-253-8
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                                                                                                                                                                                                                                                                                                              Sequence 8, Application US/08818253 Patent No. 5998204
                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Tsien, Roger Y.
APPLICANT: Miyawaki, Atsushi
TITLE OF INVENTION: FLUORESCENT PROTEIN SENSORS FOR
TITLE OF INVENTION: DETECTION OF ANALYTES
NUMBER OF SEQUENCES: 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
STATE: CA
COUNTRY: USA
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 4225 Executive Square, Suite 1400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local
                                                                                CITY: La Jolla
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                            23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
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Pred. No. 0.58;
2; Mismatches
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COMPUTER:

IBM Compatible

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APPLICANT: Tsien, Reger Y.
APPLICANT: MYNWAKI, ALBUSHI
TITLE OF INVENTION: FLUORESCENT PROTEIN SENSORS FOR
TITLE OF INVENTION: DETECTION OF ANALYTES
FILE REFERENCE: 07257/042001
CURRENT APPLICATION NUMBER: US/08/818,252B
CURRENT FILING DATE: 1997-03-14
NUMBER OF SEQ ID NOS: 56
SOTTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 8
LENGTH: 656
TYPE: PRT
ORGANISM: Aequorea victoria
                                                                                  US-08-818-253-56
; Sequence 56, Application US/08818253
; Patent No. 5998204
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                                                                                                                                         RESULT 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-818-252-8
                                                                                                                                                                                                                                                                                                                                 US-08-818-252-8
GENERAL INFORMATION:
APPLICANT: Teien, ROGI
APPLICANT: Miyawaki, J
TITLE OF INVENTION: FI
TITLE OF INVENTION: D)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 8, Application US/08818252B
Patent No. 6197928
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                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 619/678-5099
INFORMATION FOR SEQ ID NO: 8:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM: Windows 95
SOFTWARE: FASTSEQ for Windows
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION: TELEPHONE: 619/678-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/0 FILING DATE: 14-MAR-1997 PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Haile, Ph.D., Lisa A. REGISTRATION NUMBER: 38,347 REFERENCE/DOCKET NUMBER: 07
                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity les 10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY:
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                                                                                                                                                                                                                                                              10;
                                                                                                                                                                                                                 2 LPLLLGLLGPAA 13
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KGY: linear
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                                                    Tsien, Roger Y.
                                                                                                                                                                                                                                                                          54.0%;
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FLUORESCENT PROTEIN SENSORS FOR DETECTION OF ANALYTES
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                                                                                                                                                                                                                                                                              Score 47;
Pred. No.
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Pred. No.
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                                                                                                                                                                                                                                                                                                DB 3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 656;
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US-08-818-253-61
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Sequence 61, Apprix
No. 5998204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Tsien, Rog
APPLICANT: Miyawaki,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: 619/678-5099
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Haile, Ph.D., Lisa A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 0725
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/678-5070
TELEFAX: 619/678-5099
                                                                                                                                                                                                           COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
ATTORNEY/AGENT INFORMATION:
NAME: Haile, Ph.D., Lisa
REGISTRATION NUMBER: 38,
                                                                   SOFTWARE: PASTSEQ for Windows CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/818, FILING DATE: 14-MAR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/0: FILING DATE: 14-MAR-1997 PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: FastSEQ for Windows Version 2.0b CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: FLUORESCENT PROTEIN SENSORS FOR TITLE OF INVENTION: DETECTION OF ANALYTES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
                                                                                                                                                                      COMPUTER: IBM COU
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid TOPOLOGY: linear
                                                                                                                                                                                                                                                                                      CITY: La Jolla
STATE: CA
                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Fish & Richardson P.C. STREET: 4225 Executive Square, Suite 1400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: La Jolla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Match 51.7%;
Local Similarity 83.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ψ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Application US/08818253
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                USA
                                                                                                                                                                               IBM Compatible
SYSTEM: Windows 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IBM Compatible
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                                                                                                                                                                                                                    Diskette
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TELECOMMUNICATION INFORMATION:

619/678-5070

61:

TELEPHONE:

REFERENCE/DOCKET NUMBER:

07257/043001

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US-08-818-252-56
; Sequence 56, Application US/08818252B
; Patent No. 6197928
                                                                                                                                                                                                                                                                                                                                                                                      US-08-375-962B-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; ORGANISM: Rattus norvegicus
US-08-818-252-56
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Tsien, Roger Y.
APPLICANT: Miyawaki, Areushi
TITLE OF INVENTION: FLUORESCENT PROTEIN SENSORS FOR
TITLE OF INVENTION: DETECTION OF ANALYTES
FILE REFERENCE: 07257/042001
CURRENT PRILICATION NUMBER: US/08/818,252B
CURRENT FILING DATE: 1997-03-14
NUMBER OF SEQ ID NOS: 56
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPAX: 619/0/0 61
INFORMATION FOR SEQ ID NO: 61
SEQUENCE CHARACTERISTICS:
TENGTH: 18 amino acids
                                                                                                                                                                                                                                                                                                                                                    Sequence 14, Application US/08375962B Patent No. 5731195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
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                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: CHRISTER; ERIKSSON, ULF.
TITLE OF INVENTION: Isolated Nuclei
TITLE OF INVENTION: which Codes for
TITLE OF INVENTION: behydrogenase A
TITLE OF INVENTION: a Portion of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 18
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                  tent No.
                                                                    relfe & Lynch
CITY: New York City
STATE: New York
ZIP: 10022
MPUTEP
                                                                                                                                                               NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Felfe & Lynch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: peptide
                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity nes 10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
TOPOLOGY: linear
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect (ASCII standard)
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es 10; Conserv
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                                       IBM
                                                        Diskette, 3.5 inch,
                                                                                                                                                                                                                                                                                                              ANDRAS; HELLMAN, ULF; WERNSTEDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     51.7%;
83.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      51.7%;
83.3%;
                                                                                                                                                                                                                     Isolated Nucleic Acid Molecule Which Codes for A 32 kDa Protein Having 11-CIS Retinol Dehydrogenase Activity, and Which Associates With P63, a Portion of a Retinol Binding Protein Receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 45; DB Pred. No. 0.8;
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Pred. No. 0.
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                                                        144 kb
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                                                        storage
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RESULT 9
US-08-465-343A-11
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                                                                                               Sequence 11,
Patent No. 6
                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn Ver. 2.0 SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                 Matches
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Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
GENERAL INFORMATION:
APPLICANT: Wyler, David J.
APPLICANT: Prakash, Sadhana
APPLICANT: Zhang, Xiaoping
TITLE OF INVENTION: FSF-1 AND THE EARLY DETECTION
TITLE OF INVENTION: OF FIBROSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: POTENT INHIBITORS OF HUMAN 9-c18 RETINOL DEHYDROGENASE FILE REFERENCE: 0575/54544
CURRENT APPLICATION NUMBER: US/08/940,424A
CURRENT FILING DATE: 1997-09-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Blaner, William S. APPLICANT: Zott, Roseann P. APPLICANT: Gamble, Mary V. APPLICANT: Mertz, James R.
                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 13
                                                                                                                                                                                                                                                                                                                                                                LENGTH: 318
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                               ORGANISM: rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: LUTELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: 08/2
FILING DATE: 6-October-1
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: p32;11-cis retinol dehydrogenase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/08/375,962B FILING DATE: 20-January-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Pasqualini, P
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE:
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                                                                                                                                                                                                                                                                              Similarity
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                                                                                                                                                                                                                              LPLLLGLLGPAACW 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Application US/08940424A
                                                                                                                  Application US/08465343A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           318 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
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                                                                                                                                                                                                                                                                            50.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            08/258,418
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                                                                                                                                                                                                                                                                              Score 44; DB
Pred. No. 25;
                                                                                                                                                                                                                                                                 Mismatches
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                                                                                                                                                                                                                                                                 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 318,
                                                                                                                                                                                                                                                                                             Length 318;
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NUMBER OF SEQUENCES: CORRESPONDENCE ADDRESS

ADDRESSEE: F: STREET: 225 | CITY: Boston

E: Fish & Richardson P.C. 225 Franklin Street

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RESULT 10
US-09-199-637A-389
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                                                APPLICANT: TSONGALIS, JOHN
TITLE OF INVENTION: VIRULENCE-ASSOCIATED NUCLEIC
TITLE OF INVENTION: SEQUENCES AND USES THEREOF
FILE REPERENCE: 00786/361002
CURRENT APPLICATION NUMBER: US/09/199,637A
CURRENT FILING DATE: 1998-11-25
PRIOR APPLICATION NUMBER: 60/066,517
PRIOR FILING DATE: 1997-11-25
PRIOR FILING DATE: 1997-11-25
NUMBER OF SEQ ID NOS: 437
SOFTWARE: Fab
SEQ ID NO 389
SEQTH: 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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OPERATING SYSTEM: Windows95
SOFTWARE: FastSEQ for Windows Version 2.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,343A
FILING DATE: 05-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/395,674
FILING DATE: 28-FEB-1995
APPLICATION NUMBER: 08/152,904
FILING DATE: 15-NOV-1993
APPLICATION NUMBER: 07/40,426
FILING DATE: 24-FEB-1992
ATTORNEY/AGENT INFORMATION:
NAME: Meiklejohn, Ph.D., Anita L.
PEGIGTPATTON NUMBER: 35,283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 96 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REGISTRATION NUMBER: 35,283
REFERENCE/DOCKET NUMBER: 00:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617,542-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX:
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ZIP: 02110-2804
                                                                                                                                                                                                                                                                                                                                                          INFORMATION:
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                                        FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                     Ausubel,
                                                                                                                                                                                                                           Drenkard, Eliana
                                                                                                                                                                                                                                            Cao, Hui
                                                                                                                                                                                                                                                                               Rahme, Laurence G.
Mahajan-Miklos, Shalina
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               96 amino acids
                                                                                                                                                                                                                                                                                                                                                                                              Application US/09199637A
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                                                                                                                                                                                      VIRULENCE-ASSOCIATED NUCLEIC ACID
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Pred. No. 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 96
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; TYPE: PRT ; ORGANISM: Pseudomonas aeruginosa US-09-199-637A-389
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-252-991A-19814
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQ ID NO 19814
LENGTH: 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 19814, Application US/09252991A
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Best Local
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Patent No. 582133
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Marc J.
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                    APPLICANT: Godfrey, Way APPLICANT: Buck, David APPLICANT: Engleman, ENTITLE OF INVENTION: RETITLE OF INVENTION: CD.

NUMBER OF SEQUENCES: 2
                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ATTORNEY/AGENT INFORMATION NAME: Smith, Willaim M
                               APPLICATION NUMBER: US/0 FILING DATE: 03-NOV-1993 CLASSIFICATION: 424
                                                                                                                                                                                                                                         STREET: 379 Lytton Avenue CITY: Palo Alto STATE: California
                                                                                                                                                                                                      COUNTRY: UZIP: 94301
                                                                                                                                                                                                                                                                                                 ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30 LPLLMFCLGLAAC 42
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9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Application US/08147784
                                                                                                                                                                                                                                                                                                                                                                                                                                Godfrey, Wayne
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NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                David
                                                                                                                                                                                                                                                                                                                                                        RECEPTOR ON THE SURFACE OF ACTIVATED CD4+ T-CELLS: ACT-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             48.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             47.1%;
                                                                                                                                                                                                                                                                                                                                                                                              Edgar G.
                                                                       US/08/147,784
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 41; DB Pred. No. 19;
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US-08-195-967-2
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                                                             Matches
                                                                                           Query Match
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Patent No. 6242566
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (415) 326-2422 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                      TELEPHONE: (415) 326-240
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                   CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 0549
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Godfrey, Wayne
APPLICANT: Engleman, Edgar G.
TITLE OF INVENTION: LIGAND (ACT-4-L) TO A RECEPTOR ON THE SURFACE OF ACTIVATED
TITLE OF INVENTION: CD4+ T-CELLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 05
TELECOMMUNICATION INFORMATION:
                                                                                                                                          MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
                                                          Local Similarity res 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                47.18;
Local Similarity 75.08;
les 9; Conservation
                                                                                                                                                         TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                       LENGTH:
                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 10-FEB-1994
                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 94301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ENGTH:
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                              2 LPLLLGLLGPAA 13
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LGLVLGLLGPLA 232
LGLVLGLLGPLA 232
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                                                             Conservative
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                                                                                                                                                           linear
                                                                                                                                                                                                                                                         (415) 326-2400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Townsend and Townsend Khourie and Crew
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                                                                           47.1%;
75.0%;
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                                                                            Score 41;
Pred. No.
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Pred. No.
                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
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63;
                                                                                           DB 3; Length 277;
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                                                            <u>.</u>.
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RESULT 14

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US-08-472-940-2
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                                                                                                                                                                                                                                                                                     Sequence 2, Application US/08472940 Patent No. 6277962
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 12, Application US/09006353A
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (301) 309-851
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                        GENERAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                        APPLICANT: Godfrey, Wa
APPLICANT: Buck, David
APPLICANT: Engleman, E
TITLE OF INVENTION: RE
TITLE OF INVENTION: CD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                            ZIP: 94301
COMPUTER READABLE FORM:
                                                                                                                                         NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: PF
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/006,353A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                            MEDIUM TYPE:
                                                                                                                            STREET:
COMPUTER: IBM PC OPERATING SYSTEM:
                                                                            COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REGISTRATION NUMBER: 36,373
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                     221 LGLVLGLLGPLA 232
                                                                                                                                                                                                                                                                      INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                   2 LPLLLGLLGPAA 13
                                                                                           T: 379 Lytton Avenue
Palo Alto
California
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity 75.0
9; Conservative
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YU, GUO-LIANG
GENTZ, REINER
RUBEN, STEVEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             277 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3: HUMAN GENOME SCIENCES, INC
9410 KEY WEST AVENUE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (301) 309-8512
                                                                                                                                                                                                                                                       Godfrey, Wayne
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (301) 309-8504
                             Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           single
                                                                                                                                                                                                                                        David
                                                                                                                                                                                        ), Edgar G.
RECEPTOR ON THE SURFACE OF ACTIVATED
CD4+ T-CELLS: ACT-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  47.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TUMOR NECROSIS FACTOR RECEPTOR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12:
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 41; DB Pred. No. 63; 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PF341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 3; Length 277;
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SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION UNMER: US/08/472,940

FILING DATE: 06-JUN-1995

CLASSIFICATION: 530

PRIOR APPLICATION UNMER: US O8/147,784

FILING DATA: 06-JUN-1995

APPLICATION UNMER: US O8/147,784

FILING DATA: 08-JUN-1993

APPLICATION UNMER: US O8/147,784

FILING DATA: 08-JUN-1993

APPLICATION UNMER: 30,223

ATTORNEY/ACENT INFORMATION:
RESISTRATION UNMER: 30,223

REFERENCE/DOCKET NUMER: 30,223

REFERENCE/DOCKET NUMER: 05-490A-220

TELECOMMUNICATION INFORMATION:
TELEPAN: (415) 326-2400

TELECOMMUNICATION INFORMATION:
TELEPAN: (415) 326-2422

INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LEUGHH: 277 amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: protein

US-08-472-940-2

Query Match
Best Local Similarity 75.0%; Pred. No. 63;
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps

QY 2 LPLICGLIGPLA 13

Db 221 LGLVLGLIGPLA 232

Search completed: January 12, 2004, 08:20:07

Job time: 2.81437 secs
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

January 12, 2004, 08:12:09; Search time 8.27744 Seconds (without alignments) 1661.397 Million cell updates/sec

Title: Perfect score: Sequence: US-10-085-167-2\_COPY\_17\_159 745

1 LGPTPGPGSSELRSAFSAAR......PHYALGAPGATFSGYLVYAD 143

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : ...... PIR 76:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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ALIGNMENTS  tein precursor - human ose specific collagen-like factor quence revision 19-Jul-1996 #text 4944 Shimomura, I.; Funahashi, T.; Ma Commun. 221, 286-289, 1996 commun. 221, 286-289, 1996 nd expression of a novel adipose 708; MUID:96224171; PMID:8619847	1; NID:9871886; PIDN:BAA082: tissue iura, N.H.; Mazda, T.; Tomii erization of GBP28, a novel ID:97103474; PMID:8947845  12;135-149;173-178 <naksendogenous #status="" 28kda="" <sigs="" bindagens;="" carbozycoprotein;="" clq="" complement="" es<="" factor="" hydroxyproline="" ing="" predicted="" protein="" th="" that=""><th>A;Residues: 1-244 <mae> A;Residues: 1-244 <mae> A;Cross-references: DDBJ.D45371; NID:g871886; PIDN:BAA08227.1; PID:gA;Cross-references: DDBJ.D45371; NID:g871886; PIDN:BAA08227.1; PID:gA;Experimental source: adipose tissue R;Baxperimental source: Adipose tissue R;Nakano, Y; Tobe, T; Choi-Miura, N.H.; Mazda, T.; Tomita, M. Biochem. 120, 803-812, 1996 R;Nakano, Y; Tobe, T; Choi-Miura, N.H.; Mazda, T.; Tomita, M. Biochem. 120, 803-812, 1996 R;Nakano, Y; Tobe, T; Choi-Miura, N.H.; Mazda, T.; Tomita, M. Biochem. 120, 803-812, 1996 R;Nakano, Y; Tobe, T; Choi-Miura, N.H.; Mazda, T.; Tomita, M. Biochem. 120, 803-812, 1996 R;Nakano, Y; Tobe, T; Choi-Miura, N.H.; Mazda, T.; Tomita, M. Biochem. 120, 803-812, 1996 R;Nakano, Y; Tobe, T; Choi-Miura, N.H.; Mazda, T.; Tomita, M. Biochem. 120, 803-812, 1996 R;Nakano, Y; Tobe, T; Tomita, M. Biochem. 120, 803-812, NID:g871845 R;Nakano, Y; Tobe, T; Tomita, M. Best Local Similarity 31.8%; Score 191; DB 2; Length 244; Best Local Similarity 31.8%; Pred. No. 6.3e-124</mae></mae></th><th>Residues: 1-244 AMABS Cross-references: DDBJ:D45371; NID:g871886; PIDN:BAA08227.1; PID:g871887 Experimental Source: adipose tissue Nakano, Y.; Tobe, T.; Choi-Miura, N.H.; Mazda, T.; Tomita, M. Biochem. 120, 803-812, 1996 Title: Isolation and characterization of GBP28, a novel gelatin-binding Reference number: JC4944 Molecule type: protein Reference number: JC4944; MUID:97103474; PMID:8947845 Accession: JC4944 Molecule type: protein Scomment: This protein is an endogenous factor that binds with a collagen Genetics: Genetics: Genetics: Genetics: J-2494 Froduct: gelatin-binding 28kDa protein #status experimental homo Reywords: adipose tissue; glycoprotein; hydroxyproline 1-18/Domain: signal sequence #status predicted <sigs #status="" 114-241="" 19-244="" 28kda="" 42-107="" <amats="" <c1q="" c1q="" carboxyl-terminal="" collagen-like="" complement="" domain:="" experimental="" gelatin-binding="" homology="" product:="" protein="" region:=""> 5/Modified site: 4-hydroxyproline (Pro) #status experimental 230/Binding site: carbohydrate (Asn) (covalent) #status predicted Query Match Query Match 25.6%; Score 191; DB 2; Length 244; Matches 47; Conservative 29; Mismatches 54; Indels 18; Gaps Matches 47; Conservative 29; Mismatches 54; Indels 18; Gaps Matches 47; Conservative 29; Mismatches 54; Indels 18; Gaps Matches 47; Conservative 19; Score 191; Since Sinc</sigs></th><th>A;Residues: 1-244   A;Cross-references: DDBJ.D45371; NID:g871886; PIDN:BAA08227.1; PID:g871887  A;Experimental source: adipose tissue  R;Nakano, Y; Tobe, T; Choi-Miura, N.H.; Mazda, T; Tomita, M.  Biochem. 120, 803-812, 1996  A;Title: Isolation and Characterization of GBP28, a novel gelatin-binding  A;Reference number: JC4944; MUID:97103474; PMID:8947845  A;Rocession: JC4944  A;Molecule type: protein  A;Residues: 19-38;93-100;101-112;135-149;173-178 <nak>  C;Comment: This protein is an endogenous factor that binds with a collagen  C;Comment: B;  A;Gene: apM1  C;Superfamily: unassigned collagens; complement C1q carboxy1-terminal homo  C;Reywords: adipose tissue; glycoprotein; hydroxyproline  E;11-18/Domain: signal sequence #status predicted <sig>  F;19-244/Product: gelatin-binding 28kDa protein #status experimental   E;41-107/Region: collagen-like  F;230/Binding site: carbohydrate (Asn) (covalent) #status predicted  Query Match  Query Match  Best Local Similarity 31.8%; Pred. No. 6.3e-12;  Matches 47; Conservative 29; Mismatches 51;  Best Local Similarity 31.8%; Pred. No. 6.3e-12;  Matches 47; Conservative 29; Mismatches 54; Indels 18; Gaps  Oy 5 pGpGSSELRSAFSAFTPLEGTSEMAVTFDKVYNNIGDFPUXGSTGKPHCNIPGLYYPAY  Qy 65 TAGKAPHKSLSVMLVRNRDEVQALAFDEQRRPGARRAASQSAMLQLDYGDTVWLR  Db 104 PGEGAYVTSAFSVGLETYVT-IPMMPIRFTKIFYNQQNHYDGSTGKPHCNIPGLYYPAY  Qy 65 TAGKAPHKSLSVMLVRNANDEVQALAFDEQRRPGARRAASQSAMLQLDYGDTVWLR  Db 163HITVYMKDVKVSLFK-KDKAMLFTYDQYGENVDQ-ASGSVLLHLEVGDQVWLQ</sig></nak></th></naksendogenous>	A;Residues: 1-244 <mae> A;Residues: 1-244 <mae> A;Cross-references: DDBJ.D45371; NID:g871886; PIDN:BAA08227.1; PID:gA;Cross-references: DDBJ.D45371; NID:g871886; PIDN:BAA08227.1; PID:gA;Experimental source: adipose tissue R;Baxperimental source: Adipose tissue R;Nakano, Y; Tobe, T; Choi-Miura, N.H.; Mazda, T.; Tomita, M. Biochem. 120, 803-812, 1996 R;Nakano, Y; Tobe, T; Choi-Miura, N.H.; Mazda, T.; Tomita, M. Biochem. 120, 803-812, 1996 R;Nakano, Y; Tobe, T; Choi-Miura, N.H.; Mazda, T.; Tomita, M. Biochem. 120, 803-812, 1996 R;Nakano, Y; Tobe, T; Choi-Miura, N.H.; Mazda, T.; Tomita, M. Biochem. 120, 803-812, 1996 R;Nakano, Y; Tobe, T; Choi-Miura, N.H.; Mazda, T.; Tomita, M. Biochem. 120, 803-812, 1996 R;Nakano, Y; Tobe, T; Choi-Miura, N.H.; Mazda, T.; Tomita, M. Biochem. 120, 803-812, 1996 R;Nakano, Y; Tobe, T; Tomita, M. Biochem. 120, 803-812, NID:g871845 R;Nakano, Y; Tobe, T; Tomita, M. Best Local Similarity 31.8%; Score 191; DB 2; Length 244; Best Local Similarity 31.8%; Pred. No. 6.3e-124</mae></mae>	Residues: 1-244 AMABS Cross-references: DDBJ:D45371; NID:g871886; PIDN:BAA08227.1; PID:g871887 Experimental Source: adipose tissue Nakano, Y.; Tobe, T.; Choi-Miura, N.H.; Mazda, T.; Tomita, M. 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Biochem. 120, 803-812, 1996 A;Title: Isolation and Characterization of GBP28, a novel gelatin-binding A;Reference number: JC4944; MUID:97103474; PMID:8947845 A;Rocession: JC4944 A;Molecule type: protein A;Residues: 19-38;93-100;101-112;135-149;173-178 <nak>  C;Comment: This protein is an endogenous factor that binds with a collagen  C;Comment: B;  A;Gene: apM1  C;Superfamily: unassigned collagens; complement C1q carboxy1-terminal homo  C;Reywords: adipose tissue; glycoprotein; hydroxyproline  E;11-18/Domain: signal sequence #status predicted <sig>  F;19-244/Product: gelatin-binding 28kDa protein #status experimental   E;41-107/Region: collagen-like  F;230/Binding site: carbohydrate (Asn) (covalent) #status predicted  Query Match  Query Match  Best Local Similarity 31.8%; Pred. No. 6.3e-12;  Matches 47; Conservative 29; Mismatches 51;  Best Local Similarity 31.8%; Pred. No. 6.3e-12;  Matches 47; Conservative 29; Mismatches 54; Indels 18; Gaps  Oy 5 pGpGSSELRSAFSAFTPLEGTSEMAVTFDKVYNNIGDFPUXGSTGKPHCNIPGLYYPAY  Qy 65 TAGKAPHKSLSVMLVRNRDEVQALAFDEQRRPGARRAASQSAMLQLDYGDTVWLR  Db 104 PGEGAYVTSAFSVGLETYVT-IPMMPIRFTKIFYNQQNHYDGSTGKPHCNIPGLYYPAY  Qy 65 TAGKAPHKSLSVMLVRNANDEVQALAFDEQRRPGARRAASQSAMLQLDYGDTVWLR  Db 163HITVYMKDVKVSLFK-KDKAMLFTYDQYGENVDQ-ASGSVLLHLEVGDQVWLQ</sig></nak>
IGNMENTS  - human  19-Jul-1996 #text_change 20-Sep-1999  19-Jul-1996 #text_change 20-Sep-1999  Funahashi, T.; Matsuzawa, Y.; Matsubara, K.  6-289, 1996  6-289, 1996  6 a novel adipose specific collagen-like factor,  171; PMID:8619847	371886; PIDN:BAA08227.1; PID:g871887  H.; Mazda, T.; Tomita, M.  of GBP28, a novel gelatin-binding protein purifing PMID:8947845  19;173-178 <nak> 18;173-178 clarboxyl-terminal homology prodicted cSIGsprotein #status experimental <mat></mat></nak>	Mazda, T.; Tomita, M.  Mazda, T.; Tomita, M.  [GBP28, a novel gelatin-binding protein protein state of the protein	Mazda, T.; Tomita, M.  E GBP28, a novel gelatin-binding protein; PMID:8947845  173-178 <nak> Eactor that binds with a collagen-like defeator that binds with a c</nak>	Mazda, T.; Tomita, M.  E GBP28, a novel gelatin-binding protein; PMID:8947845  173-178 <nak> Eactor that binds with a collagen-like delement C1g carboxyl-terminal homology hydroxyproline delement SIG&gt; Cotein #status experimental <mat> -terminal homology <c1q> #status experimental vMAT&gt; -terminal homology c1Q&gt; -termin</c1q></mat></nak>

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submitted to the Protein Sequence Database, A;Reference number: Z18184
A;Accession: T14782
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N;Alternate names: complement subcomponent Clq beta chain C;Species: Homo sabiens (man)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: mRNA
A; Residues: 1-219 <OTT>
                                                                                                                                                                                                  Biochem. J. 179, 367-371, 1979
Biochem. J. 179, 367-371, 1979
A;Title: Complete amino acid sequences of the three collagen-like
A:Reference number: A90304; MUID:80020137; PMID:486087
                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Title: Molecular cloning a A;Reference number: A23422;
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                                                                                             Biochem. J. 173, 863-868; 1978
A;Title: Amino acid sequence of the N-terminal 108 amino acid
A;Reference number: A90301; MUID:79041552; PMID:708376
                                                                                                                                A; Molecule type: protein
A; Residues: 'E', 29-84, D', 86-99, 'P', 101-135
R; Reid, K.B.M.; Thompson, E.O.P.
Biochem, J. 173, 863-868; 1978
                                                                                                                                                                                                                                                                                   A;Residues: 28-253 <RE1>
A;Cross-references: EMBL:X03084
A;Note: the authors translated
                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: DNA
A; Residues: 'HS', 1-32 < REI>
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                                               A; Molecule type: protein
A; Residues: 28-99, 'P', 101-195 < RE3 >
                                                                                                                                                                                                                                                                       R; Reid, K.B.M
                                                                                                                                                                                                                                                                                                                                      A; Molecule type: mRNA
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Accession: T14782
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;Species: Homo sapiens (man)
;Date: 22-May-1981 #sequence revision 31-May-1996 #text_change·08-Dec-2000
;Accession: B23422; A23422; B90304; A90301; B90315; A03206
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              ;Reid, K.B.M.; Gagnon, J.; Fi
iochem. J. 203, 559-569, 1983
                                                                                  Accession: A90301
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3; Mismatches 57
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C;Superfamily: complement subcomponent Clq chain A; complement Clq carboxyl-terminal how C;Keywords: complement pathway; glycoprotein; heterodimer; hydroxylysine; hydroxyprolin: F;1-27/Domain: signal sequence #status predicted <SIG>F;28-253/Product: complement subcomponent Clq chain B #status experimental <MAT>F;33-116/Domain: collagenous, triple helix <COL>F;123-249/Domain: collagenous, triple helix <COL>F;123-249/Domain: complement Clq carboxyl-terminal homology <ClQ>F;123-249/Domain: complement Clq carboxyl-terminal homology <ClQ>F;123-249/Domain: complement Clq carboxyl-terminal homology <ClQ>F;123-249/Domain: collagenous carboxyl-terminal homology <ClQ>F;123-249/Domain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement protein Clq beta chain precursor - C;Species: Rattus norvegicus (Norway rat) C;Date: 16-Feb-1995 #sequence_revision 12-May-C;Accession: S49158 C;Schwaeble, W.; Petry, F.; Loos, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: protein
A; Residues: 136-253 < RE4 >
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Description: cDNA cloning and expression A;Reference number: S49158 A;Accession: S49158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Map position: 1p36.3-1p34.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: mRNA
A; Residues: 1-253 <SCH>
A; Cross-references: EMBL; X71127; NID: g510191; PIDN: CAA50440.1; PID: g510192
A; C; Superfamily: complement subcomponent Clq chain A; complement Clq carboxy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R;Schwaeble, W.; Petry, F.; Loos, M. submitted to the EMBL Data Library, March 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Gene: GDB:C1QB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              F;121-249/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              95
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          44;
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45; Conserv
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YGDTVWLRLHGAPHYALGAPGAT--FSGYLVYAD 143
                                                                                                                                                            RCRVPGAYFFSFTAGKAPHKSLSVMLVRNRDEVQ-ALAFDEQRRPGARRAASQSAMLQLD
                                                                                                                                                                                                                                      GP-PGPRGPKGGSGDYKATOKVAFSALRTVNSALRPNOAIRFEKVITNVNDNYEPRSGKF
                                                                                                                                                                                                                                                                                                                    GPTPGP----GSSELRS----AFSAARTTPLEGTSEMAVTFDKVYVNIGGDFDVATGQF
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 163.5; DB 2
Pred. No. 4.2e-09;
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C;Accession: S19018
C;Accession: S19018
R;Petry, F.; Reid, K.B.M.; Loc
J. Immunol. 147, 3988-3993, 19
A;Title: Gene expression of the companion of the companio
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C;Species: Homo sapi
C;Date: 22-May-1981
C;Accession: S14351;
                                                                                                                                                                                                                                                                                                                          RESULT
S19018
                                                                                                                                                                   complement subcomponent C1q chain A precursor C;Species: Mus musculus (house mouse) C;Date: 22-Nov-193 #sequence_revision 10-Nov-C;Accession: S19018
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A;Residues: 29-56,'p',58-65,'K',67-71,'p',73-83,'K',85-86,'D',88-89,'N',91-122 RRIP
C;Comment: The first component of complement is a calcium-dependent complex of the three ivation of C1r (enzyme), C1s (proenzyme), and the other eight components of complement.
C;Comment: The C1q subcomponent is composed of nine subunits, six of which are disulfide dimers of the C chain. Equimolar amounts of the A, B, and C chains are found after reductions.
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A;Title: Complete amino acid sequences of the three collagen-like
A;Reference number: A90304; MUID:80020137; PMID:486087
A;Accession: A03207
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131-1244/Domain: complement Clq carboxyl-terminal homology <CIO>
132/Disulfide bonds: interchain #status experimental
136,39,42,45,54,63,81,93,96,99,105/Modified site: 4-hydroxyproline
157,72,75/Modified site: 5-hydroxylysine (Lys) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Superfamily: complement subcomponent Clq chain A; complement Clq carboxyl-terminal hom; keywords: complement pathway; glycoprotein; homodimer; hydroxylysine; hydroxyproline; 1-28/Domain: signal sequence #status predicted <SIG>
;1-28/Domain: signal sequence #status predicted <SIG>
;29-245/Product: complement subcomponent Clq chain B #status predicted <MAT>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 44; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  75/Binding site: carbohydrate (Lys)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GPTPGPG-----SSELRSAFSAARTTPLEGTSEMAVTFDKVYVNIGGDFDVATGQFR 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EEVWLAVN--DYYDMVGIQGSDSVFSGFLLFPD
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                                                                                       K.B.M.; Loos, M.
988-3993, 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                D.J.; Reid, K.B.
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               the A- and B-chain of mouse MUID:92043789; PMID:1940381
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 160; DB 1;
Pred. No. 9.1e-09;
8; Mismatches 63
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mponent Clq gamma
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PMID:1706597
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                                                   different tissues
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Brain Res. Mol. Brain Res. 9, 71-77, 1991
A,Title: Molecular cloning of rat cerebellin-like
A,Reference number: A60032, MUID:91203483; PMID:18
A,Accession: A60032
A,Status: not compared with conceptual translation
                                                                                                                                                                                                                                   cerebellin-like glycoprotein - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 03-Mar-1993 #sequence_revision 03-Mar-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement subcomponent Clq chain C - r (;Species: Mus musculus (house mouse) C;Date: 13-Jan-1995 #sequence revision C:Date: C
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S29328
                                                                                                                                                                                R; Wada, C.; Ohtani, H.
                                                                                                                                                                                                                C; Accession:
                                                                                                                                                                                                                                                                                                             cerebellin-like
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Eur. J. Biochem. 2
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A; Molecule type:
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Pred. No. 5.3e-08;
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Pred. No. 2.3e-08;
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A,Molecule type: mRNA
A,Residues: 1-114,'R',116-253 <PET>
A,Residues: 1-114,'R',116-253 <PET>
A,Gross-references: EMBL:X16874; NID:g50222; PIDN:CAA34757.1; PID:g50223
C,Superfamily: complement subcomponent Clq chain A; complement Clq carbox
F,1-25/Domain: signal sequence #status predicted <SIG>
F,26-253/Product: complement subcomponent Clq chain B #status predicted <F;121-249/Domain: complement Clq carboxyl-terminal homology <ClQ>
                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: mRNA, Residues: 1-253 «RE2» A; Residues: 1-253 «RE2» A; Cross-references: GB:M36293; NID:g192147; R; PELY, F; Reid, K.B.M.; Loos, M. FEBS Lett. 258, 89-93, 1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement Clq B chain precursor - mouse (Species: Mus musculus (house mouse) C;Species: Mus musculus (house mouse) C;Date: 02-Jul-1996 #sequence revision 02-Jul-1996 #text_change 20-Aug-1999 C;Accession: I4950; I49527; S06836 R;Wood, L.; Pulaski, S.; Vogeli, G.
                                                                                                                                                                                                                                                                                                                                                                                             A;Title: Molecular cloning and characterization of the A;Reference number: S06836; MUID:90076497; PMID:2591537 A;Accession: S06836
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Reference number: I49527; MUID:88168728; PMID:3258283 A;Accession: I49527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: GB:M22531; NID:g192266; PIDN:AAA37335.1; PID:g309121
R;Wood, L.; Pulaski, S.; Vogeli, G.
Immunol. Lett. 17, 59-62, 1988
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A; Residues: 1-253 < RES>
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A; Accession: I49560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Immunol. Lett. 17, 115-120, 1988
A;Title: cDNA clones coding for the complete murine B chain A;Reference number: I49560; MUID:88197296; PMID:3258843
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                                                                                                                                                                   Query Match
Best Local S
Matches 44
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;Keywords: glycoprotein; transmembrane protein;32-49/Domain: transmembrane #status predicted <TMM>
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Best Local
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                                                                                                                                                                     44;
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                                                                                                                                                                                        Similarity
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                                          DFDVATGQFRCRVPGAYFFSFTAGKAPHKSLSVMLVRNRDEVQALAFDEQRRPGARRAAS 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KVHLKLERGNLMGGWKY----STFSGFLVF 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KGIYSFSFHVVKVYNRQTIQVSLMQNGYPVISAFAGDQD---VTREAASNGVLLLMERED
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                                                                                   VGPKGTPGPSGPRGPKGDSGDYGATQ-KVAFSALRTINSPLR--PNQVIRFEKVITNANE 149
    NYEPRNGKFTCKVPGLYYFTYHASSRGNLCVNLVRGRDRDSMQKVVTFCDYAQNTFQVTT
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27.2%;
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Pred. No. 8.6e-08;
6; Mismatches 51;
                                                                                                                                                                                      Score 149.5; DB 2;
Pred. No. 1.1e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   from
                                                                                                                          GSSELRSAFSAART--TPLEGTSEMAVTFDKVYVNIGG
                                                                                                                                                                     Mismatches
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C;Species: Homo sapiens (man)
C;Date: 30-Apr-1991 #sequence_revision 30-Apr-1991 #text
C;Accession: A37873
R;Urade, Y.; Oberdick, J.; Molinar-Rode, R.; Morgan, J.I
Proc. Natl. Acad. Sci. U.S.A. 88, 1069-1073, 1991
A;Title: Precerabellin is a cerebellum-specific protein A;Reference number: A37873; MUID:91126057; PMID:1704129
A;Accession: A37873
                                                                                                                                                                                                                                                                                                                                                            A;Residues: 1-193 <URA>
A;Cross-references: GB:M58583; NID:g180250; PIDN:AAA35676.1; PID:g180251
C;Superfamily: complement subcomponent C1q chain A; complement C1q carbo
                                                                                                                                                                                                                                                                                                                                          F;63-192/Domain: complement Clq carboxyl-terminal homology <ClQ>
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                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Status: preliminary
                                                                                                                                                                                                                                                                                              Query Match
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166 RAYLKLERGNLMGGWKY--
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                                                                                                                                                                                                                                                                            Similarity
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                                                                                                                          PGAYFFSFTAGKAPHK-SLSVMLVRNR-DEVQALAFDEQRRPGARRAASQSAMLQLDYGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QSAMLQLDYGDTVWLRLHGAPHYALGAPGAT - - FSGYLVYAD
                                                                                  KGIYSFNFHVVKVYNRQTIQVSLMLNGWPVISAFAGDQD---VTREAASNGVLIQMEKGD
                                                                                                                                                                      IGISVRSGSAKV--AFSAIRSTNHEPSEMSNRTMIIYFDQVLVNIGNNFDSERSTFIAPR
                                                                                                                                                                                                                                                      Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (man)
                                                                                                                                                                                                                                                                          20.0%;
                                       GAPHYALGAPGATFSGYLVY
                                                                                                                                                                                                                                                    ; Score 149; DB 2; 1; Pred. No. 9.2e-08; 27; Mismatches 52;
    STFSGFLVF 191
                                            141
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                                                                                                                                                                                                                                                                                              Length 193;
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                                                                                                                                                                                                                                                                                                                                                                 carboxyl-terminal
                                                                                                                                                                                                                                                          Gaps
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A; MCGCCA. (175 cLUV)
A; Residues: 1-75 cLUV)
A; Residues: 1-75 cLUV)
R; Ninomiya, Y.; Gordon, M.; van der Rest, M.; Schmid, T.; LL
Q. Biol. Chem. 261, 5041-5050, 1986
A; Title: The developmentally regulated type X collagen gene
A; Title: The mimber: I50218; MUID:86168227; PMID:3082876
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     collagen alpha 1(X) chain precursor - chicken

NAlternate names: type X collagen
C;Species: Gallus gallus (chicken)
C;Date: 07-Oct-1994 #sequence revision 10-Nov-1995 #text_change 13-Aug-1999
C;Accession: S23297; A31896; $65594; $77711; I50218
R;Ninomiya, Y; Castagnola, P.; Gerecke, D.; Gordon, M.K.; Jacenko, O.; LuVa maguchi, N.; Olsen, B.R.
in Extracellular Matrix Genes, Sandell L.J. and Boyd C.D., eds., pp.79-114, h.Pittle: The molecular biology of collagens with short triple-helical domain
                                                                                                                                                                                                                                                                             A;Residues: 1-674 <NIN>
R;LuValle, P.; Ninomiya, Y.; Rosenblum, N.D.; Olsen, B.R. J. Biol. Chem. 263, 18378-18385, 1988

A;Title: The type X collagen gene. Intron sequences split A;Reference number: A31896; MUID:89054019; PMID:2461368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Reference number: A; Accession: S23297
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                                                                                                                                                   Linsenmayer,
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A;Accession: S77711
A;Mclecule type: protein
A;Mcsidues: 104-112,'X',114-117;453-466 <NIN2>
C;Superfamily: collagen alpha 1 (VIII) chain; complement Clq carboxyl-terminal homology
C;Keywords: colled coil; extracellular matrix; glycoprotein; homotrimer; hydroxyproline;
F;1-18/Domain: signal sequence #status predicted <SIG>
F;1-18/Domain: signal sequence #status predicted <SIG>
F;457-673/Domain: complement Clq carboxyl-terminal homology <ClQ>
F;453,456/Modified site: hydroxyproline (Pro) #status experimental
F;611/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                          RESULT 13
C1HUQA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Keywords: coiled coil; extracellular matrix; glycoprotein; homotr: F;1-18/Domain: signal sequence #status predicted <SIG> F;19-674/Product: collagen alpha 1(X) chain #status predicted <MAT> F;547-673/Domain: complement Ciq carboxyl-terminal homology <CiQ>
                                                                          N;Alternate names: complement subcon
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Biochem. J. 273, 141-148, 19
A;Title: Isolation of cDNAs
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C;Date: 21-Nov-1993 #sequence_revision 23-Feb-1996 #text_change 13-Aug-1999
C;Accession: S13301
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A; Residues: 1-674 < THO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Reference number: S13301;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  collagen alpha 1(X) chain precursor - bovine
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Accession: S13301
;Species: Homo sapiens (man)
;Date: 24-Apr-1984 #sequence_revision
;Accession: S14350; A90304; A90315; A(
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;Superfamily: collagen alpha 1(VIII) chain; co; Keywords: colled coll; extracellular matrix;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cross-references: EMBL:X53556; NID:g263; PIDN:CAA37624.1; PID:g264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Accession: S13301
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47; Conserv
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                                                                                                                                                                                                                                                                                                                    NKQQHYDPRTGIFTCKIPGIYYFSYHIHVKGTH--AWVGLYKNGTPVM-YTYDEYIK-GY 626
                                                                                                                                                                                                                                                                                                                                                                                                                   GPPGPPGQVALPEDFVKAGQRPFVSANQGVTGMPVSAFTVILSKAYPAIGTPIPFDKILY 570
                                                                                                                                                                                                                                                               RRAASQSAMLQLDYGDTVWLRLHGAPHYALGAP---GATFSGYLV 140
                                                                                                                                                                                                                                                                                                                                              NIGGDFDVATGQFRCRVPGAYFFSFTAG-KAPHKSLSVMLVRNRDEVQALAFDEQRRPGA 98
                                                                                                                                                                                                                      LDQASGSAVIDLTENDQVWLQLPNAGSNGLYSPEYVHSSFSGFLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GPTPGPGSSELRSAFSAARTTPL----EGTSEMAVT----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                    onent Clq chain A precursor [validated] - complement subcomponent Clq alpha chain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            encoding the complete sequence of MUID:91113131; PMID:1703407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23;
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9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 148; DB 2;
Pred. No. 4.9e-07;
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Pred. No. 4.3e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 M.E.; Boot-Handford, R
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                    #text_change 08-Dec-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 674;
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C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence revision 03-Nov-1995 #text change 22-Jun-1999
C;Accession: S26396; S30086; S15826; S18249; A43901; I51870; S21856
R;Reichenberger, E.; Beier, F.; LuValle, P.; Olsen, B.R.; von der Mark, K.;
FEBS Lett. 311, 305-310, 1992
A;Title: Genomic organization and full-length cDNA sequence of human collage A;Reference number: S26396; MUID:93012005; PMID:1397333
A;Accession: S26396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Superfamily: complement subcomponent Clq chain A; complement Clq carboxyl-terminal C;Keywords: complement pathway; glycoprotein; heterodimer; hydroxylysine; hydroxyprol F;1-22/Domáin: eignal sequence #status predicted <SIG>
F;23-245/Product: complement subcomponent Clq chain A #status experimental <MAT>
F;31-109/Domain: collagenous, triple helix #status predicted <COL>
F;11-109/Domain: complement Clq carboxyl-terminal homology <ClQ>
F;26/Disulfide bonds: Interchain (to chain B-31) #status experimental F;26/Disulfide bonds: Interchain (to chain B-31) #status experimental F;33,48,67,100,103/Binding site: carbohydrate (Lys) (covalent) #status experimental F;33,48,67,100,103/Binding site: carbohydrate (Lys) (covalent) #status experimental F;39,45,54,57,73,55,97/Modified site: 4-hydroxyproline (Pro) #status experimental F;346/Binding site: carbohydrate (Asn) (covalent) #status experimental
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A;Introns: 55/1
C;Supperface:
                                                                                                                                                                                                                                               CGHUID

collagen alpha 1(X) chain precursor - hum
N;Alternate names: procollagen alpha 1(X)
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A;Residues: 131-171,'N',173-177,'W',179-239,'ILPGFSA' <RE2>
C;Comment: The first component of complement is a calcium-dependent complex of the thre ivation of C1r (enzyme), C1s (proenzyme), and the other eight components of complement. C;Comment: The C1q subcomponent is composed of nine subunits, six of which are disulfice (see PIR:C1HUQC) chain. Equimolar amounts of the A, B, and C chains are found after red
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Molecule type: protein
A;Residues: 23-96,'K',98-102,'P',104-130 <REI>
R;Reid, K.B.M.; Gagnon, J.; Frampton, J.
Biochem. J. 203, 559-569, 1982
A;Title: Completion of the amino acid sequences of the A and A;Reference number: A90315; MUID:82283890; PMID:6981411
A;Accession: A90315
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A;Accidence number: A90304
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A; Title: Characterization and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P-HYALGAPG-ATFSGYLVY 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KGHIYQGSEADSVFSGFLIF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FQVLSQWEICLSIVSSSRGQVRRSLGFCDTTNKGLFQVVSGGMVLQLQQGDQVWVEKDPK 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SPGNIKDQPRPAFSAIRRNPPMGGN--VVIFDTVITNQEEPYQNHSGRFVCTVPGYYYFT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FTAGKAPHKSLSVMLVRNRDEVQALAFDEQRRPGARRAASQSAMLQLDYGDTVWLRLHGA 123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19.7%; Score 147; DB 1; 30.7%; Pred. No. 1.9e-07;
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PMID:1706597
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                                                                                                                                   Mark, K.; Bertling,
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A;Readus: transpace mRNA
A;Molecule type: mRNA
A;Residues: 520-597, D',599-680 <WAL>
A;Residues: 520-597, D',599-680 <WAL>
A;Residues: 520-597, D',599-680 <WAL>
A;Cross-references: GB:S68531; NID:g545180; PIDN:AACG0615.1; PID:g545181
A;Cross-references: GB:S685181; PIDN:AACG0615.1; PID:g545181
A;Cross-references: GB:S685181; PIDN:AACG0615.1; PID:g545181
A;Cross-references: GB:S685181; PID:g545181; PIDN:AACG0615.1; PID:g545181
A;Cross-references: GB:S685181; PID:g545181; PIDN:AACG0615.1; PID:g545181
A;Cross-references: GB:S685181; PID:g545181; PIDN:AACG0615.1; PID:g545181; PID:g545
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A; Residues: 561-647, 'G', 649-666 < AP2>
A; Residues: 561-647, 'G', 649-666 < AP2>
A; Cross-references: EMBL: K58879; NID: 930013; PIDN: CAA41686.1; PI
R; Thomas, J.T.; Cresswell, C.J.; Rash, B.; Nicolai, H.; Jones, T
Biochem. J. 280, 617-623, 1991
A; Title: The human collagen X gene. Complete primary translated
A; Reference number: S18249; MUID: 92109659; PMID: 1764025
A; Accession: S18249
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A; Residues: 'TIPFYGWVCWVCLL',52-680 <APT>
A; Cross-references: EMBL:X65120; NID:g23129
A; Note: the initial difference is probably of R; Apte, S.; Mattei, M.G.; Olsen, B.R.
FEBS Lett. 282, 393-396, 1991
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 547-656 <-KE2>
A;Cross-references: GB:M74050; GB:D57494; NID:g339884; PIDN:AAA61221.1;
A;Cross-references: GB:M74050; GB:D57494; NID:g339884; PIDN:AAA61221.1;
A;Note: sequence extracted from NCBI backbone (NCBIN:69012, NCBIP:69014)
A;Note: sequence extracted from NCBI backbone (NCBIN:69012, NCBIP:69014)
A;Note: sequence extracted from NCBI backbone (NCBIN:69012, NCBIP:69014)
A;Note: sequence extracted from NCBI backbone
A;Note: Amino acid substitutions of conserved residues in the carboxyl-
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A;Accession: S15826
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                                                                                                                                                                                                                                                                                               C;Superfamily: collagen alpha 1(VIII) chain; complement Ciq carboxy C;Keywords: coiled coil; extracellular matrix; glycoprotein; homotr F;1-18/Domain: signal sequence #status predicted <SIG>
F;19-680/Product: collagen alpha 1(X) chain #status predicted <MAT>
F;19-65/Domain: amino-terminal nonhelical #status predicted <MC2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Note: a defect in this gene may C;Complex: type X collagen may be
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A;Note: the sequence from Fig. 3 is inconsistent with that from Fig. 2 in
R;Restchenberger, E; Aigner, T.; von der Mark, K.; Stoss, H.; Bertling, W.;
Dev. Biol. 148, 562-572, 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 be important for skeletogenesis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C; Function:
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A;Map position: 6q21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Accession: I51870
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Query Match
Best Local S
Matches 52
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                                                                                                                                             ;57-519/Region: interrupted helical
;520-680/Domain: amino-terminal non
;553-679/Domain: complement C1g car;
;617/Binding site: carbohydrate (As;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;Description:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Status: translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Reference number: I51870; MUID:94136476;
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                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    structural component of extracellular fibrous
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6q21-6q22
       Conservative
                                   19.5%;
       22;
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                                                                                                                                                         carboxyl-terminal
(Asn) (covalent) ;
                                                                                                                                                                                                                                    nonhelical #status
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   Pred. No. 9.9e
2; Mismatches
                                                                              Score
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                                                                                                                                                         (covalent) #status
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                                           9e-07
                                                                              DB 1;
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                                                                      Length 680;
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, T.; Solomon,
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       36;
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A;Molecule type: protein
A;Molecule type: protein
A;Residues: 31-40,'A',42-50,'Q',52-215 <RON>
C;Superfamily: complement subcomponent Clq chain A; complement Clq carbox C;Superfamily: complement subcomponent Clq chain A; complement Clq carbox C;Keywords: glycoprotein; hibernation; plasma
F;1-30/Domain: signal sequence #status predicted <SIG>
F;31-215/Product: hibernation-related protein HP-27 #status experimental F;31-214/Domain: complement Clq carboxyl-terminal homology <ClQ>
F;31-214/Domain: complement Clq carboxyl-terminal homology <ClQ>
F;155/Binding site: carbohydrate (Asn) (covalent) #status predicted
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C48150
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A;Accession: A41752
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A; Title: Identification of
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48; Conserv
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                                      WLRLH-GAPHYALGAPGATFSGYLVY 141
                                                                                                                                                                                  GPTPGPG-----SSELRSAFSAARTTPLEGTSEMAVTFDKVYVNIGGDFDVATGOFRCRV
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WLENKLSQTDLERGTVQAVFSGFLIH
                                                                        PGLYQFGFHI-EAVQRAVKVSLMRNGTQVMEREAEAQ---DGYEHISGTAILQLGMEDRV
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RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
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RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Willalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RG Roherch A., Schein J.E., Jones S.J.M., Marra M.A.;
"Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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PiddLington C.S., Bishop P.;

"Homo saplens complement-clq tumor necrosis factor-related protein.";

Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
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Mammalia; Eutheria; Primates;
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                                                                                                                                                                                                                                                                                                                                       or send an email to license@isb-sib.ch).
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15-SEP-2003
                                                                                                                                                                                                                                               Genew; HGNC:14325; C1QTNF2.
InterPro; IPR001073; C1q.
                                                                                                                                                          PRINTS; PR00007; COM
SMART; SM00110; C1Q;
                                                                                                                                        PROSITE; PS01113; C1Q; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIMILARITY: Contains 1 collagenous domain. SIMILARITY: Contains 1 C1Q domain.
                                                                                                                                                                                         PF00386; Clq; 1.
PF01391; Collagen; 2.
                                                                                                                     Signal.
                                                                                                                                                                                                                              IPR000087; Collagen.
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S., Bishop I
                                  40
143
                                                                                    16
                                                                                                                                                                             COMPLEMNICIO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PubMed=12477932;
                141
285
29952
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285
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Last annotation update)
                  ₩
;
                                               POTENTIAL.

COMPLEMENT-C1Q TUMOR N

RELATED PROTEIN 2.

COLLAGEN-LIKE.
C1Q.
; 7E31FF9868D4EDFA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Craniata; Vertebrata; Catarrhini; Hominidae;
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                                                                                      NECROSIS FACTOR
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; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N
                                                                                                                                                                                                                                                                                                                                                                                                             restrictions
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                                                                                                                                                                                                                                                                                                                                                                                                                                              collaboration
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RESULT 3
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HUMAN
                                                                                                                                                                           TNF's and to genes expressed in activated T cells, inchromosome 1g21.3-g23, a susceptibility locus identi combined hyperlipidemia (FCH).";
                                                                                                                                                                                                                                                                                                  MEDLINE=99196984; PubMed=10095105; Saito K., Tobe T., Minoshima S., Asakawa S., Sumiya J., Yoda M., Nakano Y., Shimizu N., Tomita M.; "Organization of the gene for gelatin-binding protein (GBP28)."; Gene 229:67-73(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APM1 OK ACCOUNTS (Human).
Homo sapiens (Human) Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1997
15-SEP-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q15848;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APM1
MEDLINE=20440368;
Ouchi N., Kihara
                                                                                                                                                                                                                                                   Schaeffler A.,
                                                                                                                                                                                                                                                              MEDLINE=99333693; PubMed=10403784;
                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                   tactor,
                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE=Adipose tissue;
MEDLINE=96224171; PubM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Adiponectin
                                                                                                                                                                                                                                      Schaeffler A., Orso E., Palitzsch K.D., Fuerst A., Schoelmerich J., Schmitz G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (ACRP30) (Adipose most abundant
                                                            negatively regulates the functions of macrophages.
                                                                                                              Ouchi N.,
                                                                                                                                                                                                                                                                                                                                                                                     "cDNA cloning and expression of a novel adipose specific collagen-like factor, apM1 (AdiPose Most abundant Gene transcript 1)."; iochem. Biophys. Res. Commun. 221:286-289(1996).
                         CHARACTERIZATION
                                                                                                                                    MEDLINE=20417747;
                                                                                    Adiponectin,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OR ACRP30 OR GBP28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HUMAN
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                                                                                                                         Τ.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YYFTYDITLA-NKHLAIGLVHN-GQYRIRTFD--ANTGNHDVASGSTILALKQGDEVWLQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IFYSEQNGLFYDPYWT----DSLFTGFLIYAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YFFSFTAGKAPHKSLSVMLVRNRDEVQALAFDEQRRPGARRAASQSAMLQLDYGDTVWLR 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                      Okubo K.,
                                                                                                            Oritani K.
Kihara S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (Rel. 35, Last sequence update)
(Rel. 42, Last annotation update)
(Rel. 42, Last annotation update)
(precursor (30 kDa adipocyte complement-related)
(precursor abundant gene transcript 1) (apM-1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                         N.A
                                                                                    a new member of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -GSSELRSAFSAA--RTTPLEGTSEMAVTFDKVYVNIGGDFDVATGQFRCRVPGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                            PubMed=10961870;
i K., Takahashi I., Ishil
s., Funahashi T., Tenner
                                                                                                                                                                                                                                                                                                                                                                                                                                               PubMed=8619847;
           PubMed=10982546;
                                                                                                                                                                                                                                                                                                                                                                                                                                       Shimomura
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26.3%;
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  Arita
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                                                               growth of .";
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Pred. No. 4.
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Catarrhini; Hominidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                         260:416-425(1999).
  Okamoto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                       Funahashi
                                                                                    family of soluble defense collagens
                                                                         myelomonocytic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     244
                                                                                                             Ishikawa J., Matsuy
enner A.J., Tomiyama
                                                                                                                                                                                                   ed T cells, is mapped to locus identified for familial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 1;
.5e-13;
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  Maeda
                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  46;
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                                                                                                                Matsuyama
omiyama Y.
                                                                          progenitors and
                                                                                                                                                                                                                             to the family
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Euteleostomi;
                                                                                                                                                                                                                                                     Drobnik W.,
  Kuriyama
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(Gelatin-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24;
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EMBL; D45371; BAA08227.1; --
EMBL; AB012165; BAA86716.1;
EMBL; AB012164; BAA66716.1;
EMBL; AJ131460; CAB52413.1;
EMBL; AJ131461; CAB52413.1;
                                                                                                                                                                                                                                                                                                                                  use by non-profit institute modified and this statement entities requires a license
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hara K., Boutin P., Mori Y., Tobe K., Dina C., Yasuda K., Yamauchi T., Otabe S., Okada T., Eto K., Kadowaki H., Hagura R., Akanuma Y., Yazaki Y., Nagai R., Taniyama M., Matsubara K., Yoda M., Nakano Y., Kimura S., Tomita M., Kimura S., Ito C., Froguel P., Kadowaki T.; "Genetic variation in the gene encoding adiponectin is associated with an increased risk of type 2 diabetes in the Japanese population."; Diabetes 51:536-540(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Shudo K., Youa ...,
Shudo K., Youa ...,
Froquel P., Kadowaki T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hotta K., Nishida M., Takahashi M., Muraguchi M., Ohmoto Y., Nakamura T., Yamashita S., Funahashi T., Matsuzawa Y.; "Adiponectin, an adipocyte-derived plasma protein, inhibits endothelial NF-kappaB signaling through a cAMP-dependent pathway."; Circulation 102:1296-1301(2000).
                                                                                                                                                                                                                                                                                                        or send
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Takahashi M., Arita Y., Yamagata K., N
Horie M., Shimomura I., Hotta K., Kuri
Yamashita S., Funahashi T., Matsuzawa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hotta K., Nishida M., 1
Nakamura T., Yamashita
                                                                       GO; GO:0006091; P:energy pathways;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=21671103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=20378830;
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InterPro; IPR001073; Cīq.
InterPro; IPR000087; Collagen
Pfam; PF00386; Clq; 1.
                                                                                                                                                                                                                                                                                                                                                                                                            the European
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VARIANTS ARG-84;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              adiponectin.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Secreted into plasma.

DISEASE: Defects in APM1 are the cause of adiponectin (MIM:605441), resulting in very low concentration of padiponectin. Decreased adiponectin plasma levels are awith obesity insulin resistance, and diabetes type 2. PHARMACEUTICAL: Adiponectin might be used in the treating the type 2 and insulin resistance.

SIMILARITY: Contains 1 collagenous domain.

SIMILARITY: Contains 1 ClQ domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EXPRESSION OF ENDOTHBLIAL ADHESION MOLECULES. INVOLVED CONTROL OF FAR METABOLISM AND INSULIN SENSITIVITY. SUBUNIT: HOMODLIGOMER (POTENTIAL).
SUBCELLULAR LOCATION: Secreted.
TISSUE SPECIFICITY: Synthesized exclusively by adipocyt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FUNCTION: IMPORTANT NEGATIVE REGULATOR SYSTEMS; MAY BE INVOLVED IN ENDING INFERIS ENDITY INHIBITS ENDITY INHIBITS ENDITY FUNCTIONS, INHIBITS ENDITY FOR A CAMP-DEPENDENT PATHWAY, INHIB
                                                                                                                                                                                                                                                                                                                                                                             SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  fat-derived hormone adiponectin ciated with both lipoatrophy and Med. 7:941-946(2001).
                                                                                                    JC4708; JC4708.
605441; -.
                                                                                                                                                                                                                                                                                                        s requires a license agreement an email to license@isb-sib.cl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADIPONECTIN DEFICIENCY CYS
=20378830; PubMed=10918532;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 T., Kamon J., Waki H., Terauchi Y., Kubota N., Hara K., Ide T., Murakami K., Tsuboyama-Kasaoka N., Ezaki O., Y., Gavrilova O., Vinson C., Reitman M.L., Kagechika H., Yoda M., Nakano Y., Tobe K., Nagai R., Kimura S., Tomita
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   structure and
                                                                                                                                                                                                                                                                                                                                                  Bioinformatics Institute. The profit institutions as long this statement is not removed.
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Hotta K., Kuriyama H.,
T., Matsuzawa Y.;
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Kihara
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RESULTI
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ID CQT6-PU
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AC QQ
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Best Local S
Matches 47
                                                                                                                                                          CQTS_HUMAN STANDARD
QSBXJ0; QSUFX4;
28-FEB-2003 (Rel. 41, C
28-FEB-2003 (Rel. 41, L.
28-FEB-2003 (Rel. 41, L.
28-FEB-2003 (Rel. 41, L.
Complement-clq tumor ne.
ClQTNF5 OR CTRP5.
Homo sapiens (Human).
Eukaryota; Metazoa; Cho
Mammalia; Eutheria; Prin
                                                                                                                                                                                                                                                                                                                                               LT 4
HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DISULFID
MOD_RES
                                                   SEQUENCE FROM N.A.
Sheppard P.O., Humes J.M.;
"Homo sapiens complement-clq
submitted (DEC-2000) to the E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIGNAL
CHAIN
DOMAIN
SEQUENCE OF 29
TISSUE=Uterus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF01391; Collagen; 1. PRINTS; PR00007; COMPLEMNTC1Q. ProDom; PD000007; Clg_helix; 1.
                                                                                                                                           NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VARIANT
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PROSITE; PS01113; C10; 1.
Hormone; Collagen; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               163
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47; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----HITVYMKDVKVSLFK-KDKAMLFTYDQYQENNVDQ-ASGSVLLHLEVGDQVWLQ
                                                                                                                                                                                                                                                                                                                                                                                                                       VYGEGERNGLYADNDNDSTFTGFLLYHD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PGEGAYVYRSAFSVGLETYVT-IPNMPIRFTKIFYNOQNHYDGSTGKFHCNIPGLYYFAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TAGKAPH----KSLSVMLVRNRDEVQALAFDEQRRPGARRAASQSAMLQLDYGDTVWLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PGPGSSELRSAFSAARTTPLEGTSEMAVTFDKVYVNIGGDFDVATGQFRCRVPGAYFFSF
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                   25-243 FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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                                                                                                                                                                                                                                                                                                                              STANDARD;
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                                                                                                                                                               Chordata;
Primates;
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                                                                                                                                                                                                                                      necrosis
                                                                                                                                                                                                                                  Last sequence update)
Last annotation update)
necrosis factor-related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        mutation;
                                                                                                                                                                                                                                                                                         Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                29;
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tion; Obesity; Diabetes
                                                   [ tumor necrosis f
EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INTERCHAIN (BY HYDROXYLATION (I)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. 1.25
9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 191;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /FTId=VAR_013273.
R -> C (in adiponectin
/FTId=VAR_013274.
V -> M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FTId=VAR_013277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HYDROXYLATION
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                                                                                                                                                              Craniata; V
Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FTId=VAR_013278.
64D8C6C1204B1018
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /FTId=VAR_013276
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                                                                                                                                                                                                                                                                                                                              243
                                                                                                                                                                                                                                                                                                                                                                                                                           242
                                                                                                                                                                                                                                                                                                                                                                                                                                                         143
                                                                                                                                                                             Vertebrata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             . 2e-1
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(BY SIMILARI)
                                                     factor-related
3J databases,
                                                                                                                                                                                                                                      protein
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Y SIMILARITY)
Y SIMILARITY)
Y SIMILARITY
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mellitus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                               Euteleostomi, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        deficiency)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  244;
                                                                                                                                                                                                                                      precursor.
                                                                  protein.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    119
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RESULT 5
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   RACE RAPERS OF THE RESERVE OF THE RE
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Best Local s
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DOMAIN
SEQUENCE
                                                                                                                                                                                                                                                                                                              CQT6_HUMAN
Q9BXI9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PIR; T14782; T14782.
Genew; HGNC:14344; C1QTNF5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AF329841; AAK17965.1; -. EMBL; AL110261; CAB53702.1; -.
                                                                                                                                                                                                                               O9BXI9;
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00386; Clq; 1.
Pfam; PF01391; Collagen; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Collagen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR001073; Clq.
InterPro; IPR000087; Collagen.
             SEQUENCE FROM N.A. TISSUE=Placenta; MEDLINE=22388257;
                                                                                SEQUENCE FROM N.A.

PiddLington C.S., Sheppard P.O.;

"Homo sapleans complement-clq tumor necrosis f.
Submitted (DEC-2000) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                 Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                              CBI_TaxID=9606;
                                                                                                                                                                                                                  sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; PR00007; COMPLEMNTC1Q.
SM00110; C1Q; 1.
B; PS01113; C1Q; FALSE_NEG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GPTPGPGSSEL--RSAFSAART-TPLEGTSEMAVTFDKVYVNIGGDFDVATGQFRCRVPG
                                                                                                                                                                                                                                                                                                                                                                                                                   WVQVGVGDYIGIYASIKTDSTFSGFLVYSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VYYFAVHA-TVYRASLQFDLVKNGESIASFFQFFGGWPKPA---SLSGGAMVRLEPEDQV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AYFFSFTAGKAPHKSLSVMLVRNRDEVQAL--AFDEQRRPGARRAASQSAMLQLDYGDTV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 WLRLHGAPH---
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97
243
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B
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                                                                                                                                                                                                                   (Human)
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                                                                                                                                                                                                                                                                                                                                  STANDARD;
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; PubMed=12477932;
Feingold E.A., Gr
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243
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25298
                                                                                                                                                                                 Chordata;
Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25.4%;
35.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                YALGAPGATESGYLVYAD
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COMPLEMENT-C1Q TUMOR RELATED PROTEIN 5.

COLLAGEN-LIKE.
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; 7CCDA65CDA7EB784
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 189; DB 1
Pred. No. 2e-12;
                                                                                                                                                                                 Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
 Grouse L.H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               H.-W.,
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                                                                                                   factor-related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                57;
                                                                                                                                                                                                                                                  protein 6
 Derge
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                                                                                   databases
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 J.G.,
                                                                                                                                                                                                                                                    precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12;
                                                                                                 protein.";
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                                                                                   APM1_MOUSE
                                                                                                   RESULT
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Best Local S
Matches 59
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DOMAIN
CARBOHYD
CONFLICT
SEQUENCE
_APM1_MOUSE STANDARD;

Q60994; Q62400; Q9DC68;

Q1-NOV-1997 (Rel. 35, Creat

Q1-NOV-1997 (Rel. 35, Last

15-SEP-2003 (Rel. 42, Last
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This
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RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., RA Brownstein M.J., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hullyk S.W., RICHARD S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., RA Richards J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Ra Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Ra Hikkesley R.W., Touchman J.W., Green E.D., Dickson M.C., Ra Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Ra Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Ra Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Ra Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Ra Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Ra Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Ra Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Ra Butterfield Y.S.N., Krzywinski M.I., Skalaka U., Smailus D.E., Ra Green E.D., Dickson M.C., Scheun J.E., Jones S.J.M., Marra M.A.; Thuman and mouse cDNA sequences."; Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AF329842; AAK17966.1; --
EMBL; BC020551; AAH30551.1; --
Genew; HGNC:14343; C1QTNF6.
InterPro; IPR001073; C1q.
InterPro; IPR000087; Collagen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       between the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and for entities requires a license agreement (See http://www.isb-sib-entities requires a license agreement (See http://www.isb-sib-entities.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00386; Clq; 1.
Pfam; PF01391; Collagen; 1.
PRINTS; PR00007; COMPLEMNTCLQ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- SIMILARITY: Contains 1 collagenous -!- SIMILARITY: Contains 1 C1Q domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PR00007; COMPLEMNTCIC; PS01113; C1Q; FALSE
                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                             SQSAMLQLDYGDTVWLRL----HGAPHYALGAPGATFSGYLVYAD
                                                                                                                                      CFDMATGQFAAPLRGIYFFSLNVHSWNYKETYVHIMHNQKEAVIL----YAQPSERSIMQ
                                                                                                                                                                                                  DFDVATGOFRCRVPGAYFFSFTAGKAPHKSLSVMLVRNRDEVQALAFDEORRPGARR-AA
                                                                                                                                                                                                                                                                     GPQGEPGPQGSKGDKGEMGSPGAPCQKRFFAFSVGRKTALHSGEDFQTLLFERVFVNLDG
                                                                                                                                                                                                                                                                                                                                        GP--TPGPGSS-----ELRS-----AFSAARTTPL-EGTSEMAVTFDKVYVNIGG
SQSVMLDLAYGDRVWVRLFKRQRENAIYSNDFDTYITFSGHLIKAE
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278
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278
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35.5%; Pred. No. 3e-12;
tive 18; Mismatches
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C1Q.
N-LINKED (GLCNAC. .
G -> V (IN REF. 2).
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COMPLEMENT-C1Q TRELATED PROTEIN
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RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Kelischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazazarelli J., Mombaerts P.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Sasaki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
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MEDIJUNE 96209999; PubMed=86318//,
Hu E., Liang P., Spiegelman B.M.;
"AdipoQ is a novel adipose-specific
"AdipoQ is a novel adipose-specific
"I Biol. Chem. 271:10697-10703(1996)
                                                                           MEDLINE=21372499; PubMed
Berg A.H., Combs T.P., I
"The adipocyte-secreted
                                                                                                                                                                                                                                   Froguel P., Kadowaki T.;
"The fat-derived hormone adiponectin associated with both lipoatrophy and
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Scherer P.E., Williams S., Fogliano M.,
"A novel serum protein similar to Clq, ;
                                                                                                                                                                                                                                                                                                                                                                                              Yamauchi T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Functional annotation of a Nature 409:685-690(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  of the mouse gene encoding Acrp30.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PubMed=11162643;
                                                        action.
                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=21372498; PubMed=11479627;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Das K., Lin Y., Widen E., "Chromosomal localization,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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J. Biol. Chem
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                                                                                                                                                                  FUNCTION
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(ACRP30) (Adipocyte specific
     FUNCTION:
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OR ACRP30 OR AL
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  7:947-953(2001)
ION: IMPORTANT N
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                                                                                                                                                                                                                7:941-946(2001).
                                                                                                                                                                                                                                                                                                                                          Gavrilova O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   270:26746-26749(1995).
                                                                                                                                                                                                                                                                                                          on J., Waki H., Terauchi Y., Kubota N., Hara
Murakami K., Tsuboyama-Kasaoka N., Ezaki O.,
ilova O., Vinson C., Reitman M.L., Kagechika
I., Nakano Y., Tobe K., Nagai R., Kimura S., 1
                                                                                                         PubMed=11479628;
I.P., Du X., Brow
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Res.
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                                                                           Du X., Brownlee
d protein Acrp30
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     NEGATIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Zhang Y., Scherer P.E.;
, expression pattern, and promo
g adipocyte-specific secretory
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Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       280:1120-1129(2001).
  REGULATOR
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                                                                                                                                                                                                                                      reverses insulin obesity.";
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produced
                                                                           M., Scherer P.E.;
enhances hepatic
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HEMATOPOIESIS AND
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; Murinae; Mus.
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PRODOM; PD000007; Clg helix; 1.
SMART; SM00110; ClQ; 1.
PROSITE; PS01113; ClQ; 1.
PROSITE; PS01113; ClQ; 1.
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or send a
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GO; GO:0005515; F:protein binding activity; 1
GO; GO:0006635; P:fatty acid beta-oxidation;
InterPro; IPR001073; Clq.
InterPro; IPR000087; Collagen.
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                                                                                                                                                                                                                                                                                     DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUBUNIT: Homooligomer.
SUBCELLULAR LOCATION: Secreted.
TISSUE SPECIFICITY: Synthesized exclusively by
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           secreted into plasma.
INDUCTION: DURING HORMONE-INDUCED
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MGI:106675; Acrp30.
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U49915; AAB06706.1; -.
AF304466; AAK13417.1; -.
AK003138; BAB22597.1; -.
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                                                                                 l Similarity
47; Conser
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                   TAGKAPH-----KSLSVMLVRNRDEVQALAFDEQRRPGARRAASQSAMLQLDYGDTVWLR
                                                            PGPGSSELRSAFSAARTTPLEGTSEMAVTFDKVYVNIGGDFDVATGQFRCRVPGAYFFSF
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RX Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Brownstein M.J., Walland, J., Abramson R.D., Mullahy S.J.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Villalon D.K., Muzny D.M., Sodergran E.J., Lu X., Gibbs R.A.,

RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Blakeeley R.W., Touchman J.W., Schmutz J., Myers R.M.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

RA Rodriguez A.C., Grimcood J., Schmutz J., Myers R.M.,

RA Rodriguez A.C., Grimcood J., Schmutz J., Myers R.M.,

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RA Rodriguez A.C., Grimcood J., Schmutz J., Myers R.M.,

RA Rodriguez A.C., Grimcood J., Schmutz J., Myers R.M.,

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RA Rodriguez A.C., Grimcood J., Schmutz J., Myers R.M.,

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Mammalia; Eutheria;
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                                                                                                                                                use by non-profit institutions as long as modified and this statement is not removed. Usentities requires a license agreement (See htt
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EMBL; AF410771; AAK95248.1; -.
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16-OCT-2001
                                                                                                                                                                                                                       Berube N.G., Swanson X.H., Bertram M.J., Kittle J.D., Didenko Baskin D.S., Smith J.R., Pereira-Smith O.M.;
"Cloning and characterization of CRF, a novel Clq-related fact expressed in areas of the brain involved in motor function.";
Brain Res. Mol. Brain Res. 63:233-240(1999)
-!- TISSUE SPECIFICITY: EXPRESSED IN BRAINSTEM. MORE ABUNDANT OF THE NERVOUS SYSTEM INVOLVED IN MOTOR FUNCTION, SUCH AS PURKINJE CELLS OF THE CEREBELLUM, THE ACCESSORY OLIVARY NUTTER PONS AND THE RED NUCLEUS.
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                                                                                                     use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
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Mammalia; Eutheria; Rodentia;
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                                                   EMBL; AF095155; AAC64187.1; -
MGD; MGI:1344400; Clgrf.
GG:0005737; C:cytoplasm;
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                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=10090;
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                                  InterPro; IPR001073; Clq.
InterPro; IPR000087; Collagen.
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XX Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

XX Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

XX Altachel S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

XX Altachelko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

XX Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

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XX Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

XX Altachelko J., Jones G.J., Davawant T.L., Scheetz T.E.,

XX Altachelko J., Wolley K.C., Hole S., Carninci P., Prange C.,

XX Altachelko J., McEwan P.J., McKernan K.J., Abramson R.D., Mullahy S.J.,

XX Altachelko J., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

XX Altachelko J., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

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XX Altachelko J., McKernan K.J., J., J., Gunaratne P.H.,

XX Altachelko J., McKernan K.J., Malek J.A.,

XX Altachelko J., McKernan K.J., Marka M.,

XX Altachelko J., McKernan K.J., Marka M.,

XX Altachelko J., McKernan K.J., Marka M.,

XX Altachelko J., McKernan K.J., McKernan M.A.,

XX Altachelko J., McKernan K.J., Jones S.J.M., Marka M.A.,

Young A.C., Shevchenko Y., Bouffard G.G.,

XX Altachelko J., McKernan K.J., Jones S.J.M., Marka M.A.,

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28-FEB-2003
15-SEP-2003
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Mammalia; Eutheria;
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     SWISS-PROT entry is copyright.
een the Swiss Institute of Bio
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COLLAGEN-LIKE.
C1Q.
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Catarrhini; Hominidae;
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InterPro; lrnu:
Pfam; PF00386; C1q; l.
Pfam; PF01391; Collagen; 2.
Pfam; PF01391; COMPLEMNTC1Q.
MEDLINE=22388257; PubMed=12477932;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., S.
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., I
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CQT1 HUMAN STANDARD;
Q9BXJI; Q96NF2; Q9GZR4;
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Complement-clq tumor necrosis factor-related
(G protein coupled receptor interacting prote
C1QTNF1 OR CTRP1.
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Mammalia; Eutheria;
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PROSITE; PS01113; C1Q; 1.
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                                                                                                                                                                                                    SEQUENCE
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"GIP, a putative GPCR
Submitted (FEB-2000) t
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InterPro; IPR000087; Collagen.
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tted (DEC-2000) to the EMBL/GenBank/DDBJ
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                                                                                                                                                                                                                                                                                                                            FROM N.A.
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COMPLEMENT-C1Q TUMOR NECROSIS
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   Schuler G
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Hsieh F.,
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Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
A Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
A Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
A Villano D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
A Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
A Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
A Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
A Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
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Generation and initial analysis of more than 15,000 full-length
Thuman and mouse cDNA sequences.",
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                 Query Match
Best Local S
Matches 51
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Ighibashi T., Kanehori K., Yosida M., Watanabe S., Ishida S., Ono Y
Hotuta T., Hiraoka S., Murakawa K., Takiguchi S., Kusano J.,
Hotuta T., Hiraoka S., Murakawa K., Takiguchi S., Kusano J.,
Watanabe M., Fujimori K., Tanai H., Ishida M., Yamashita H., Chiba
Sugiyama T., Irie R., Otsuki T., Sacto H., Wakamatsu A., Ishii S.,
Yamamoto J., Isono Y., Kawai-Hio Y., Saito K., Nishikawa T.,
Kimura K., Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K.,
Magatsuma M., Takahashi-Pujii A., Oshima A., Sugiyama A., Kawakami
Magatsuma M., Takahashi-Pujii A., Oshima A., Sugiyama A., Kawakami
                                                                                                                                                                                                                                                                                                                            CONFLICT
CONFLICT
SEQUENCE
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EMBL; AF232905; AAG44303.1; AL

EMBL; AF2329840; AAK17964.1; ---

EMBL; BC021553; AAH21553.1; ---

EMBL; AK055541; BAB70947.1; ---
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DOMAIN
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Pfam; PF01391; Collagen; 1.
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                                                                                                                                                                                                                                             Similarity
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                                                  FTAGKAPHKSLSVMLVRNRDEVQALAFDEQRRPGARR-AASQSAMLQLDYGDTVWLRLH-
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IPR000087; Collagen.
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147
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COMPLEMENT-C1Q TUMOR NECROSIS FACTOR-
RELATED PROTEIN 1.
COLLAGEN-LIKE.
C1Q.
L -> P (IN REF. 1).
R -> Q (IN REF. 1).
MW; 49E248CB8BACFB7C CRC64;
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                                                                                                                                                                                                                      18;
                                                                                                                                                                                                                 Score 170.5;
Pred. No. 2e-1
L8; Mismatches
                                                                                                                                                                                                                                                170.5; DB
. No. 2e-10;
  -AQVGDRSIMQSQSLMLELREQDQVWVRLYK
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RESULT 11
C1QB HUMAN
ID C1QB HUMAN
IS EQUENCE FROM N.A.
IS EQUENCE FROM N.A.
IN MEDLINE=86076906; P.
RA MEDLINE=86076906; P.
RA MEDLINE=22388257; P.
RA MEDLINE=22388257; P.
RA SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=22388257; P.
RA STRAUSDE-BRAIN;
RX MEDLINE-22388257; P.
RA STRAUSDE-BRAIN;
RX MEDLINE-20388257; P.
RA HODKINS R.F., Jordal
RA BLAKESLEY R.W., TOW
RA RICHAR'S S., MCEWAN
RA RICHAR'S S., WCEWAN
RA RICHAR'S S., WCEWAN
RA BLAKESLEY R.W., TOW
RA ROMITINE=80020137; P.
RA BLAKESLEY R.W., TOW
RA ROMITINE=80020137; P.
RA BLAKESLEY R.W., TOW
RA SCOUENCE OF 26-133.
RN MEDLINE=80020137; P.
RA BLAKESLEY R.W., TOW
RA SCOUENCE OF 26-133.
RN MEDLINE-80020137; P.
RA GEOUENCE OF 26-133.
RN MEDLINE-80020137; P.
RA MEDLINE-80020309; P.
RA MEDLINE-80020309; P.
RA MEDLINE-80020309; P.
RA MEDLINE-800203090; P.
RA
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SEQUENCE OF 134....
MEDLINE=82283890; PubMed=698141..,
Reid K.B.M., Gagnon J., Frampton J.;
Reid K.B.M., Gagnon J., Frampton J.;
"Completion of the amino acid sequences of subcomponent C1q of the first component of subcomponent O1 203:559-569(1982).
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Biochem. J. 231:729-735(1985).
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Mammalia; Eutheria;
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Reid K.B.M., Thompson E.O.P.;
"Amino acid sequence of the N
                                                                                                                                                                                                                                                                         chain of subcomponent
omplement.";
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42, Last annotation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PubMed=486087;
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Catarrhini;
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SMART; SM00110; C1Q; 1.
PROSITE; PS01113; C1Q;
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Pfam; PF01391; Collagen; 1.
PRINTS; PR00007; COMPLEMNTC1Q.
                                                                                                                                                                                                                                                                                                                                                      EMBL; X03084; CAA26880.1; EMBL; BC008983; AAH08983.1; EMBL; M36278; AAC41692.1;
                                                                                                                                                                                                                                                                                                                                                                                                            use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               [6]
                                                                                                                                                                                                                                                                        InterPro; IPR001073; Clq.
InterPro; IPR000087; Collagen
                                                                                                                                                                                                                                                                                                  GO; GO:0005602; C:complement component C1q complex; GO; GO:0003811; F:complement activity activity; TAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Reid K.B.M., Bentley D.R., Wood K.J.; "Cloning and characterization of the complementary DNA for the chain of normal human serum C1g."; "philos. Trans. R. Soc. Lond., B, Biol. Sci. 306:345-354(1984).
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Reid K.B.M., Benti
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-i- FUNCTION: C1Q ASSOCIATES WI
C1, THE FIRST COMPONENT OF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'Molecular basis of hereditary Clq deficiency.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the oxygen atom of post-translationally added hydroxyl groups.

DISEASE: Defects in C1QB are a cause of C1Q deficiency [MIM:120570]. It is a rare genetic disorder which is associated with recurrent infections and a high prevalence of lupus erythematosus-like symptoms. It is characterized by a loss of activation of the complement classical pathway.

SIMILARITY: Contains 1 collagenous Armain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         s SWISS-PROT entry is copyright. It is produced through a collab
ween the Swiss Institute of Bioinformatics and the EMBL outst
European Bioinformatics Institute. There are no restrictions
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C1, THE FIRST COMPONENT OF THE SERUM COMPLEMENT SYSTEM. THE COLLAGEN-LIKE REGIONS OF C10 INTERACT WITH THE CA(2+) - DEPENDENT C1R(2) C1S(2) PROENZYME COMPLEX, AND EFFICIENT ACTIVATION OF C1 TAKES PLACE ON INTERACTION OF THE GLOBULAR HEADS OF C10 WITH THE PC REGIONS OF IGG OR IGM ANTIBODY PRESENT IN IMMUNE COMPLEXES. SUBUNIT: C1 IS A CALCIUM-DEPENDENT TRIMOLECULAR COMPLEX OF C10, R SUBUNIT: C1 IS A CALCIUM OF 1:2:2. C10 SUBCOMPONENT IS COMPOSED OF NINE SUBUNITS, SIX OF WHICH ARE DISULFIDE-LINKED DIMERS OF THE A AND B CHAINS, AND THREE OF WHICH ARE DISULFIDE-LINKED DIMERS OF THE CHAINS.
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                                   Submitted (MAR-1995) to the SWISS-PROT data bank.
-!- FUNCTION: FORMS A MICROSTRUCTURAL MATRIX WITHIN THE
-!- TISSUE SPECIFICITY: SPECIALIZED SECRETORY SUPPORTING
OUTER PERIMETER OF THE SACCULAR EDITHELIUM.
-!- SIMILARITY: Contains 1 C1Q domain.
-!- SIMILARITY: THIS IS A CONCEPTUAL TRANSLATION; A FRAMESH
-!- CAUTION: THIS IS A CONCEPTUAL TRANSLATION; A FRAMESH
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Davis J.G., Oberholtzer J.C., Burns F.R.
"Molecular cloning and characterization
structural protein.";
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VARIANT
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Centrarchidae; Lepomis.
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Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei
                                                                                                                                                                                                                                                            Ol-NOV-1995 (Rel. 32, Created)
Ol-NOV-1995 (Rel. 32, Last Sequence update)
15-JÜL-1998 (Rel. 36, Last annotation update)
Inner ear-specific collagen precursor (Saccular
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                                                                                                                  CONCEPTUAL TRANSLATION
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                     WITH OTHER SHORT-CHAIN COLLAGENS
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Pfam; PF01391; Collagen; 3.
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InterPro; IPR001073; Clq.
InterPro; IPR000087; Collagen.
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                  This SWISS-PROT entry is copyright. It is produced through a collaboratic between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it use by non-profit institutions as long as its content is in no was
                                                                                                                                                                                                                                                                           Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=10090;
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PROSITE; PS01113; C1Q;
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                                                                                                                                                                                        MEDLINE=20428709; PubMed=10862616;
Koide T., Aso A., Yorihuzi T., Nagata K.;
"Conformational requirements of collagenous
                                                                                                                                                                                                                                                                                                                                    Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                        Gliacolin
                                                                                                                                                                                                                                                                                                                                                                                                                                                         GLIC_MOUSE
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                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                 the chaperone protein HSP47.",
Biol. Chem. 275:27957-27963 (2000).
- TISSUE SPECIFICITY: EXPRESSED IN GLIAL CEL-
- SIMILARITY: Contains 1 collagenous domain.
- SIMILARITY: Contains 1 C1Q domain.
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275 41
272 41
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419
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(Rel. 40, Last sequence up
(Rel. 41, Last annotation
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419
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Rodentia;
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TRIPLE-HELICAL REGION (NC1).
C1Q.
N-LINKED (GLCNAC. . .) (F
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Pred.
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. 7.3e-10;
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(GLCNAC. . .) (POTENTIAL)
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 Usage
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MBL outstation -
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Matches 48
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or send a
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SIGNAL
                                                                                                                                                                                                                                                                                                                          Q9EXJ4; Q96KY1;
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sec
15-SEP-2003 (Rel. 42, Last and
Complement-clq tumor necrosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
DOMAIN
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                                                                                                                                                                                              SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

Bishop P.;

Piddington C.S., Bishop P.;

"Homo sapiens complement-olq tumor necrosis factor-related submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00386; Clq; 1.
Pfam; PF01391; Collagen; 1.
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausmer R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.
                                                                                                                                                                                                                                                                  Homo sapiens (Human)
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                    (Secretory protein C1QTNF3 OR CTRP3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
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GO; GO:0005515; F:proclein binding
InterPro; IPR001073; Clq.
InterPro; IPR000087; Collagen.
                                                                                                                                                  Maeda T., Hayashi A., "Molecular cloning, c
                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                             MEDLINE=22388257; PubMed=12477932;
                                                                                                                            Submitted
                                                                                                                                                                                                                                                     NCBI_TaxID=9606;
                                                                                           TISSUE=Placenta;
                                                                                                     SEQUENCE
                                                                                                                                        human
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; SM00110; C1Q; 1.
cc01113; C1Q; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                           218
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                                                                                                                                                                                                                                                                    Chordata;
Primates;
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GLIACOLIN.
COLLAGEN-LIKE.
C1Q.
C1Q.
W; 529FBAF4B2191BC1 (
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Pred. No. 5.
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Catarrhini;
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                                                                                                                                                                                                                                                                                                                                                                                    246
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RESULT 15
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                                                                                                                                                                                                                                                                                                                                                                                   Matches
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Best Local
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P31721;
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DOMAIN
CONFLICT
Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia; NCBI_TaxID=10116;
                                                                                    01-JUL-1993 (Rel.
01-NOV-1995 (Rel.
16-OCT-2001 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it
                                                          Complement C1QB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AF329837; AAK17961.1; -.
EMBL; AF326976; AAK70344.1; -.
EMBL; BC016021; AAH16021.1; -.
Genew; HGNC: 14326; C1QTNF3.
                                          Rattus norvegicus (Rat)
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Pfam; PF01391; Collagen; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          modified
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InterPro; IPR000087; Collagen.
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3; PS01113; C1Q;
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                                                                                                                                                                                                                                                                    MMK--HEDVEEVYVYLMHNGNTVFSMYSYEMK--GKSDTSSNHAVLKLAKGDEVWLRMGN
                                                                                                                                                                                                                                                                                          AGKAPHKSLS----VMLVRNRDEVQALAFDEQRRPGARRAASQSAMLQLDYGDTVWLRL-H
                                                                                                                                                                                                                                                                                                                                          PG-SSELRSAFSAARTTPLEGTSEMAVTFDKVYVNIGGDFDVATGQFRCRVPGAYFFSFT
                                                                                                                                                                                                                GALH-----
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114
214
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                                                                     subcomponent,
                                                                                                                                          STANDARD;
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1. 32, Last sequence update)
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1. 40, Last annotation update)
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Fran K.J., Malek J.A.,
                                                                                                                                                                                                                                                                                                                                                                                Score 163.5; |
Pred. No. 9.1e
24; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                     CIQ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POTENTIAL.
COMPLEMENT-C1Q TUMOR NECROSIS FACTOR-
RELATED PROTEIN 3.
COLLAGEN-LIKE.
              Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                         C589B6C3A73E5D29
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                                                                                                                                          253
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SALAR BARRARA BARRA
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Wing M.G., Seilly D.J., Bridgman D.J., Harrison R.A.;

Wing M.G., Seilly D.J., Bridgman D.J., Harrison R.A.;

Rapid isolation and blochemical characterization of rat C1 and C1q.";

M. Immunol. 30:433-440(1993).

C. Holdton. C1Q ASSOCIATES WITH THE PROENZYMES CIR AND C1S TO YIELD C1. THE FIRST COMPONENT OF THE SERUM COMPLEMENT SYSTEM. THE CC1, THE FIRST COMPONENT OF THE SERUM COMPLEMENT SYSTEM. THE COLLAGEN-LIKE REGIONS OF COMPLEX, AND EFFICIENT ACTIVATION OF C1 TAKES PLACE ON INTERACTION OF THE GLOBULAR HEADS OF C1Q MITH THE FC REGIONS OF IGG OR IGM ANTIBODY PRESENT IN IMMUNE COMPLEXES.

C. -I- SUBUNIT: C1 IS A CALCIUM-DEPENDENT TRIMOLECULAR COMPLEX OF C1Q, R AND S IN THE MOLAR RATION OF 1:2:2. C1Q SUBCOMPONENT IS COMPOSED OF NINE SUBUNITS, SIX OF WHICH ARE DISULFIDE-LINKED DIMERS OF THE A AND B CHAINS, AND THREE OF WHICH ARE DISULFIDE-LINKED DIMERS OF THE C CHAIN. IN ADDITION TO THE MAJOR A:B AND C:C DIMER BANDS, C-I- SIMILARITY: Contains 1 C01 domain.
Query Match
                                                          MOD RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             [2]
SEQUENCE OF 71-79 AND 141-146.
MEDLINE=93218657; PubMed=8464426;
Wing M.G., Seilly D.J., Bridgman I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             [1].
SEQUENCE FROM N.A.
STRAIN-Sprague-Dawley; TISSUE-Spleen;
MEDLINE-96062319; PubMed-7594503;
MEDLINE-96062319; Schaefer M.K.-H., Petry
                                                                                                                                                                                                                                                                                                                                                                                     CHAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                       SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00386; Clq; 1.
Pfam; PF01391; Collagen; 1.
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InterPro; IPR000087; Collagen.
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PIR; S49158; S49158.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                pathway;
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COMPLEMENT C1Q
COLLAGEN-LIKE.
C1Q.
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MPLEMENT C1Q SUBCOMPONENT,
163.5;
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78)
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Best L Matche	Best Local Similarity 29.2%; Pred. No. 9.4e-10; Matches 45; Conservative 36; Mismatches 58; Indels 15; Gaps
₹	2 GPTPGPGSSELRSAFSAARTTPLEGTSEMAVTFDKVYVNIGGDFDVATGQF 52
ਲੋ	100 GP-PGPRGPKGGSGDYKATOKVAFSALRTVNSALRPNQAIRFEKVITNVNDNYEPRSGKF 158
¥	53 RCRVPGAYFFSFTAGKAPHKSLSVMLVRNRDEVQ-ALAFDEQRRPGARRAASQSAMLQLD 111
ŏ	159 TCKVPGLYYFTYHASSRGNLCVNIVRGRDRDRMQKVLTFCDYAQ-NTFQVTTGGVVLKLE 217
¥	112 YGDTVWLRLHGAPHYALGAPGATFSGYLVYAD 143
ŏ	218 QEEVVHLQATD-KNSLLGVEGANSIFTGFLLFPD 250
earch c	earch completed: January 12, 2004, 08:12:58 Job time : 6.13772 secs

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Title:
Perfect score:
Sequence:
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Maximum DB seq length: 2000000000
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Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query
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         Q81V25
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Q8TE71
Q8TE71
Q9DBU4
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Q95DBU4
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Q98R0W2
Q8BRW2
Q8BRW2
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O9h667 homo sapien
Q8te71 homo sapien
Q8te10 mus musculu
Q9d8u4 mus musculu
Q95jd7 macaca mula
Q8n6p2 homo sapien
Q8brw2 mus musculu
Q8v20 mus musculu
Q8v100 mus musculu
Q8k3r4 rattus norv
Q95mq4 bos taurus
Q8k479 mus musculu
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	16.3	16.9	17.0	17.1	17.1	17.1	17.4	17.6	17.8	18.1	18.2	18.7	18.9	18.9	19.1	19.4	19.7	20.1	20.1	20.9			•		•			
583	347	198	198	1017	295	102	222	185	195	213	705	675	744	744	173	333	197	224	224	245	281	182	289	246	120	194	287	312
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homo	5	Q8bme9 mus musculu	Bru		Q9z1k4 rattus norv	æ	Q8ji26 salvelinus	etro:	Q8bzs3 mus musculu	P83425 mytilus edu	Omo	s sn	mus	Bru	a sne	omo		mus	nomo		aum	Bnw	Bru	Bru	Q8rlz2 mus musculu	Q95j95 canis famil	Q8cfr0 mus musculu	Q8chx9 mus musculu

## ALIGNMENTS

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121 HGAPHYALGAPGATFSGYLVYAD 143                      137 HGAPQYALGAPGATFSGYLVYAD 159	61 FFSSTAGKAPHKSLSVMLVRNRDEVQALAFDEQRRPGARRAASQSAMLQLDYGDTVWLRL 120	1 LGPTPGPGSSELRSAFSAARTTPLEGTSEMAVTFDKVYVNIGGDFDVATGQFRCRVPGAY 60 	Query Match 98.9%; Score 737; DB 4; Length 329; Best Local Similarity 99.3%; Pred. No. 1.3e-68; Matches 142; Conservative 0; Mismatches 1; Indels 0; Gaps 0	TLT 1  725  725  726  727  727  728  728  728  728  728

RESULT 2 Q8R066

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RESULT 3
       RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Arakawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Salto T., Okazaki Y., Gojbbori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baddarelli R., Barsh G.,
RA Sakai K., Okido T., Furuno M., Aono H., Baddarelli R., Barsh G.,
RA Blake J., Okido T., Furuno M., Aono H., Baddarelli R., Barsh G.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
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Best I
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MGD; MGI:1914695; 0710001E10Rik.
Interpro; IPR001073; C1q.
Pfam; PF00306; C1q; 2.
SMART; SM00110; C1Q; 2.
SPOSITE; PS01113; C1Q; 2.
PROSITE; PS01113; C1Q; 2.
SPONIENCE 326 AA; 35057 MW; 72
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01-JUN-2002
01-JUN-2002
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Similar to Clq and
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Submitted (APR-2002) to the
EMBL; BC027315; AAH27315.1;
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Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus (Mouse)
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                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Embryo;
MEDLINE=21085660; PubMed=11217851;
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                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus (Mouse).
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01-OCT-2002
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Rodentia;
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Rodentia;
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21,
23,

    Last sequence update)
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    necrosis factor related protein

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L; Mismatches
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Lee N.H.,
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Best Local (
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PRINTS; PRODOOT; CIQ; 1.
SMART; SMODILO; CIQ; 1.
PROSITE; PSOIII13; CIQ; 1.
PROSITE; PSOIAA; 22190 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JUN-2001
01-JUN-2001
01-OCT-2002
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MGD; MGI:1914695; 0710001E10Rik.
InterPro; IPR001073; C1q.
Pfam; PF00386; C1q; 1.
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0010001E10RIK.
Mus musculus (Mouse).
Mus musculus (Mouse).
Metazoa; Chordata;
Metazoa; Rodentia;
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Hayashizaki Y.;
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                                                                                      EMBL; AK002948; b. MGD; MGI:1914695;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=C57BL/6J;
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     SMART; SM00110;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=21085660; PubMed=11217851;
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                                                                                                                           Nature 409:685-690(2001).
EMBL; AK002948; BAB22473.1;
                                                    Pfam; PF00386;
                                                                                                                                                                                                Hayashizaki Y.;
                          PRINTS;
                                                                         InterPro;
                                                                                                                                                                             Functional annotation
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                                                                            IPR001073;
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6U; TISSUE=Brain;
                                                    C1q;
     CTO;
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                            COMPLEMNTC10
                                                                                                      0710001E10Rik.
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17,
22,
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2; Mismatches
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Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
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. 5.3e-29;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         update)
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                                                                                                                                                                                collection.";
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; Murinae; Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    205;
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                                                                                                                                                                                                                                                          Wilming
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                                                                                                                                                                                                                                                                                    K. -F.,
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Best Local
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Best Local
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Sthausberg R.;
Submitted (MAY-2001) to the EN EMBL; AK026222; BAB15398.1; -
EMBL; BC007520; AAH07520.1; -
InterPro; IPR001073; C1q.
Pfam; PF00386; C1q; 1.
PRINTS; PR00007; COMPLEMNTC1Q
SMART; SM00110; C1Q; 1.
PROSITE; PS01113; C1Q; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Watanabe K., Kumagai A., Itakura S., Yamazal
Suzuki Y., Obayashi M., Nishi T., Shibahara
Nakamura Y., Isogai T., Sugano S.;
"NEDO human cDNA sequencing project.";
Submitted (AUG-2000) to the EMBL/GenBank/DDF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                   Hypothetical protein. SEQUENCE 158 AA; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAR-2001 (TrEMBLrel 16, Cr
01-MAR-2001 (TrEMBLrel 16, La
01-OCT-2002 (TrEMBLrel 22, La
Hypothetical protein FLJ22569.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=Small intestine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q9Н667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FISSUE=Uterus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q9Н667;
                                                                                                                                                                                                                                                                                                                                                                Local Similarity
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205 AA;
                                                              IYGSSWKYSTFSGYLLYQD
                                                                                                         HYALGAPGATFSGYLVYAD
                                                                                                                                                         MLKLAVNVPLYVNLMKN
                                                                                                                                                                                               AGK-APHKSLSVMLVRNRDEVQALAFDEQRRPGARRAASQSAMLQLDYGDTVWLRLHGAP 124
                                                                                                                                                                                                                                             PLPQQMRVAFSAARTSNLAPGTLDQPIVFDLLLNNLGETFDLQLGRFNCPVNGTYVFIFH
                                                                                                                                                                                                                                                                                          PGSSELRSAFSAARTTPL-EGTSEMAVTFDKVYVNIGGDFDVATGQFRCRVPGAYFFSFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TVWLRLH---GAPHYALGAPGATFSGYLVYAD 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PTPGPGSSELRSAFSAARTTPLEGTS-----EMAVTFDKVYVNIGGDFDVATGQFRCRV 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AVWLLSHDHDGYGAYSNHGKYITFSGFLVYPD 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PGAYFFSFTLGKLPRKTLSVKLMKNRDEVQAMIYDDGASRR----REMQSQSVRLPLRRGD
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                                                                                                                                                                                                                                                                                                                                          Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                17625 MW;
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41.7%;
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                                                                                                                                                                                                                                                                                                                                        18;
                                                                                                                                                         -EEVLVSAYANDGAPD-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             project.";
EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Created)
                                                                                                                                                                                                                                                                                                                                        Score 222; DB 4;
Pred. No. 2.9e-15;
B; Mismatches 59
                                                                                                           143
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Pred. No. 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Craniata; Vertebrata; l
Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                47DB10EDD6DC9760 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  56AD37793C437300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Yamazaki M.,
ibahara T., Ta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            158
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              databases
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                                                                                                                                                                                                                                                                                                                                                                                Length 158;
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                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tashiro H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Euteleostomi;
; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    205;
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Best Local :
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Pfam; PF00386; C1q; 1.
SMART; SM00110; C1Q; 1.
PROSITE; PS01113; C1Q; 1.
SEQUENCE 1077 AA; 12097.
                                                                                                                                                                                                                                 Strausberg R.;
Submitted (APR-2002) to the
EMBL; BC027523; AAH27523.1;
InterPro; IPR001073; C1q.
Pfam; PF00386; C1q; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q8TE71;
Q8TE71;
01-JUN-2002
                                                                                                                                                 PRINTS; PR00007; COMPLEMN'SMART; SM00110; C1Q; 1.
PROSITE; PS01113; C1Q; 1.
Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similar to hypothetical protein FLJ22569. Mus musculus (Mouse).
                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                 rissuE=Uterus;
                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                      Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-OCT-2002
01-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q8K1I0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Aerbajinai W., Miller J.L.;
Submitted (JAN-2002) to the
EMBL; AY074490; AAL71549.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (Human)
Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JUN-2002
01-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               941
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  58;
      7
                                            l Similarity
57; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
PGSSELRSAFSAARTTPL-EGTSEMAVTFDKVYVNIGGDFDVATGQFRCRVPGAYFFSFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MLKLAVNVPLYVNLMKN-EEVLVSAYANDGAPD-HETASNHAILQLFQGDQIWLRLHRGA 1058
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PGSSELRSAFSAARTTPL-EGTSEMAVTFDKVYVNIGGDFDVATGQFRCRVPGAYFFSFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AGK-APHKSLSVMLVRNRDEVQALAFDEQRRPGARRAASQSAMLQLDYGDTVWLRLHGAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PLPQQMRVAFSAARTSNLAPGTLDQPIVFDLLLNNLGETFDLQLGRFNCPVNGTYVFIFH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IYGSSWKYSTFSGYLLYQD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HYALGAPGATFSGYLVYAD 143
                                                                                                                                 158 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (TrEMBLrel. 22, Created)
(TrEMBLrel. 22, Last sequence update)
(TrEMBLrel. 23, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (TrEMBLrel. (TrEMBLrel. (TrEMBLrel.
                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                  COMPLEMNTC1Q
                                                                                                                                                                                                                                                                                                                                                                                                                                    Chordata;
Rodentia;
                                                                                                                               17533 MW;
                                                              29.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29.8%;
41.7%;
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21,
23,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       W.
                                                                                                                                                                                                                                                                                                       EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Last sequence up
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1077
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 222;
Pred. No. 3
                                                                   Pred.
                                                                                       Score
                                                                                                                                                                                                                                                                                                                                                                                                                                  Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                 86E9321C99225FCB
                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2B88BF3C47D032D6 CRC64;
                                                                216;
No. 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              158
                                                                2e-14;
                                                                                       DB 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .4e-14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                update)
                                              59;
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                                                                                                                                 CRC64;
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                                              Indels
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                                                                                       158;
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22

PLPQQMRVAFSAARTSNLAPGTLDQPIVFDLLLNNLGETFNLQLGRFNCPVNGTYVFIFH

81

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RESULT 8
Q9D8U4
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RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Arakawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashina J., Mazazarelli J., Mombaerts P.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Mynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.;
                                                                                                                                                                                                                                  Query Match
Best Local S
Matches 53
                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR001073; Clq.
InterPro; IPR001087; Collagen.
Pfam; PF001386; Clq; 1.
Pfam; PF01391; Collagen; 2.
PRINTS; PR00007; COMPLEMNTC1Q.
PROSSITE; PS01113; ClQ; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q9D8U4
Q9D8U4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JUN-2001 (TrEMBLrel. 17, 01-JUN-2001 (TrEMBLrel. 17, 01-MAR-2003 (TrEMBLrel. 23,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=C57BL/6J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases. EMBL; AK007683; BAB25187.1; -. EMBL; BC03034; AAH30324.1; -. EMBL; BC03034; AAH30324.1; -. MGD; MGI:1916433; 1810033K05Rik.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=21085660; PubMed=11217851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hayashizaki Y.; "Function of a
                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Strausberg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nature 409:685-690(2001).
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                                                                                                           147
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204
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                                                                                                                                                                                                                                     53;
                                                                                                                                                                                                                                                                    Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HYALGAPGATFSGYLVYAD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AGK-APHKSLSVMLVRNRDEVQALAFDEQRRPGARRAASQSAMLQLDYGDTVWLRLHGAP
YYFTYDITLA-NKHLAIGLVHN-GQYRIRTFD--ANTGNHDVASGSTILALKEGDEVWLQ
                                                    YFFSFTAGKAPHKSLSVMLVRNRDEVQALAFDEQRRPGARRAASQSAMLQLDYGDTVWLR
                                                                                                              294 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                     GSSELRSAFSAA--RTTPLEGTSEMAVTFDKVYVNIGGDFDVATGQFRCRVPGA
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Rodentia;
                                                                                                                                                                                                                                                                                                                                                         30865 MW;
                                                                                                                                                                                                                                                              26.8%;
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Last annotation update)
N cDNA 1810033K05 gene).
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                                                                                                                                                                                                                                  Score 200; DB 11;
Pred. No. 1.3e-12;
0; Mismatches 45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                         6D3905AE7C19E6FA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           294
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cDNA collection.";
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Ti, Fukuda (
                                                                                                                                                                                                                                                                                            Length
                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                  24;
                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   124
                                                       119
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259
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POR RATION RESULTS REPORTED TO SERVICE REPORT OF SERVICE REPORT OF
                                                                                                                                                                                                                                                                                        RESULT 10
Q8N6P2
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밁
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Best Local S
Matches 47
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Q95JD7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Collagen.
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Circulating concentrations of the adipocyte protein adiponectin are decreased in parallel with reduced insulin sensitivity during the progression to type 2 diabetes in rhesus monkeys."; Diabetes 50:1126-1133(2001).

EMBL; AF404407; AAK92202.1; -. InterPro; IPR001073; Clq.
InterPro; IPR001073; Collagen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Macaca mulatta (Rhesus macaque).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
                                                                                                                                   01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Clq and tumor necrosis factor related protein 5.
                                                                                                                                                              01-OCT-2002 (TrEMBLrel.
01-OCT-2002 (TrEMBLrel.
01-MAR-2003 (TrEMBLrel.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cercopithecinae;
SEQUENCE FROM N.A
                                  NCBI_TaxID=9606;
                                                                                                                                                                                                                                         Q8N6P2;
                                                                                                                                                                                                                                                                    Q8N6P2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRINTS; PR00007; COMPLEMNTC10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00386; Clq; 1.
Pfam; PF01391; Collagen; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hotta K., Funahashi T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=Adipose tissue;
MEDLINE=21232234; PubMed=11334417;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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                                                                       Mammalia;
                                                                                         Eukaryota; Metazoa;
                                                                                                                    Homo sapiens (Human)
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                                                                     Eutheria;
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                                                                                                                                                                                                                                                                  PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                               YALGAPGATFSGYLVYAD
                                                                     Chordata;
Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26264 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25.8%; Score 192; DB 6; I 31.8%; Pred. No. 6.8e-12; tive 29; Mismatches 54;
                                                                                                                                                                   22,
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                                                                     Craniata; Vertebrata;
Catarrhini; Hominidae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          49A45DAF2B4613FD CRC64;
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                                                                                                Euteleostomi;
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RESULT 12
Q8R002
ID Q8R00
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Best Local S
Matches 47
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Best Local
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Pfam; PF01391; Collagen; 1.
PRINTS; PR00007; COMPLEMNTCLQ.
SMART; SM00110; ClQ; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nature 420:563-573(2002).
EMBL; AK041214; BAC30866.1; -
SEQUENCE 247 AA; 26751 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the RIKEN Genome Exploration Research Group "Analysis of the mouse transcriptome based 60,770 full-length cDNAs.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAR-2003 (TrEMBLrel. 23,
01-MAR-2003 (TrEMBLrel. 23,
01-MAR-2003 (TrEMBLrel. 23,
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Submitted (MAY-2002) to the
  Q8R002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=C57BL/6J; TISSUE=Aorta and MEDLINE=22354683; PubMed=12466851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Adipocyte complement related Mus musculus (Mouse).
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47; Conserv
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PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                29;
                                                                                                                                                                                                                                                                                                                                                                                           Score 185; DB
Pred. No. 3.7e
29; Mismatches
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3; Mismatches
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.7e-11;
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on functional
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                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                     119
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RESULT 13
Q8BKR0
                                     밁
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Best Local
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Best Local
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InterPro; IPR000087; Collagen.
Pfam; PF00386; Clq; 1.
Pfam; PF01391; Collagen; 1.
SMART; SM00110; ClQ; 1.
                                                                                                                                                                                                                     .QBBKR0;
01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Weakly similar to complement-ClQ tumor necrosis fac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q8R002;
01-JUN-2002
01-JUN-2002
01-MAR-2003
                                  "Analysis of the mouse transcriptome 60,770 full-length CDNAs.";
Nature 420:563-573 (2002).
EMBL; AKO51058; BAC34512.1; -.
SEQUENCE 264 AA; 29062 MW; 054B5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-UN-2002 (TrEMBLrel. 21, Created)
01-UN-2002 (TrEMBLrel. 21, Last sequence update)
01-WAR-2003 (TrEMBLrel. 23, Last annotation updats)
Similar to DKFZP586B0621 protein (Hypothetical 25
                                                                                    the RIKEN Genome Exploration Research Group "Analysis of the mouse transcriptome based o
                                                                                                          The
                                                                                                                       SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Body;
MEDLINE=22354683; PubMed=12466851;
                                                                                                                                                                                   Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                Q8BKR0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hypothetical protein. SEQUENCE 243 AA; 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; BC023068; AAH23068.1;
EMBL; BC025174; AAH25174.1;
MGD; MGI:2385958; Clqtnf5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Strausberg R
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus
                                                                                                                                                                     NCBI_TaxID=10090;
                                                                                                                                                                                                            Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted
                                                                                                            FANTOM Consortium
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LGPTPGPGSSELRSAFSAART-TPLEGTSEMAVTFDKVYVNIGGDFDVATGQFRCRVPGA
                                                                                                                                                                                                                                                                                                                                                                                   LRLHGAPH---YALGAPGATFSGYLVYAD
                                                                                                                                                                                                                                                                                                                                                            VQVGVGDYIGIYASIKTDSTFSGFLVYSD
                                                                                                                                                                                                                                                                                                                                                                                                             YYFAVHA-TVYRASLQFDLVKNG---QSIASFFQYFGGWPKPASLSGGAMVRLEPEDQVW
                                                                                                                                                                                                                                                                                                                                                                                                                                    YFFSFTAGKAPHKSLSVMLVRNRDEVQALAFDEQRRPGARRAASQS--AMLQLDYGDTVW
                                                                                                                                                                                                                                                                                                                                                                                                                                                             IGPA-GECSVPPRSAFSAKRSESRVPPPADTPLPFDRVLLNEQGHFDPTTGKFTCQVPGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (MAR-2002)
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                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Clqtnf5.
                                                                                                                                                                                    Chordata;
Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chordata;
Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25420 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24.4%;
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24.2%;
35.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 181.5; DB 11; Pred. No. 8.4e-11; 7; Mismatches 55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL/GenBank/DDBJ
Score
Pred.
                                                                                                                                                                                   Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Craniata; Vertebrata; l
Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            498129CD051DB97B CRC64;
                                     054B50E7D2E56826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             annotation update) (Hypothetical 25.4
180.5; DB 1
No. 1.2e-10;
                                                                                                                                                                                                                                                                                                 264
                                                                                                                                                                                                                                                                                                                                                                                    143
                                                                                                                                                                                                                                                                                                                                                            235
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on functional
            11;
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                                      CRC64;
                                                                                                                                                                                                                                     factor-related
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4
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           Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein)
                                                                                       annotation
                                                                                                Team;
              264;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     243;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11;
                                                                                                                                                                                     Mus
                                                                                     of.
                                                                                                                                                                                                                                                                                                                                                                                                                                    117
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Similarity

Matches

56;

Conservative

15;

Mismatches

61;

Indels

25;

Gaps

6

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RESULT 15
Q95MQ4
ID Q95MQ
AC Q95MQ
DT 01-DE
DT 01-DE
DT 01-MA
DT 01-MA
DE Adipo
OS Bos t
OC Eukar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q8K3RA
AC Q8K3R
AC Q8
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Best Local S
Matches 45
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Pfam; PF01391; COllagen; 1.
PRINTS; PR00007; COMPLEMNTC1Q.
ProDom; PD000007; COllagen; 1.
SMART; SM00110; C1Q; 1.
PROSITE; PS01113; C1Q; 1.
                                              Q95MQ4 PRELIMINARY; PRT; 2
Q95MQ4;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last seque
01-MAR-2003 (TrEMBLrel. 23, Last annot
Adipose tissue-specific protein adipo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                protein of 30 kDa.";
Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases
EMBL; AY033885; AAK61608.1; -.
InterPro; IPR001073; C1q.
InterPro; IPR000087; Collagen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=Sprague-Dawley;
Berg A.H., Scherer P.E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30 kDa adipocyte complement-related protein. Rattus norvegicus (Rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-OCT-2002 (TrEMBLrel. 22,
01-OCT-2002 (TrEMBLrel. 22,
01-MAR-2003 (TrEMBLrel. 23,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q8K3R4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q8K3R4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Berg A.H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             loning of the rat homolog to murine adipocyte complement-related
                         taurus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        118
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                                                                                                                                                                                                                                                                                                                                        215
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     104 PGEAAYMYHSAFSVGLETRVT-VPNVPIRFTKIFYNQQNHYDGSTGKFHCNIPGLYYFSY 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 232 VRLFKRERENGIYSDDVDTY----ITFSGHLIKAE 262
                                                                                                                                                                                                                                                                                                                                                                                         120 LHGAPH----YALGAPGATFSGYLVYAD 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       65
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TAGKAPH-----KSLSVMLVRNRDEVQALAFDEQRRPGARRAASQSAMLQLDYGDTVWLR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GPTPGPGSS--ELRSAFSAARTTPLEGTSE-MAVTFDKVYVNIGGDFDVATGQFRCRVPG
                                                                                                                                                                                                                                                                                                                                     VYGEGDNNGLYADNVNDSTFTGFLLYHD
                                                                                                                                                                                                                                                                                                                                                                                                                                                -----HITVYMKDVKVSLFK-KDKAVLFTYDQYQEKNVDQ-ASGSMLLHLEVGDQVWLQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PGPGSSELRSAFSAARTTPLEGTSEMAVTFDKVYVNIGGDFDVATGQFRCRVPGAYFFSF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   244 AA;
                         (Bovine)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26410 MW;
Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24.2%; Score 180; DB 11; 30.4%; Pred. No. 1.2e-10; tive 29; Mismatches 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .
[3]
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                                                      Last sequence update)
Last annotation updat
Stein adipo Q.
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Rattus.
  Craniata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            244
                                                                                                                                                                                              240
                                                                                                                                                                                                                                                                                                                                     242
  Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            B
                                                                                                                                                                                              B
                                                                                update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 244;
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Search completed: January 12, Job time: 20.6946 secs
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                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
NCBI_TaxID=9913;
[1]
                                                                                                                                                                                                                                                                                                Pfam; PF00386; C1q; 1.
Pfam; PF01391; Collagen; 1.
PRINTS; PR00007; COMPLEMNTC10.
ProDom; PD000007; Collagen; 1.
SMART; SM00110; C1Q; 1.
                                                                                                                                                                                                                                                                                                                                                                                                              Sato C., Yasukawa Z., Honda N., Matsuda T., Kitajima K., "Identification and Adipocyte Differentiation-dependent Expression the Unique Disialic Acid Residue in an Adipose Tissue-specific Glycoprotein, Adipo Q.";
                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                               EMBL; AF269230; AAK58902.1; -.
InterPro; IPR001073; Clq.
InterPro; IPR000087; Collagen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=21369933;
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                                                   VYEGENHNGVYADNVNDSTFTGFLLY 235
                                                                            LH-GAPH---YALGAPGATFSGYLVY 141
                                                                                                      ----HITVYMKDVKVSLFK-KDKAVLFTYDQYQEKNVDQ-ASGSVLLHLEVGDQVWLQ
                                                                                                                              TAGKAPH-----KSLSVMLVRNRDEVQALAFDEQRRPGARRAASQSAMLQLDYGDTVWLR
                                                                                                                                                      PGEAAYVYRSAFSVGLETRVT-VPNVPIRFTKIFYNQQNHYDGSTGKFYCNIPGLYYFSY
                                                                                                                                                                               PGPGSSELRSAFSAARTTPLEGTSEMAVTFDKVYVNIGGDFDVATGQFRCRVPGAYFFSF 64
                                                                                                                                                                                                                                                             240 AA;
                                                                                                                                                                                                          Conservative
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31.5%;
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             2004,
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Pred. No. 1.5e-10;
9; Mismatches 53
              08:19:09
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Database
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Maximum Match 10
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1: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1980.DAT:*

2: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1981.DAT:*

3: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1982.DAT:*

4: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1984.DAT:*

5: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1986.DAT:*

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Copyright (c) 1993 - 2004 Compugen Ltd.
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AAB61469	AAB61488	AAB61424	ABG79643	AAB61466	AAB61423	ABG70384	AAB61606	ABG70385	ID
Human MANGO 245 CI	Murine MANGO 245 p	Monkey MANGO 245 p	Human novel secret	Human MANGO 245 ma	Human MANGO 245 pr	Adipocyte compleme	Human ZACRP4. Hom	Adipocyte compleme	Description

25-JUL-2002.

WO200257453-A2 Homo sapiens.

## ALIGNMENTS

RESULT 1 ABG70385 gastro-intestinal disease; reproductive; neurological disease; bone marrow transplantation; endocrine disease; allergy; inflammation; nephrological disorder; urinary system disorder; age-related disorder; neuropsychiatric disorder; EGF-related protein; SCUBEI; TEN-M4; adipocyte complement-related Clq tumour necrosis factor; out at first; beta adrenergic receptor kinase; EphA6/ehk-2; glucose transporter; type la membrane sushi-containing domain; butyrophilin; type la membrane-sushi domain containing. Human; NOVX; NOVX-associated disorder; cardiomyopathy; atherosclerosis; cell signal processing; metabolic pathway modulation; metabolic disorder obesity; diabetes; infectious disease; neurodegenerative disorder; acne; Alzheimer's disease; takinson's disease; immune disorder; cancer; haematopoietic disorder; cirrhosis; pancreatitis; learning defect; memory defect; infertility; congenital heart defect; hair growth; pigmentation disorder; endocrine disorder; respiratory disease; health; ABG70385; ABG70385 standard; Protein; 299 Adipocyte complement-related Clq Tumour Necrosis Factor-like protein #3. 05-NOV-2002 (first entry) B

disorder;

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The present invention relates to new NOVX polypeptiues. The invention of treating or preventing a NOVX-associated disorder such as CC cardiomyopathy or atherosclerosis, where the disorder is related to cell cignal processing and metabolic pathway modulation in a subject, CC preferably human. The invention is also useful for treating metabolic CC disorders (e.g. Alzheimer's disease, parkinson's disease), immune CC disorders, haematopoietic disorders and various cancers. The molecules of CC the invention are also useful for treating or preventing cirrhosis, CC pancreatitis, learning and memory defects, infertility, congenital heart CC defects, acne, hair growth, pigmentation disorders, endocrine disorders, cc reurological disease, gastro-incestinal diseases, reproductive, health, CC neurological disease, pone marrow transplantation, endocrine disorders. CC callergy and inflammation, nephrological disorders, urinary system CC disorders, neuropsychiatric disorders and age-related disorders.
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20-DEC-2000;
02-MAY-2001;
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24-JUL-2001;
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10-AUG-2001;
29-AUG-2001;
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Stone DJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel isolated NOVX polypeptide useful for treating cardiomyopathy, atherosclerosis, metabolic disorders, diabetes, obesity, infectious disease, anorexia, neurodegenerative disorders, Alzheimer's disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19-DEC-2001;
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N-PSDB; ABS52097.
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                                                    standard;
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                                                                                                          HGAPHYALGAPGATFSGYLVYAD 159
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Casman SJ, B
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2001US-307506P.
2001US-311590P.
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ilarity 100.0%;
Conservative (
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2001US-315617P.
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2001US-288153P.
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           (first entry)
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                                                    Protein;
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Shimkets RA, Burgess CE, Zerhusen BD,
Boldog FL, Smithson G, Li L, Ji W;
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Pred. No. 1.5e-76;
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Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Key
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                                                                                                                                                                                                                                                                                                                                                                                                      protein is useful as an autocrine factor, particularly during development, in mediating the processes of an organism, in regulating cellular processes such as cell proliferation and/or differentiation.
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                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; Page 77-78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cellular processes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel secreted protein ZACRP4 polypeptides having tandem C1q globular domains, useful for studying cell-cell communication and regulation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-138140/14.
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                                                                                                                                                                                                                                                                                                                                                                                           survival and
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137
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Pred. No. 1.7e-76;
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standard; Protein; 284

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(first entry)

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gastro-intestinal disease; reproductive, neurological disease; health bone marrow transplantation; endocrine disease; allergy; inflammation; neurological discase; urinary system disorder; age-related disorder; neuropsychiatric disorder; EGF-related protein; SCUBE1; TEN-M4; adipocyte complement-related Clq tumour necrosis factor; out at first; beta adrenergic receptor kinase; EphA6/ehk-2; glucose transporter; type la membrane sushi-containing domain; butyrophilin; type la membrane-sushi domain containing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Alzhalmer's disease; Parkinson's disease; hammune disorder; cancer; haematopoietic disorder; cirrhoats; pancreatitis; learning defect; memory defect; infertility; congenital heart defect; hair growth;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; NOVX; NOVX-associated disorder; cardiomyopathy; atherosclerosis; cell signal processing; metabolic pathway modulation; metabolic disorder; obesity; diabetes; infectious disease; neurodegenerative disorder; acne;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Alzheimer's disease;
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19-DEC-2001; 2001WO-US50331

20-DEC-2000; 02-MAY-2001; 29-MAY-2001; 24-JUL-2001; 10-AUG-2001; 19-DEC-2000; 2000US-257314P. 2001US-288153P. 2001US-294075P. 2001US-307506P. 2001US-311590P. 2000US-265704P

10-AUG-2001; 29-AUG-2001; 2001US-322358P. 2001US-311613P. 2001US-315617P

(CURA-) CURAGEN CORP

Stone ğ EA, Anderson D, Casman SJ, Patturajan 1 M, Vernet CAM, Malyankar UM, Keku Shimkets RA, Burgess CE, Zerhusen B Boldog FL, Smithson G, Li L, Ji W; Kekuda Liu

WPI; 2002-590744/63.

Novel isolated NOVX polypeptide useful for treating cardiomyopathy, atherosclerosis, metabolic disorders, diabetes, obesity, infectious disease, anorexia, neurodegenerative disorders, Alzheimer's disease ő

Claim 1; Page 30; 318pp; English

useful for treating or preventing a NOVX-associated disorder such as cardiomyopathy or atherosclerosis, where the disorder is related to cell signal processing and metabolic pathway modulation in a subject, preferably human. The invention is also useful for treating metabolic disorders (e.g. obesity), diabetes, infectious disease, neurodegenerative disorders (e.g. Alzheimer's disease, Parkingon's disease), immune disorders, haematopoietic disorders and various cancers. The molecules of the invention are also useful for treating or preventing cirrhosis, pancreatitis, learning and memory defects, infertility, congenital heart defects, acne, hair growth, pigmentation disorders, endocrine disorders, cespiratory disease, gastro-intestinal diseases, reproductive, health, neurological diseases, reproductive, health, allergy and inflammation, nephrological disorders, urinary system consorders, neuropsychiatic disorders, urinary system consorders, neuropsychiatic disorders and age-related disorders. The present invention relates to new NOVX polypeptides. The invention

284 AA

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LGPTPGPGSSELRSAFSAARTTPLEGTSEMAVTFDKVYVNIGGDFDVATGQFRCRVPGAY

LGPTPGPGSSELRSAFSAARTTPLEGTSEMAVTFDKVYVNIGGDFDVATGQFRCRVPGAY

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                                                                                   The present invention relates to cDNAs encoding TANGO 244, TANGO 246, TANGO 275, TANGO 300 and MANGO 245 proteins.

The nucleic acide, proteins and protein modulators are useful for treating colonic disorders, inflammatory diseases, tumors, renal disorders, liver disorders, lung disorders, autoimmune diseases, allergic diseases, cardiovascular diseases, brain disorders, diseases, cardiovascular diseases, brain disorders, degenerative diseases placental, pancreatic, skeletal and muscle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TANGO; MANGO; colon; inflammation; tumor; renal; liver; lung; autoimmune; allergy; cardiovascular; brain; degenerative; placental; pancreatic; skeletal; muscle.
                                                                                                                                                                                                                        Isolated cDNAs encoding TANGO 244, TANGO 246, TANGO 275, TANGO 300 a MANGO 245 proteins, useful in the treatment of inflammatory diseases (e.g. idiopathic ulcerative colitis), tumors, renal disorders and li
                                                  Sequence
                                                                                                                                                                                       Claim
                                                                                                                                                                                                               disorders
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                                                                           disorders.
                                                                                                                                                                                                                                                                                                  Holtzman
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Score 737; DB
Pred. No. 1.5e
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                                                                                                                                                                                                                                                                                                                                                                        Isolated CDNAs encoding TANGO 244, TANGO 246, TANGO 275, TANGO 300 and MANGO 245 proteins, useful in the treatment of inflammatory diseases (e.g. idiopathic ulcerative colitis), tumors, renal disorders and liver disorders (e.g. jaundice) -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        pancreatic;
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                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                              degenerative diseases
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123
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                                                                                                                               LGPTPGPGSSELRSAFSAARTTPLEGTSEMAVTFDKVYVNIGGDFDVATGQFRCRVPGAY
                       HGAPHYALGAPGATFSGYLVYAD 143
 HGAPQYALGAPGATFSGYLVYAD 145
                                                                                                     LGPTPGPGSSELRGAFSAARTTPLEGTSEMAVTFDKVYVNIGGDFDVATGQFRCRVPGAY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         skeletal; muscle.
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cardiovascular; brain; degenerative; placental;
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                                                                                                                                                                                                                                                                                                                                                     English.
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Pred. No. 4.1e-75;
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09-FEB-2001;
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07-SEP-2001;
21-DEC-2001;
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2001US-267924P.

2001US-267816P.

2001US-268112P.

2001US-271639P.

2001US-317818P.

2001US-343553P.
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Tang . Ku Y, `e EA, New human secreted proteins and nucleic acids useful in diagnosing, treating and preventing cell proliferative, autoimmune/inflammatory, cardiovascular, neurological, and developmental disorders -Yang, Yue H, Ga (ang J, Than Richardson Thangavelu dson TW, Ba Baughn Yao MG, Warren BA, D: Lal PG, Honchell CD, hn MR, Elliott VS; Ding L, Duggan Br ), Walia NK, Lee s

BM;

Claim 1; Page 140; 158pp; English.

The invention relates to twenty four human secreted proteins (SECP1-24), proteins 90% identical to them and active fragments of them. (CR Also included are nucleic acids encoding the SECP proteins, a recombinant polynucleotide comprising a promoter sequence operably linked to the convergence of convergence of the comprising the recombinant polynucleotide, and can transgenic organism comprising the recombinant polynucleotide, and convergence of convergence of the convergence of the convergence of the convergence of convergence of the conver recombinant

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                                                                          The present invention relates to cDNAs encoding TANGO 244, TANGO 246, TANGO 275, TANGO 300 and MANGO 245 proteins. TANGO 246 proteins and protein modulators are useful for treating colonic disorders, inflammatory diseases, tumors, renal disorders, liver disorders, lung disorders, autoimmune diseases, allergic diseases, cardiovascular diseases, brain disorders, degenerative diseases placental, pancreatic, skeletal and muscle
                                             Sequence
                                                                                                                                                                                            Isolated cDNAs encoding TANGO 244, TANGO 246, T
MANGO 245 proteins, useful in the treatment of
(e.g. idiopathic ulcerative colitis), tumors, r
disorders (e.g. jaundice) -
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pancreatic; skeletal; muscle.
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mune; allergy;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  standard; protein; 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FFSFTAGKAPHKSLSVMLVRNRDEVQALAFDEQRRPGARRAASQSAMLQLDYGDTVWLRL
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                                                                                                                                                                                           (e.g.
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                                                                                                                                                                                                                                                                         Barnes
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                                                                                                                                                                    262pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                           inflammation; tumor; renal; liver; lung; cardiovascular; brain; degenerative; pla
           95.0%;
95.1%;
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Score 708; DE
Pred. No. 2.9e
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Pred. No. 2.5e-74;
D; Mismatches 2;
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 DB 22;
2.9e-72;
hes 7;
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                                                                                                                                                                                                    TANGO 275, TANGO 300 and f inflammatory diseases renal disorders and live
                      Length 329;
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RESULT 8
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                                                                                                                                                                                                   Query Match
Best Local Sim
Matches 137;
                                                                                                                                                                                                                                                                                                                                                                            The present invention relates to cDNAs encoding TANGO 244, TANGO 246, TANGO 275, TANGO 300 and MANGO 245 proteins.

The nucleic acids, proteins and protein modulators are useful for treating colonic disorders, inflammatory diseases, tumors, renal disorders, liver disorders, lung disorders, autoimmune diseases, allergic diseases, cardiovascular diseases, brain disorders, degenerative diseases placental, pancreatic, skeletal and muscle
                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Isolated cDNAs encoding TANGO 244, TANGO 246, TANGO 275, TANGO MANGO 245 proteins, useful in the treatment of inflammatory dis (e.g. idiopathic ulcerative colitis), tumors, renal disorders a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TANGO; MANGO; colon;
autoimmune; allergy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; Fig 29; 262pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              disorders (e.g. jaundice)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29-JUN-2000; 2000WO-US18184
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                                                                                                                                                                                                                                                                                                                                                            disorders
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (MILL-) MILLENNIUM PHARM
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                                                                                                                                1 LGPTPGPGSSELRSAFSAARTTPLEGTSEMAVTFDKVYVNIGGDFDVATGQFRCRVPGAY
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                  FFSFTAGKAPHKSLSVMLVRNRDEVQALAFDEQRRPGARRAASQSAMLQLDYGDTVWLRL
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                                                                                                                                                                                                      Conservative
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                                                                                                                                                                                                                            95.0%;
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cardiovascular; brain; degenerative; placental;
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                                                                                                                                                                                                   Score 707.5; DB 2
Pred. No. 1.7e-72;
3; Mismatches 2
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RESULT 10
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Matches 125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         autoimmune;
pancreatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human MANGO 245 Clq
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TANGO; MANGO; colon;
                                                                                                                                                                                                                                                                                                                              Disclosure; Fig 26; 262pp; English
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                                                                                                                                                                                                              Sequence
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25; Conservative
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                                          FSGYLV 126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   inflammation; tumor; renal; liver; lung;
cardiovascular; brain; degenerative; placental;
                                                                                                                                                                               86.7%;
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Pred. No. le-65;
0; Mismatches
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RESULT 11
AAB61477
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                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                     degenerative disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Page 260-261; 262pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Isolated cDNAs encoding TANGO 244, TANGO 246, TANGO 275, TANGO 300 and MANGO 245 proteins, useful in the treatment of inflammatory diseases (e.g. idiopathic ulcerative colitis), tumors, renal disorders and lives disorders (e.g. jaundice) -
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                                  (first entry)
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                                                                                                                                                                                                                                                                                Score 639; DB 22;
Pred. No. 6.5e-65;
3; Mismatches 1
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Human MANGO

245 extracellular

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Best Local Similarity
Matches 123; Conserv
                                                                               Catarrhini sp..
                                                                                                                               TANGO; MANGO; colon; inflammation; tumor; renal; liver; lung, autoimmune; allergy; cardiovascular; brain; degenerative; plapancreatic; skeletal; muscle.
                                                                                                                                                                                                                                                                                                    04-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention relates to cDNAs encoding TANGO 244, TANGO 246, TANGO 275, TANGO 300 and MANGO 245 proteins. TANGO 275, TANGO 300 and mANGO 245 proteins. The nucleic acids, proteins and protein modulators are useful for treating colonic disorders, inflammatory diseases, tumors, renal disorders, liver disorders, lung disorders, autoimmune diseases, renal disorders, liver disorders, lung disorders, autoimmune diseases, allergic diseases, cardiovascular diseases, brain disorders, degenerative diseases placental, pancreatic, skeletal and muscle
                                                                                                                                                                                                                                              Monkey
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                                                                                                                                                                                                                                                                                                                                                                                                          AAB61472 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Page 246; 262pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                disorders (e.g. jaundice) -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Isolated cDNAs encoding TANGO 244, TANGO 246, TANGO 275, TANGO 300 MANGO 245 proteins, useful in the treatment of inflammatory disease (e.g. idiopathic ulcerative colitis), tumors, renal disorders and i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-050127/06
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                                                                                                                                                                                                                                                                                                                                                                                                             protein; 126
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                                                                                                                                                                                                                                                                                                 entry)
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100.0%;
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cardiovascular; brain; degenerative; placental;
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Pred. No. 1.8e-64;
0; Mismatches 0;
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ARBSULT 13
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Best Local
                                               Human; open reading frame; ORFX; detection; cytostatic; hepatotropic; vulnerary; antipsoriatic; antiparkinsonian; nootropic; neuroprotective; anticonvulsant; osteopathic; antiarthritic; immunosuppressant; cardiant; immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic; hypotensive; dermatological; immunosuppressive; antiinflammatory; antiviral; antibacterial; antifungal; antiheumatic; antithyroid; antianaemic; gene therapy; cancer; proliferative disorder; hypertension; neurodegenerative disorder; osteoarthritis; graft vs host disease; cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS; cholesterol ester storage; systemic lupus erythematosus; infection; severe combined immunodeficiency; malaria; autoimmune disorder; asthma; allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound; bone damage; cartilage damage; antiinflammatory disease; coagulation;
                                                                                                                                                                                                                                                                                                                        Human ORFX ORF1953 polypeptide sequence SEQ ID NO:3906
                                                                                                                                                                                                                                                                                                                                                                                                                                         AAB42189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention relates to cDNAs encoding TANGO 244, TANGO 245, TANGO 300 and MANGO 245 proteins. TANGO 275, TANGO 300 and MANGO 245 proteins. The nucleic acids, proteins and protein modulators are useful for treating colonic disorders, inflammatory diseases, tumors, renal disorders, liver disorders, lung disorders, autolmmune diseases, allergic diseases, cardiovascular diseases, brain disorders, degenerative diseases placental, pancreatic, skeletal and muscle
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Fig 28; 262pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AFSAARTTPLEGTSEMAVTFDKVYVNIGGDFDVATGQFRCRVPGAYFFSFTAGKAPHKSL
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Pred. No. 5
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Homo sapiens

WO200058473-A2

05-OCT-2000

31-MAR-2000; 2000WO-US08621

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RESULT 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CC which represent the human ORFX open reading frames 1 to 3161. The ORFX CC which represent the human ORFX open reading frames 1 to 3161. The ORFX CC sequences have activities such as: cytostatic; hepatotropic; vulnerary; CC antipacviatic; antiparkinsonian; noctropic; neuropyotective; continuous that; cardiant; thrombolytic; coagulant; vasotropic; coaminostimulant; cardiant; thrombolytic; coagulant; vasotropic; cc antiinfammatory; antibacterial; antiviral; antifungal; antirheumatic; cardiant antibacterial; antiviral; antifungal; antirheumatic; cc antiinflammatory; antibacterial; antiviral; antifungal; antirheumatic; cc antithyroid; and antianaemic. The sequences can be used for determining cc pathological conditions associated with an ORFX-associated disorder. The couleic acids can be used to express ORFX proteins in gene therapy coefficies. The proteins and nucleic acids may be used to treat cancers, cordiferative disorders, neurodegenerative disorders, osteoarthritis, cc proliferative disorders, neurodegenerative disorders, osteoarthritis, cc graft vs host disease, cardiovascular disease, diabetes mellitus, conjection, hypothyroidism, cholesterol ester storage, systemic lupus crythematosus, severe combined immunodeficiency (SCID), AIDS, viral, collarics anament human woman and carrilare damane.
BXXXI
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Best Local :
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02-APR-1999; 99US-0127636.
05-APR-1999; 99US-0127728.
30-MAR-2000; 2000US-0540763.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel nucleic acids and peptides derived from open reading useful for treating e.g. cancers, proliferative disorders, neurodegenerative disorders and cardiovascular disease -
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N-PSDB; AAC76398.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    allergies, aplastic anaemia, burns, wounds, bone and cartilage nocturnal haemoglobinuria, antiinflammatory disease; to enhance coagulation; to inhibit thrombosis; and as a contraceptive.
05-NOV-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                     Seguence
                                                                  ABG70383 standard;
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                                                                                                                                                       LGA 123
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                                                                                                                                                                                                                                                                                                GSSELRSAFSAARTTPLEGTSEMAVTFDKVYVNIGGDFDVATGQFRCRVPGAYFFSFTAG
                                                                                                                                                                                                                           KAPHKSPSVMLVRNRDEVQALAFDEQRRPGARRAASQSAMLQLDYGDTVWLRLHGAPQYA
                                                                                                                                                                                                                                                                                                                                                                                                                                     123
                                                                                                                                                                                                                                                                                                                                                                   Conservative
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Leach M;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Ŗ,
                                                                  Protein; 221
                                                                                                                                                                                                                                                                                                                                                                                   83.0%;
98.4%;
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Pred. No. 1.
                                                                    ₽
                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                   DB 21;
                                                                                                                                                                                                                                                                                                                                                                                                   Length 123;
                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cartilage damage,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 frame
                                                                                                                                                                                                                                                                                                                                                                    0
                                                                                                                                                                                                                                                                                                                                                                    Gaps
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pigmentation disorder; endocrine disorder; respiratory disease; health; gastro-intestinal disease; reproductive; neurological disease; bone marrow transplantation; endocrine disease; allergy; inflammation; nephrological disorder; urinary system disorder; age-related disorder; neuropsychiatric disorder; EGF-related protein; SCUBEI; TEN-M4; adipocyte complement-related C1q tumour necrosis factor; out at first; beta adrenergic receptor kinase; EphA6/ehk-2; glucose transporter;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cell signal processing; metabolic pathway modulation; metabolic disorder obesity; diabetes; infectious disease; neurodegenerative disorder; acne; Alzheimer's disease; Parkinson's disease; immune disorder; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Adipocyte complement-related Clq Tumour Necrosis Factor-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    memory defect;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                haematopoietic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              la membrane sushi-containing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NOVX;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             membrane sushi-containing domain; butyrophilin; membrane-sushi domain containing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NOVX-associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   disorder; cirrhosis; pancreatitis; learning defect; infertility; congenital heart defect; hair growth;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cardiomyopathy; atherosclerosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  disorder;
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Homo sapiens.

WO200257453-A2

19-DEC-2001; 2001WO-US50331

19-DEC-2000; 2000US-265704P.
20-DEC-2000; 2000US-257314P.
02-MAY-2001; 2001US-288153P.
29-MAY-2001; 2001US-294075P.
24-JUL-2001; 2001US-307506P.
10-AUG-2001; 2001US-311513P.
29-AUG-2001; 2001US-315617P.
14-SEP-2001; 2001US-322358P.

(CURA-) CURAGEN CORP.

Spytek Stone DJ, ξ EA, Anderson Anderson D, Casman SJ, Patturajan M, Vernet CAM, Malyankar UM, derson D, Shimkets RA, Burgess CE, Zerh asman SJ, Boldog FL, Smithson G, Li L, Zerhusen i L, Ji W Kekuda usen BD, Liu

WPI; 2002-590744/63. N-PSDB; ABS52095.

Novel isolated NOVX polypeptide useful for treating cardiomyopathy, atherosclerosis, metabolic disorders, diabetes, obesity, infectious disease, anorexia, neurodegenerative disorders, Alzheimer's disease cancer disease, anorexia, neurodegenerative or

Claim 1; Page 28; 318pp; English

The present invention relates to new NOVX polypeptides. The invention is cuseful for treating or preventing a NOVX-associated disorder such as cardiomyopathy or atherosclerosis, where the disorder is related to cell cising processing and metabolic pathway modulation in a subject, competerably human. The invention is also useful for treating metabolic cising processing and metabolic pathway modulation in a subject, considered (e.g. obesity), diabetes, infectious disease, neurodegenerative disorders (e.g. Alzheimer's disease, parkinson's disease, immune considered (e.g. Alzheimer's disease, parkinson's disease), infertility, congenital heart constitute, learning and memory defects, infertility, congenital heart constitute, learning and memory defects, infertility, congenital heart constitute, acne, hair growth, pigmentation disorders, endocrine diseases, consupposital diseases, reproductive, health, consupration diseases, bone marrow transplantation, endocrine diseases, consupposition disorders, uninary system constituted diseases, endocrine diseases, and age-related disorders. amino acid sequence represents a NOVX protein

Sequence 221

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                                                      Query Match
Best Local Similarity
Matches 90; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 60.1%; Score 448; DB 23; Best Local Similarity 66.0%; Pred. No. 8.5e-43; Matches 95; Conservative 10; Mismatches 31
                                                                                                                                  The present invention relates to cDNAs encoding TANGO 244, TANGO 246, TANGO 275, TANGO 300 and MANGO 245 proteins. The nucleic acids, proteins and protein modulators are useful for treating colonic disorders, inflammatory diseases, tumors, renal disorders, liver disorders, lung disorders, autoimmune diseases, allergic diseases, cardiovascular diseases, brain disorders, degenerative diseases placental, pancreatic, skeletal and muscle disorders.
                                                                                                                                                                                                                                                                                 Isolated cDNAs encoding TANGO 244, TANGO 246, TANGO 275, TANGO 300 and MANGO 245 proteins, useful in the treatment of inflammatory diseases (e.g. idiopathic ulcerative colitis), tumors, renal disorders and liver disorders (e.g. jaundice) -
                                                                                                            Sequence
                                                                                                                                                                                                                                                       Disclosure; Page 243; 262pp; English.
                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-050127/06.
                                                                                                                                                                                                                                                                                                                                                                                Holtzman DA,
                                                                                                                                                                                                                                                                                                                                                                                                                                   29-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             29-JUN-2000; 2000WO-US18184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        04-JAN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TANGO; MANGO; colon; inflammation; tumor; renal; liver; lung; autoimmune; allergy; cardiovascular; brain; degenerative; placental; pancreatic; skeletal; muscle.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     04-APR-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAB61468 standard; protein; 130 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Catarrhini sp..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mature monkey MANGO 245 protein.
                                                                                                                                                                                                                                                                                                                                                                                                         (MILL-) MILLENNIUM PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         183 HDGYGAYSNHGKYITFSGFLVYPD 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  122 -- GAPHYALGAPGATFSGYLVYAD 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           126 TLGKLPRKTLSVKLMKNRDEVQAMIYDDGASRR---REMQSQSVMLALRRGDAVWLLSHD 182
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                                                                                                          130 AA;
                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                Barnes TM,
                                                                                                                                                                                                                                                                                                                                                                                                                                    99US-0342687
                                                                    57.2%;
62.1%;
                                                                                                                                                                                                                                                                                                                                                                              Fraser CC,
                                                   Score 426.5; DB 22;
Pred. No. 1.2e-40;
Pred. No. 1.2e-20;
                                                                                                                                                                                                                                                                                                                                                                             Sharp JD;
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                                                       Indels
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Search completed: January 12, 2004, 08:15:35 Job time : 21.5499 secs THIS PAGE BLANK (USPTO)

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Result
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Maximum DB
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Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Title:
Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
              Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         seq length: 0
seq length: 2000000000
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1: /cgn2=6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*

2: /cgn2=6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*

3: /cgn2=6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*

4: /cgn2=6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*

5: /cgn2=6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep:*

6: /cgn2=6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep:*

7: /cgn2=6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*

7: /cgn2=6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
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99.2
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745
1 LGPTPGPGSSELRSAFSAAR......PHYALGAPGATFSGYLVYAD 143
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          Copyright
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/cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep:*
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/cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*
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                                                                                                                                                                                                                                                                                                                                  DB
    US-10-085-167-2
US-10-236-055A-14
US-10-236-055A-16
US-10-236-055A-2
US-09-738-973-185
US-09-854-133-185
US-09-854-133-185
US-10-309-422-10
US-10-309-422-12
US-10-309-422-18
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                                                                                                                                                                                                                                                                                                                                Description
Sequence 2, Appli
Sequence 14, Appl
Sequence 16, Appl
Sequence 2, Appli
Sequence 185, App
Sequence 185, App
Sequence 185, App
Sequence 185, App
Sequence 17, Appl
Sequence 14, Appl
Sequence 26, Appl
Sequence 26, Appl
Sequence 30, Appl
Sequence 8, Appl
Sequence 8, Appl
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45	44	43	42	41	40	39	38	37	36	35 5	34	ω ω	32	31	0	29	28	27	26	25	24	23	22	21	20	19	18	17	16
191	191	191	191	191	191	191	191	191	191	191	191	191	192	192	192	192	193	193	196	196	197	200	200	$\vdash$	222	Ν	Ν	222	Ν
25.6		5	.5	.5	5	5	5	5	25.6	ū	5		5	ŗ	5	5	5	5	٥,	٥.	٥,	٥.	٥,	9	9	9	9	9	29.8
203	203	193	193	187	187	163	163	157	145	145	144	144	163	163	163	146	163	146	330	285	285	294	294	409	1127	1126	1092	1091	1043
12	12	12	12	12	12	12	12	12	12	12	12	12	12	12	12	12	12	12	12	16	11	12	11	12	12	12	12	12	12
-325-71	-10-325-717-3	-10-325-717-	-10-325-717-1	-10-325-717-	-10-325-717-1	-10-325-717-	-10-325-717-	-10-325-717-	-10-325-717-	-10-325-717-1	-10-325-717-	-10-325-717-	0-325-717-5	-10-325-717-5	-10-325-717-	0-325-717-2	-10-325-717-	0-325-717-2	-10-236-055A	-10-	9	-10-236-055A-8	9-866-050A-	-10-236-055A-	-10-309-422-	-10-309-422-1	0-309-422-2	-10-309-422-1	US-10-309-422-20
equenc	equenc	equenc	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	ដ	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	equenc	Sequence	Sequence	equenc	Sequence	equenc	equenc	equenc	Sequence	Seguence		equenc	Sequence	Sequence
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Appl	βρli	Appl	Appl	Appl	App1	Appl	Appl	Appli	Appl	Appl	Appl	Appli	Appl	App1	Appl	Appl	Appl	Appl	Appli	Appli	, App	Appli	agA	Appli	Appl	Appl	Appl	Appl	App1

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## ALIGNMENTS

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; SEQ ID NO 2
; LENGTH: 329
; TYPE: PRT
; ORCANISM: Homo sapiens
US-10-085-167-2
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Publication No. US20030170781A1
GENERAL INFORMATION:
APPLICANT: HOLLOWAY, James L.
APPLICANT: Lok, Si
TITLE OF INVENTION: SECRETED PROTEIN ZACRP4
                                                                                                                                                                                                                         Matches 143;
                                                                                                                                                                                                                                             Query Match
Best Local S
                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/10/085,167
CURRENT FILING DATE: 2002-02-27
PRIOR APPLICATION NUMBER: 60/141,928
PRIOR FILING DATE: 1999-07-01
NUMBER OF SEQ ID NOS: 9
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILE REFERENCE: 99-29
   137
                       121 HGAPHYALGAPGATFSGYLVYAD 143
                                                                           77
                                                                                           61 FFSFTAGKAPHKSLSVMLVRNRDEVQALAFDEQRRPGARRAASQSAMLQLDYGDTVWLRL 120
                                                                                                                                                   17
                                                                                                                                                                   1 LGPTPGPGSSELRSAFSAARTTPLEGTSEMAVTFDKVYVNIGGDFDVATGQFRCRVPGAY
                                                                                                                                                                                                                                             Similarity
HGAPHYALGAPGATFSGYLVYAD 159
                                                                       FFSFTAGKAPHKSLSVMLVRNRDEVQALAFDEQRRPGARRAASQSAMLQLDYGDTVWLRL
                                                                                                                                                 LGPTPGPGSSELRSAFSAARTTPLEGTSEMAVTFDKVYVNIGGDFDVATGQFRCRVPGAY
                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                       100.0%; Score 745; DB 12; 100.0%; Pred. No. 3.6e-78; o. Mismatches 0;
                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                            Length 329;
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60 76

US-10-236-055A-14

Sequence 14, Application US/10236055A Publication No. US20030134328A1

INFORMATION:

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                                                                                                                                US-10-236-055A-16
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                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                 SEQ ID NO 16
LENGTH: 326
                                                        Matches 138;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Basham, Beth E.
APPLICANT: Forsythe, Ian
APPLICANT: Gorman, Daniel M.
APPLICANT: Mattson, Jeanine
APPLICANT: Mattson, Jeanine
APPLICANT: Moshrefi, Mehrdad
APPLICANT: Parham, Christi
TITLE OF INVENTION: MAMMALIAN GENES; RELATED REAGENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: US 60/317,988
PRIOR FILING DATE: 2001-09-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/10/236,055A CURRENT FILING DATE: 2003-02-28
                                                                                                                                                                                                                        SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: US (
PRIOR FILING DATE: 2001-09-06
                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/10/236,055A
CURRENT FILING DATE: 2003-02-28
                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Basham, Beth E.
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                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                  FILE REFERENCE: DX01343K
                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Parham, Christi
FITLE OF INVENTION: MAMMALIAN GENES; RELATED REAGENTS
                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 329
TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS: 36
                                                                                                                                               TYPE: PRT
ORGANISM: Mus musculus
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LGPTPGPGSSELRSAFSAARTTPLEGTSEMAVTFDKVYVNIGGDFDVATGQFRCRVPGAY 60
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                                                                                                                                                                                                                                                                                                                                                                                   Mattson, Jeanine
Moshrefi, Mehrdad
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Application US/10236055A
                                                                                                                                                                                                                                                                                                                                                                                                                           Gorman, Daniel M.
                                                                                                                                                                                                                                                                                                                                                                                                                                          Forsythe,
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                                                          Conservative
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                                                        1,
                                                      Score 706.5; DB 12; Pred. No. 1.1e-73; 1; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 739; DB 12;
Pred. No. 1.8e-77;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 12;
                                                                                        DB 12;
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                                                        Indels
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RESULT 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/10/091,458
CURRENT FILING DATE: 2002-03-07
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                              APPLICATION NUMBER: 60
FILING DATE: 2000-08-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: 60/218,290 FILING DATE: 2000-07-14
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APPLICATION NUMBER: 60/216,880
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FILING DATE:
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                60/220,964
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APPLICATION NUMBER: 60/225,759
FILING DATE: 2000-08-14
APPLICATION NUMBER: 60/225,213
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APPLICATION NUMBER: 60/249,216
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APPLICATION NUMBER: 60/246,474
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APPLICATION NUMBER: 60/241,787
                                         FILING DATE: 2000-08-14
APPLICATION NUMBER: 60/227,182
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APPLICATION NUMBER: 60/226,681
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APPLICATION NUMBER: 60/249,210
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APPLICATION NUMBER: 60/236,802
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APPLICATION NUMBER: 60/229,513
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           NUMBER: 60/225,214
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OR APPLICATION NUMBER: 60/249,213
OR FILING DATE: 2000-11-17
OR APPLICATION NUMBER: 60/249,212
OR FILING DATE: 2000-11-17
OR APPLICATION NUMBER: 60/249,207
OR FILING DATE: 2000-11-17
OR APPLICATION NUMBER: 60/249,245
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OR APPLICATION NUMBER: 60/249,264
OR FILING DATE: 2000-11-17
OR APPLICATION NUMBER: 60/249,214
OR FILING DATE: 2000-11-17
OR APPLICATION NUMBER: 60/249,297
OR APPLICATION NUMBER: 60/249,297
OR FILING DATE: 2000-11-17
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APPLICATION NUMBER: 60/233,064
FILING DATE: 2000-09-14
APPLICATION NUMBER: 60/233,063
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FILING DATE: 2000-10-20
APPLICATION NUMBER: 60/241,826
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APPLICATION NUMBER: 60/
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APPLICATION NUMBER: 60/231,414
FILING DATE: 2000-09-08
APPLICATION NUMBER: 60/231,244
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                                                     APPLICATION NUMBER: 60/
FILING DATE: 2000-10-20
APPLICATION NUMBER: 60/
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APPLICATION NUMBER: 60/232,397
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FILING DATE: 2000-09-14
APPLICATION NUMBER: 60/231,242
FILING DATE: 2000-09-08
                  FILING DATE: 2000-11-08
APPLICATION NUMBER: 60/231,243
                                                                                                                APPLICATION NUMBER: FILING DATE: 2000-10
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APPLICATION NUMBER:
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APPLICATION NUMBER: 60/249,211
FILING DATE: 2000-11-17
APPLICATION NUMBER: 60/249,215
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APPLICATION NUMBER: 60/249,244
FILING DATE: 2000-11-17
APPLICATION NUMBER: 60/249,217
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2000-09-08
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                                                     60/246,475
                                                                                            60/241,221
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7 PGSSELRSAFSAARTTPL-EGTSEMAVTFDKVYVNIGGDFDVATGQFRCRVPGAYFFSFT 65

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US-10-236-055A-2
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Best Local Similarity
                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                           Sequence 185, Application US/09738973 Patent No. US20020110563A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/10/236,055A CURRENT FILING DATE: 2003-02-28 PRIOR APPLICATION NUMBER: US 60/317,988 PRIOR FILING DATE: 2001-09-06 NUMBER OF SEQ ID NOS: 36
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TITLE OF INVENTION: MAMMALIAN GENES; RELATED REAGENTS
FILE REFERENCE: DX01343K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Basham, Beth
APPLICANT: Forsythe, Ia
APPLICANT: Gorman, Dani
APPLICANT: Mattson, Jea
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ENGTH: 420
 OF INVENTION:
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T: Mannion, Jane
T: Kalos, Michael D.
INVENTION: COMPOSITIONS AND METHODS FOR
INVENTION: THE THERAPY AND DIAGNOSIS OF LUNG CANCER
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Moshrefi, Mehrdad
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Gorman, Daniel M.
                                                                  Secrist, Heather
Indirias, Carol Yoseph
Benson, Darin R.
Elliot, Mark
                                                                                                                                                     Lodes, Michael J. Fling, Steven P. Mohamath, Raodoh
                                                                                                                                  Algate, Paul A.
                                                                                                                                                                                                           Henderson, Robert A.
                                                                                                                                                                                                                           Reed, Steven G.
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FILE REFERENCE: 210121.475C9
CURRENT APPLICATION NUMBER: US/09/738,973
CURRENT FILING DATE: 2000-12-14
NUMBER OF SEQ ID NOS: 587
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 185
LENGTH: 746
TYPE: PRT
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RESULT 8
US-10-144-649A-185
; Sequence 185, Application US/10144649A
; Publication No. US20030118599A1
; GENERAL INFORMATION:
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SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 185
LENGTH: 746
TYPE: PRT
ORGANIZM: Homo sapien
US-09-854-133-185
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Matches
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APPLICANT: Mohamath, Raodoh
APPLICANT: Henderson, Robert A.
APPLICANT: Benson, Darin R.
APPLICANT: Secrist, Heather
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: THE THERAPY AND DIAGNOSIS OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/854,133
CURRENT FILING DATE: 2001-05-11
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Local Similarity 41.7%;
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58; Conserv
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o. US20020183499A1
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41.7%; Pred. No. 8e-17;
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Pred. No. 8e-17;
8; Mismatches
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RESULT 9
US-10-309-422-10
US-10-309-422-10
; Sequence 10, Application US/10309422
; Publication No. US20030139587A1
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SEQ ID NO 185
LENGTH: 746
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                                                                                                                                                                                                                                                                                                                                               SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 10
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APPLICANT: Wilganowski, Nathaniel L.
APPLICANT: Wilganowski, Nathaniel L.
APPLICANT: Turner, C. Alexander Jr.
TITLE OF INVENTION: NO. US20030139587A1el Human Proteins and Polynucleotides Encoding
FILE REFERENCE: LEX-0142-USA
CURRENT APPLICATION NUMBER: US/10/309,422
CURRENT FILING DATE: 2002-12-03
PRIOR APPLICATION NUMBER: US/99/798,771
PRIOR FILING DATE: 2001-03-02
PRIOR PILING DATE: 2000-03-02
PRIOR FILING DATE: 2000-03-02
PRIOR FILING DATE: 2000-03-02
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CURRENT APPLICATION NUMBER: US/10/144,649A
CURRENT FILING DATE: 2002-08-21
NUMBER OF SEQ ID NOS: 749
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APPLICANT: McNeill, Patricia D.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: THE THERAPY AND DIAGNOSIS OF LUNG CANCER
                                                                                                                                                                                                                                                                                        LENGTH: 908
TYPE: PRT
ORGANISM: homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 43
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ORGANISM: Homo sapien
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                                                                                                                                                                                                                      Local Similarity
                        125
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 HYALGAPGATFSGYLVYAD 143
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                                                                                       AGK-APHKSLSVMLVRNRDEVQALAFDEQRRPGARRAASQSAMLQLDYGDTVWLRLHGAP 124
                                                                                                                                                             PGSSELRSAFSAARTTPL-EGTSEMAVTFDKVYVNIGGDFDVATGQFRCRVPGAYFFSFT 65
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                                                                                                                               PLPQQMRVAFSAARTSNLAPGTLDQPIVFDLLLNNLGETFDLQLGRFNCPVNGTYVFIFH
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41.7%; Pred. No. 8e-17;
vative 18; Mismatches
                                                                                                                                                                                                 18;
                                                                                                                                                                                                                      Score 222;
Pred. No. 1
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59;
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                                                                                                                                                                                                                                     Length 908;
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RESULT 10
US-10-309-422-22
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; TYPE: PRT
; ORGANISM: homo sapiens
US-10-309-422-22
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                                               Query Match
Best Local Similarity
Matches 58; Conserv
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SEQ ID NO 14
LENGTH: 957
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APPLICANT: Wilganowski, Nathaniel L.
APPLICANT: Turner, C. Alexander Jr.
TITLE OF INVENTION: No. US20030139587A1el Human Proteins
FILE REFERENCE: LEX-0142-USA
CURRENT APPLICATION NUMBER: US/10/309,422
CURRENT FILING DATE: 2002-12-03
PRIOR APPLICATION NUMBER: US/09/798,771
                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/10/309,422
CURRENT FILING DATE: 2002-12-03
PRIOR APPLICATION NUMBER: US/09/798,771
                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Wilganowski, Nathaniel L. APPLICANT: Turmer, C. Alexander Jr. TITLE OF INVENTION: No. US20030139587Alel Human Proteins and Polynucleotides Encoding FILE REFERENCE: LEX-0142-USA
                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: US 60/186,557
PRIOR FILING DATE: 2000-03-02
NUMBER OF SEQ ID NOS: 43
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PGSSELRSAFSAARTTPL-EGTSEMAVTFDKVYVNIGGDFDVATGQFRCRVPGAYFFSFT 65
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                                               Conservative
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                                               Score 222; DB 12;
Pred. No. 1.1e-16;
8; Mismatches 59;
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                                                                                                     APPLICANT: Walke, D. Wade
APPLICANT: Wilganowski, Nathaniel L.
APPLICANT: Turner, C. Alexander Jr.
TITLE OF INVENTION: NO. US20030139587A1el Hu
FILE REFERENCE: LEX-0142-USA
CURRENT APPLICATION NUMBER: US/10/309,422
CURRENT FILING DATE: 2002-12-03
PRIOR APPLICATION NUMBER: US/09/798,771
PRIOR FILING DATE: 2001-03-02
PRIOR FILING DATE: 2001-03-02
                                                                                                                                                                                                                                                                    Sequence 18, Application US/10309422 Publication No. US20030139587A1 GENERAL INFORMATION:
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 26
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PRIOR APPLICATION NUMBER: US 60/186,557
PRIOR FILING DATE: 2000-03-02
NUMBER OF SEQ ID NOS: 43
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 18
LENGTH: 992
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Best Local :
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APPLICANT: Wilganowski, Nathaniel L.
APPLICANT: Wilganowski, Nathaniel L.
APPLICANT: Wilganowski, Nathaniel L.
APPLICANT: Turner, C. Alexander Jr.
TITLE OF INVENTION: NO. US20030139587A1el Human Proteins and Polynucleotides Encoding FILE REFERENCE: LEX-0142-USA
FILE REFERENCE: LEX-0142-USA
CURRENT FILING DATE: 2002-12-03
CURRENT FILING DATE: 2002-12-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: US/09/798,771
PRIOR FILING DATE: 2001-03-02
PRIOR APPLICATION NUMBER: US 60/186,557
PRIOR FILING DATE: 2000-03-02
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Pred. No. 1.1e-16;
8; Mismatches 59;
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US-10-309-422-18
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Publication No.
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Best Local
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Sequence 8, Application US/10309422 Publication No. US20030139587A1 GENERAL INFORMATION:
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SEQ ID NO 30
LENGTH: 993
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APPLICANT: Walke, D. Wade
APPLICANT: Wilganowski, I
APPLICANT: Turner, C. Al
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Best Local Similarity 41.7%;
Matches 58; Conservative 1
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CURRENT FILING DATE: 2002-12-03
PRIOR APPLICATION NUMBER: US/09/798,771
PRIOR FILING DATE: 2001-03-02
PRIOR APPLICATION NUMBER: US 60/186,557
PRIOR APPLICATION NUMBER: US 60/186,557
PRIOR FILING DATE: 2000-03-02
NUMBER OF SEQ ID NOS: 43
                    APPLICANT: Wilganowski, Nathaniel L. APPLICANT: Turner, C. Alexander Jr. TITLE OF INVENTION: NO. US20030139587Alel Human Proteins and Polynucleotides FILE REFERENCE: LEX-0142-USA
                                                                    APPLICANT: Walke, D. Wade
APPLICANT: Wilganowski, I
APPLICANT: Turner, C. All
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APPLICANT: Turner, C. Alexander Jr.
TITLE OF INVENTION: No. US20030139587A1el Human Proteins and Polynucleotides Encodin
FILE REFERENCE: LEX-0142-USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT ORGANISM: homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          916 MLKLAVNVPLYVNLMKN-EEVLVSAYANDGAPD-HETASNHAILQLFQGDQIWLRLHRGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           856 PLPQQMRVAFSAARTSNLAPGTLDQPIVFDLLLNNLGETFDLQLGRFNCPVNGTYVFIFH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             974 IYGSSWKYSTFSGYLLYQD 992
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               66 AGK-APHKSLSVMLVRNRDEVQALAFDEQRRPGARRAASQSAMLQLDYGDTVWLRLHGAP
                                                                                                                                                                                                                                                                                                                                                                                                               homo sapiens
                                                                                                                                                                                                                                                                                                                    IYGSSWKYSTFSGYLLYQD 993
                                                                                                                                                                                                                                                                                                                                                                  HYALGAPGATFSGYLVYAD 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PLPQQMRVAFSAARTSNLAPGTLDQPIVFDLLLNNLGETFDLQLGRFNCPVNGTYVFIFH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PGSSELRSAFSAARTTPL-EGTSEMAVTFDKVYVNIGGDFDVATGQFRCRVPGAYFFSFT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Application US/10309422
to. US20030139587A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
NUMBER: US/10/309,422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29.8%; Score 222; DB 12;
41.7%; Pred. No. 1.2e-16;
ative 18; Mismatches 59
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Pred. No. 1.2e-16;
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                                                     Encodir
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CURRENT FILING DATE: 2002-12-03; PRIOR APPLICATION NUMBER: US/99/798,771
PRIOR APPLICATION NUMBER: US/99/798,771
PRIOR APPLICATION NUMBER: US 60/186,557
PRIOR OF SEQ ID NOS: 43
SOFTWARE: FRSTSEQ for Windows Version 4.0
:SEQ ID NO 8
: LENGTH: 1042
TYPE: PRT
: ORGANISM: homo sapiens
US-10-309-422-8

Query Match
Best Local Similarity 41,7%; Pred. No. 1.2e-16;
Matches 58; Conservative 18; Mismatches 59; Indels 4; Gaps 4;
Matches 58; Conservative 18; Mismatches 59; Indels 4; Gaps 4;

QY 7 PGSSELRSAFSARTTPL_EGTSEMAVTEDVYVNIGGDFDVATGGPFCRVPGAYFFSFT 65
Matches 58; Conservative 18; Mismatches 59; Indels 4; Gaps 4;

QY 7 PGSSELRSAFSARTTPL_EGTSEMAVTEDVYVNIGGDFDVATGGPFCRVPGAYFFSFT 65
Matches 58; Conservative 18; Mismatches 59; Indels 4; Gaps 4;

QY 7 PGSSELRSAFSARTTSNLAPGTLDQPIVFDLLLNNLGETFDLQLGRENCPVNGTYVFIFH 965

QY 66 AGK-APHKSLSVMLVRNRDEVQALAFDEQRRPGARRAASQSAMLQLDYGDTVWLRLHGAP 124

Db 966 MLKLAVNVPLYVNLMKN-EEVLVSAYANDGAPD-HETASNHAILQLPQGDQIWLRLHRGA 1023

QY 125 HYALGAPGATFSGYLLYAD 143
Db 1024 IYGSSWKYSTFSGYLLYAD 1042

Search completed: January 12, 2004, 08:33:37

Job time: 18.4112 secs
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Result
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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Perfect score:
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       Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18
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seq length: 2000000000
       derived by analysis
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Gapop 10.0 , Gapext 0.5
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745
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1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*

2: /cgn2_6/ptodata/2//iaa/6A_COMB.pep:*

3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*

4: /cgn2_6/ptodata/2/iaa/B_COMB.pep:*

5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*

6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*
     GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd
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  US-09-370-838-185
US-09-188-930-294
US-09-312-283C-294
US-09-312-283C-382
US-09-530-423-2
US-09-530-423-2
US-09-336-536-20
US-09-336-536-20
US-09-686-838B-3
US-09-911-176B-48
US-09-176-976-6
US-09-176-976-6
US-09-176-976-6
US-09-336-536-4
US-09-336-536-4
US-09-336-536-3
US-09-489-847-198
US-09-489-847-198
US-09-489-847-349
US-09-489-847-349
US-09-140-804-8
US-09-140-804-8
US-09-140-804-8
US-09-140-804-8
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US-09-140-804-8
US-09-140-805-3
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Sequence 185, App
Sequence 294, App
Sequence 294, App
Sequence 382, App
Sequence 7, Appli
Sequence 7, Appli
Sequence 10, Appli
Sequence 10, Appli
Sequence 11, Appli
Sequence 11, Appli
Sequence 12, Appli
Sequence 13, Appli
Sequence 6, Appli
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RESULT 2
US-09-188-930-294
Sequence 294, Application US/09188930A
Petent No. 6150502
GENERAL INFORMATION:
APPLICANT: Watson, James D.
APPLICANT: Strachan, Lorna
APPLICANT: Steeman, Matthew
APPLICANT: Onrust, Rene

Matches Qy Db Qy Db Oy Db	RESULT 1 US-09-370 Sequent Sequent GENERAL GENERAL APPLIC FILE FILE FILE FILE FILE FILE FILE FILE	222 222 2014 2014 2014 2014 2014 2014
58 7 610 66 670 125	110-838-18 ence 185, ence 185, ence 185, LICANT: Re LICANT: Re LICANT: LO LICANT: LO LICANT: LO LICANT: LO LICANT: LO LICANT: LO LICANT: MO LICANT: LO LICANT: LO LICANT: LO LICANT: LO LICANT: MO LICANT: LO LICANT: LO LICANT: MO ENCIPTERNO ENCIPTERNO LICANT LIER FILIN LIER FI	185 185 185 179 185 179 179 170 170 170 170 170 170 170 170 170 170
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ative	lication US/093 S. Steven G. Steven G. Michael J. Ath, Readoh St. Heather ON: LUNG CANCER 210121.475C1 TON NUMBER: US/ ATE: 1999-08-09 TON NUMBER: US/ ATE: 1999-04-02 NOS: 289 O for Windows V Sapien  sapien  29.8%; rity 41.7%;	247 247 247 247 247 247 247 243 2243 224
TPL: SNL: SNL: KN-: KN-: LYQ		<b>444444444444444444</b>
8; Mismatches 59; EGTSEMAVTFDKVYVNIGGDFD	370838  FOR THERAPY AND DIAGNOS: R AND METHODS FOR THEIR /09/370,838 9 09/285,323 2 Version 3.0 Version 3.0 Score 222; DB 4; Lenc Pred. No. 2e-18;	US-09-686-838B-8 US-09-911-176B-3 US-09-619-740-3 US-09-76-852-3 US-09-76-852-3 US-09-909-547-4 US-09-312-283C-295 US-09-312-283C-295 US-09-316-536-10 US-09-336-536-10 US-09-336-536-10 US-09-336-536-10 US-09-336-536-12 US-09-918-408-2 US-09-918-408-2 US-09-911-176B-2 US-09-511-176B-2 US-09-516-852-2 US-09-485-316A-11
Indels 4; Gaps 4  VATGOFRCRVPGAYFFSFT 65                  65  LOLGRENCPVNGTYVFIFH 669  AMLQLDYGDTVWLRLHGAP 124	IS OF USE	Sequence 8, Appli Sequence 3, Appli Sequence 4, Appli Sequence 3, Appli Sequence 4, Appli Sequence 295, App Sequence 295, Appli Sequence 10, Appli Sequence 10, Appli Sequence 2, Appli

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APPLICANT: Murison, James Greg
TITLE OF INVENTION: Compositions Isolated From Skin Cells
TITLE OF INVENTION: and Methods For Their Use
FILE REFERENCE: 11000.1011c1
CURRENT APPLICATION NUMBER: US/09/188,930A
CURRENT FILING DATE: 1998-11-09
NUMBER OF SEQ ID NOS: 348
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 294
LENGTH: 294
TYPE: PRT
ORGANISM: Rat
US-09-188-930-294
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US-09-312-283C-294
; Sequence 294, Application US/09312283C
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CURRENT APPLICATION NUMBER: US/09/312,283C

CURRENT FILING DATE: 1999-05-14

NUMBER OF SEQ ID NOS: 425

SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 294

LENGTH: 294
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Best Local Similarity
Matches 53; Conserv
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APPLICANT: Kumble, Krishanand D.
TITLE OF INVENTION: Compositions Isolated from
TITLE OF INVENTION: and Methods for Their Use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Watson, James D.
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                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Mouse
260
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                                                                                                                60 YFFSFTAGKAPHKSLSVMLVRNRDEVQALAFDEQRRPGARRAASQSAMLQLDYGDTVWLR 119
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                                  LHGA-----PHYALGAPGATFSGYLVYAD 143
                                                                                                                                                         PGPCSCGSSRAKSAFSVAVTKSYPRE---RLPIKFDKILMNEGGHYNASSGKFVCSVPGI 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IFYSEQNGLFYDPYWT----DSLFTGFLIYAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YFFSFTAGKAPHKSLSVMLVRNRDEVQALAFDEQRRPGARRAASQSAMLQLDYGDTVWLR 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PGPCSCGSSRAKSAFSVAVTKSYPRE---RLPIKFDKILMNEGGHYNASSGKFVCSVPGI 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PGP---GSSELRSAFSAA--RTTPLEGTSEMAVTFDKVYVNIGGDFDVATGQFRCRVPGA 59
IFYSEQNGLFYDPYWT----DSLFTGFLIYAD 287
                                                                                                                                                                                  PGP---GSSELRSAFSAA--RTTPLEGTSEMAVTFDKVYVNIGGDFDVATGQFRCRVPGA 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LHGA-----PHYALGAPGATFSGYLVYAD 143
                                                                           YYFTYDITLA-NKHLAIGLVHN-GQYRIRTFD--ANTGNHDVASGSTILALKEGDEVWLQ 259
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Sleeman, Matthew
Onrust, Rene
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                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                     26.8%; Score 200; DB 4; Length 294; 34.9%; Pred. No. 2.7e-16; tive 30; Mismatches 45; Indels
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RESULT 4

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RESULT 5
US-09-530-423-2
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                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 4
SOFTWARE: PatentIn Ver.
SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 425
SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION: Otsuka Pharmaceutical Co., Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2, Application US/09530423 Patent No. 6461821
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Best Local
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Best Local (
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APPLICANT:
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TITLE OF INVENTION: C
FILE REFERENCE: P98-51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILE REFERENCE: 11000.1011c2
CURRENT APPLICATION NUMBER: US/09/312,283C
CURRENT FILING DATE: 1999-05-14
                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: JP H9-297569 PRIOR FILING DATE: 1997-10-29
                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/530,423
CURRENT FILING DATE: 2000-05-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: Compositions Isolated from TITLE OF INVENTION: and Methods for Their Use
                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: Smooth muscle growth inhibitory composition,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Mouse
                                                                                                                                                                                                                 TYPE: PRT ORGANISM: Abdominal fat tissue from myoma uteri
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-----HITVYMKDVKVSLFK-KDKAMLFTYDQYQENNVDQ-ASGSVLLHLEVGDQVWLQ
                                  TAGKAPH-----KSLSVMLVRNRDEVQALAFDEQRRPGARRAASQSAMLQLDYGDTVWLR 119
                                                                     PGEGAYVYRSAFSVGLETYVT-IPNMPIRFTKIFYNQQNHYDGSTGKFHCNIPGLYYFAY
                                                                                                     PGPGSSELRSAFSAARTTPLEGTSEMAVTFDKVYVNIGGDFDVATGQFRCRVPGAYFFSF 64
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Kumble, Krishanand D.
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Sleeman, Matthew
Onrust, Rene
                                                                                                                                    25.6%; Score 191; DB 4; ilarity 31.8%; Pred. No. 2.4e-15; Conservative 29; Mismatches 54
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                                                                                                                                                                                                                                                                                                                                                                                                                          diagnostic method for arteriosclerosis
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Pred. No. 6e-16;
}1; Mismatches
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LHGAPH----YALGAPGATFSGYLVYAD 143

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RESULT 7
US-09-140-804-3
; Sequence 3, Application US/09140804
; Patent No. 6197930
; Patent No. 6197930
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Best Local S
Matches 47
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NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: WHI9
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 861-6240
TELEPAX: (617) 861-9540
INFORMATION FOR SEQ ID NO: 7:
                                                             GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                             -08-463-911-7
      APPLICANT: Sheppard, Paul O.
APPLICANT: Humes, Jacqueline M.
TITLE OF INVENTION: ADIPOCYTE-SPECIFIC
FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
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MEDIUM TYPE: Floppy disk
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CORRESPONDENCE ADDRESS:
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Harvey F.
A NOVEL SERUM PROTEIN PRODUCED
EXCLUSIVELY IN ADIPOCYTES
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Pred. No. 2.6e-15;
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             PROTEIN
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             HOMOLOGS
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US-09-530-423-1
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US-09-336-536-20
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Sequence 1, Application US/09530423 Patent No: 6461821
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SEQ ID NO 20
LENGTH: 244
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CURRENT FILING DATE: 1998-08-26
EARLIER APPLICATION NUMBER: 60/056,983
EARLIER FILING DATE: 1997-08-26
NUMBER OF SEQ ID NOS: 47
SOFTWARE: FASESEQ for Windows Version 3.0
SEQ ID NO 3
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Best Local
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CURRENT FILING DATE: 1999-06-18
NUMBER OF SEQ ID NOS: 75
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TITLE OF INVENTION: SECRETED PROTEINS
FILE REFERENCE: 7853-144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Leiby, K. APPLICANT: McKay, C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Homo sapiens
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TYPE: PRT
ORGANISM: Homo sapiens
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                                                                                                                                                                                                                   LHGAPH----YALGAPGATFSGYLVYAD 143
                                                                                                                                                                                                                                                -----HITVYMKDVKVSLFK-KDKAMLFTYDQYQENNVDQ-ASGSVLLHLEVGDQVWLQ
                                                                                                                                                                                                                                                                                 TAGKAPH-----KSLSVMLVRNRDEVQALAFDEQRRPGARRAASQSAMLQLDYGDTVWLR 119
                                                                                                                                                                                                                                                                                                                  PGEGAYVYRSAFSVGLETYVT-IPNMPIRFTKIFYNQQNHYDGSTGKFHCNIPGLYYFAY 162
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31.8%;
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Pred. No. 2.6e-15;
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Pred. No. 2.6e-15;
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                                                                                                                                                                                                                                                                                                                                                                                                                  DB 4; Length 244;
                                                                                                                                                                                                                                                                                                                                                                                     54;
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; SEQ ID NO 1
; LENGTH: 244
; TYPE: PRT
; ORGANISM: Abdominal fat tissue from myoma uteri
US-09-530-423-1
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                         SEQ ID NO 3
                                                                                                                                                                                                                                                                    Query Match
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TITLE OF INVENTION: Adipocyte-Specific Protein Homologs
FILE REFERENCE: 97-49D1
CURRENT APPLICATION NUMBER: US/09/686,838B
CCURENT FILING DATE: 2000-10-10
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CURRENT APPLICATION NUMBER: US/09/530,423
CURRENT FILING DATE: 2000-05-01
PRIOR APPLICATION NUMBER: JP H9-297569
PRIOR PILING DATE: 1997-10-29
PRIOR PILING DATE: 1997-10-29
PRIOR FILING DATE: 1997-10-29
PRIOR FILING DATE: 1997-10-29
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PRIOR FILING DATE: 1998-08-26
PRIOR APPLICATION NUMBER: US 60/056,983
PRIOR FILING DATE: 1997-08-26
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                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 50
SOFTWARE: FastSEQ for Windows Version 4.0
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ORGANISM: Homo sapiens
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Local Similarity 31.8%;
hes 47; Conservative 2:
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47; Conserv
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                                      LHGAPH----YALGAPGATFSGYLVYAD 143
                                                                                                            TAGKAPH-----KSLSVMLVRNRDEVQALAFDEQRRPGARRAASQSAMLQLDYGDTVWLR 119
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VYGEGERNGLYADNDNDSTFTGFLLYHD
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Pred. No. 2.6e-15;
29; Mismatches 54
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RESULT 11

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120 LHGAPH----YALGAPGATFSGYLVYAD 143

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APPLICANT: Sheppard, Paul O.
TITLE OF INVENTION: ANTIBODIES THAT BIND AN
TITLE OF INVENTION: ADIPOCYTE-SPECIFIC PROTEIN
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Matches
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 3
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CURRENT APPLICATION NUMBER: US/09/911,176B
CURRENT FILING DATE: 2001-07-23
CURRENT FILING DATE: 09/118,408
PRIOR APPLICATION NUMBER: 09/118,408
PRIOR FILING DATE: 1998-07-17
PRIOR APPLICATION NUMBER: 60/053,154
                                                                                                                                                                                          Query Match
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NUMBER OF SEQ ID NOS: 52
                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/552,225A CURRENT FILING DATE: 2000-04-19 PRIOR APPLICATION NUMBER: 60/130,199 PRIOR FILING DATE: 1999-04-20
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APPLICANT: Bishop, Paul
TITLE OF INVENTION: ADIPOCYTE-SPECIFIC PROTEIN HOMOLOG
FILE REFERENCE: 99-09
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ORGANISM: Homo sapiens
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                                                                                                                                                                      Match 25.6%;
Local Similarity 31.8%;
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 163 -----HITVYMKDVKVSLFK-KDKAMLFTYDQYQENNVDQ-ASGSVLLHLEVGDQVWLQ
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                                     TAGKAPH-----KSLSVMLVRNRDEVQALAFDEQRRPGARRAASQSAMLQLDYGDTVWLR 119
                                                                           PGEGAYVYRSAFSVGLETYVT-IPNMPIRFTKIFYNOONHYDGSTGKFHCNIPGLYYFAY 162
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                                                                                                                                                        Score 191; DB 4;
Pred. No. 2.6e-15;
29; Mismatches 54
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US-09-619-740-51
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LENGTH: 244
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Sequence 51, App. -
No. 6544946
SEQ ID NO 6
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                    NUMBER OF SOFTWARE:
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-09-619-740-51
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                                                                                          CURRENT FILING DATE: 2001-02-05
PRIOR APPLICATION NUMBER: US 09/758,055
PRIOR FILING DATE: 2001-01-10
PRIOR APPLICATION NUMBER: US 60/176,228
PRIOR FILING DATE: 2000-01-14
PRIOR FILING DATE: 2000-04-13
PRIOR FILING DATE: 2000-04-13
                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/776,976
CURRENT FILING DATE: 2001-02-05
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PRIOR APPLICATION NUMBER: 09/253,604
PRIOR FILING DATE: 1999-02-19
PRIOR APPLICATION NUMBER: 09/444,794
PRIOR PILING PARTOR
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CURRENT APPLICATION NUMBER: US/09/619,740
CURRENT FILING DATE: 2000-07-19
                                                    PRIOR APPLICATION NUMBER: US 60/299,881 PRIOR FILING DATE: 2000-09-01
                                                                                                                                                                                                                                                    FILE REFERENCE:
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                    Patent.pm
                                    SEQ ID NOS:
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US-09-909-547-6
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                                                                                                                                                                                                                                                                                                                                                                                                       US-09-909-547-6
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PRIOR APPLICATION NUMBER: US 09/776,976
PRIOR FILING DATE: 2001-02-05
PRIOR APPLICATION NUMBER: US 09/758,055
PRIOR FILING DATE: 2001-01-10
PRIOR APPLICATION NUMBER: US 60/29,881
PRIOR FILING DATE: 2000-09-01
PRIOR APPLICATION NUMBER: US 60/198,087
PRIOR APPLICATION NUMBER: US 60/176,228
PRIOR FILING DATE: 2000-04-13
PRIOR FILING DATE: 2000-01-14
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SEQ ID NO 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 6, Application US/09909547 Patent No. 6579852
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SOFTWARE: Patent.pm
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CURRENT FILING DATE: 2001-07-19
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                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 24
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Bihain, Bernard
TITLE OF INVENTION: OBG3 Globular Head and
FILE REFERENCE: 76.US6.CIP
                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Homo sapiens
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                                                                                                                   120 LHGAPH----YALGAPGATFSGYLVYAD 143
                                                                                                                                                                                                                                          104 PGEGAYVYRSAFSVGLETYVT-IPNMPIRFTKIFYNQQNHYDGSTGKFHCNIPGLYYFAY 162
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                244
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Pred. No. 2.6e-15;
9; Mismatches 54;
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1639
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1: pir1:*
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3: pir3:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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RESULT 2  JC4708  gelatin-binding 28K protein precursor - human  N;Alternate names: adipose specific collagen-like factor  C;Species: Homo sapiens (man)  C;Date: 10-May-1996 #sequence_revision 19-Jul-1996 #text_  C;Accession: JC4708; JC4944  R;Maeda, K.; Okubo, K.; Shimomura, I.; Funahashi, T.; Mat  Biochem. Biophys. Res. Commun. 221, 286-289, 1996  A;Title: cDNA cloning and expression of a novel adipose s  A;Reference number: JC4708; MUID:96224171; PMID:8619847  A;Accession: JC4708	RESULT 1  T14782  hypothetical protein DKFZp586B0621.1 - human (fragment) C;Species: Homo sapiens (man) C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 02-Sep-20 C;Accession: T14782 R;Ottenwaelder, B.; Obermaier, B.; Mewes, H.W.; Gassenhuber, J.; Wiemann, submitted to the Protein Sequence Database, August 1999 A;Reference number: Z18184 A;Accession: T14782 A;Accession	ALIGNMENTS	30 94 5.7 913 2 AB2587 31 94 5.7 913 2 B97369 32 94 5.7 1045 2 A39199 33 94 5.7 1045 2 A39199 34 92.5 5.6 420 2 E75130 35 91.5 5.6 13055 2 T15880 36 91 5.6 882 2 S41034 37 90.5 5.5 2124 2 H83357 38 90 5.5 268 2 D75574 40 90 5.5 366 2 T52655 41 90 5.5 1239 1 QQBE10 42 90 5.5 1239 1 QQBE10 42 90 5.5 7463 2 T36248 44 89.5 5.5 7463 2 T36248 44 89.5 5.5 7463 2 T36299
or xt_change 20-Sep-1999 Matsuzawa, Y.; Matsubara, K. e specific collagen-like factor, ag	ent)  #text_change 02-Sep-2000  senhuber, J.; Wiemann, S.  1999  B0621  cology  Length 219;  Length 219;    Indels 22; Gaps 6;  GPPAPPEPRSAFSAARTR 169		translation initia translation initia endoglucanase B (E Bassoon protein - hypothetical prote hypothetical prote hypothetical prote probable non-ribos hypothetical prote probable non-ribos hypothetical prote probable non-ribos hypothetical prote bhiosulfate sulfur Om(ID) protein - hu bullous pemphigoid CDA peptide synthe tellurium resistan hypothetical prote

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A;Cross-references: GB:D12975; NID:g287469; PIDN:BAA02352.1; PID:g287470
A;Note: the source is designated as Tamias asiaticus in Genbank entry TMSHP25,
A;Note: sequence extracted from NCBI backbone (NCBIN:125946, NCBIP:125947)
R;Kondo, N; Kondo, J
J. Biol. Chem. 267, 473-478, 1992
J. Hiol. Chem. 267, 473-478, 1992
A;Title: Identification of novel blood proteins specific for mammalian hibernal A;Reference number: A41752; MUID:92112696; PMID:1730610
A;Accession: B41752
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Accession: B48150; B41752

R;Takamatsu, N.; Ohba, K.; Kondo, J.; Kondo, N.; Shiba, T.

Mol. Cell. Biol. 13, 1516-1521, 1993

A;Title: Hibernation-associated gene regulation of plasma A;Reference number: A48150; MUID:93180798; PMID:8441393

A;Accession: B48150
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A; Residues: 1-215 < TAK>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hibernation-related protein HP-25 precursor - Siberian chipmunk
C;Species: Eutamias sibiricus (Siberian chipmunk)
C;Sate: 16-Feb-1994 #sequence_revision 25-Apr-1997 #text_change
                                                                     ;Status: preliminary
;Molecule type: protein
;Residues: 29-62;84-130;172-183;187-192;201-215 <KON>
;Residues: 29-62;84-130;172-183;187-192;201-215 <KON>
;Superfamily: complement subcomponent Clq chain A; complement Clq carboxyl-te:
;Keywords: glycoprotein; hibernation; plasma
;1-28/Domain: signal sequence #status predicted <SIG>
;29-215/Product: hibernation-related protein HP-25 #status experimental <MAT>
;91-214/Domain: complement Clq carboxyl-terminal homology <ClQ>
;167/Binding site: carbohydrate (Asn) (covalent) #status predicted
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                      Query Match
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11.2%;
30.4%;
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31.3%;
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Score
Pred.
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Pred. No. 1.4e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
184;
No. 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (covalent) #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           #status
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DB 2;
.6e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 2; Length 244
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                                                                                                                                                                                                             A; complement Clq carboxyl-terminal hom
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                      Length 215;
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A; Molecule type: protein
A; Molecule type: protein
A; Molecule type: protein
A; Residues: 136-253 < RB4>
A; Residues: 136-253 < RB4>
A; Residues: 176-61x may also be present
C; Comment: The first component of complement is a calcium-dependent complex of the three cycomment: The first component of complement.
An interval component is composed of nine subunits, six of which are disulfide-
C; Comment: The Clq subcomponent is composed of nine subunits, six of which are disulfide-
C; Comment: The Clq subcomponent is composed of nine subunits, six of which are found after reduced the composed of the A, B, and C chains are found after reduced the composed of the A, B, and C chains are found after reduced the composed of the A, B, and C chains are found after reduced the composed of the A, B, and C chains are found after reduced the composed of the A, B, and C chains are found after reduced the composed of the A, B, and C chains are found after reduced the composed of the A, B, and C chains are found after reduced the composed of the A, B, and C chains are found after reduced the composed of the A, B, and C chains are found after reduced the composed of the A, B, and C chains are found after reduced the composed of the A, B, and C chains are found after reduced the composed of the A, B, and C chains are found after reduced the composed of the A, B, and C chains are found after reduced the composed of the A, B, and C chains are found after reduced the composed of the A, B, and C chains are found after reduced the composed of the A, B, and C chains are found after reduced the composed of the A, B, and C chains are found after reduced the composed of the A, B, and C chains are found after reduced the composed of the A, B, and C chains are found after reduced the composed of the A, B, and C chains are found the composed of the A, B, and C chains are found the composed of the A, B, and C chains are found the composed of the A, B, and C chains are found the composed of the A, B, and C chains are found the composed of the A,
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A;Residues: 'E',29-84,'D',86-99,'P',101-135 <RE5>
R;Reid, K.B.M.; Thompson, E.O.P.
Biochem. J. 173, 863-868, 1978
A;Title: Amino acid sequence of the N-terminal 108 amino A;Reference number: A90301; MUID:79041552; PMID:708376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement subcomponent C1q chain B precursor [validated] N;Alternate names: complement subcomponent C1q beta chain C;Species: Homo sapiens (man) C;Date: 22-May-1991 #sequence revision 31-May-1996 #text c2-Accession: B23422; A23422; B90304; A90301; B90315; A0320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: protein
A; Residues: 28-99, 'P', 101-195 <RE3>
R; Reid, K.B.M.; Gagnon, J.; Frampton
Biochem. J. 203, 559-569, 1982
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Title: Complete amino acid sequences of the three collagen-like A; Reference number: A90304; MUID:80020137; PMID:486087
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A:Residues: 'HS',1-32 <REI>
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F;33-116/Domain: collagenous, triple helix cCOL>
F;123-249/Domain: complement Clq carboxyl-terminal homology cClQ>
F;123-249/Domain: complement Clq carboxylic acid (Gln) (in mature form) #status epsiloned in the pyrcolidone carboxylic acid (Gln) (in mature form) #status experimental
F;31/Disulfide bonds: interchain (to chain A-26) #status experimental
F;35,38,41,53,56,65,83,86,101,104,107/Modified site: 4-hydroxyproline (Iyro) #status experimental
F;59,62,77,92,98,110/Binding site: carbohydrate (Lyro) (covalent) #status experimental
C;Accession: A34246
R;YAmaguchi, N.; Benya, P.D.; van der Rest, M.; Ninomiya,
J. Biol. Chem. 264, 16022-16029, 1989
A;Title: The cloning and sequencing of alphal(VIII) collar
                                                                                collagen alpha 1(VIII) chain precursor - rabbit C;Species: Oryctolagus cuniculus (domestic rabbit) C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: DNA
A; Residues: 1-744 <NIN>
C; Superfamily: collagen
F; 617-743/Domain: comple
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     maguchi, N.; Olsen, B.R.
in Extracellular Matrix Genes,
A;Title: The molecular biology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        collagen alpha 1(VIII) chain - chicken
C;Species: Gallus gallus (chicken)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
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A; Accession: S23298
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  문
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Matches 48
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56; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LHGAPHYALGAPGATFSGYLVYADADADAPA-RGPPAPPEPRS------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GDFDAAAGVFRCRLPGAYFFSFTLGKLPRKTLSVKLMKNRDEVQAMI-YDDGASRRREMQ 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PARGPPAPPEP-----RSAFSAARTRSLVGSDAGPGPRHQPLAFDTEFVNIG 195
                                                                                                                                                                                                                                                     SAVLLLRPGDRVFLQNPSEQAAGLYAGQYVHSSFSGYLLYP 743
                                                                                                                                                                                                                                                                                               SVMLALRRGDAVWLLSHDHDGYGAYSNHGKYITFSGFLVYP 297
                                                                                                                                                                                                                                                                                                                                                                                    DFDAAAGVFRCRLPGAYFFSFTLGKLPRKTLSVKLMKNRDEVQAMIYDDGASRRREMQSQ 256
                                                                                                                                                                                                                                                                                                                                                                                                                                 LGIDGVKTPHAYAAKK-----GKNGGPAYEMPAFTAELTAPFPPVGAPIKFDRLLYNGRO 644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ----AFSAARTRSLVGSDAGPG----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LHGPP----GKPGA-----LGPQGQPGLPGPPGPPGPPGPPAVMPPTPAPQGEYLPDMG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SQSVMLALRRGDAVWLLSHDHDGYGAYSNHGKYITFSGFLVYPDL 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NNYEPRSGKFTCKVPGLYYFTYHASS---RGNLCVNLMRGRERAQKVVTFCDYAYNTFQVT
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sequencing of alpha1(VIII) collagen
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29.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 175; DB 1; I
Pred. No. 1.4e-06;
28; Mismatches 77;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 182; DB 1; Length 253 Pred. No. 1e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       and Boyd C.D., eds., pp.79-114, Avwith short triple-helical domains
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61;
                                                                                    #text_change
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  CDNAS
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    demonstrate
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C;Superfamily: complement subcomponent Clq chain A; complement Clq carboxyl-terminal home C;Keywords: complement pathway; glycoprotein; homodimer; hydroxylysine; hydroxyproline; [F;1-28/Domain: signal sequence #status predicted cSIGs F;29-245/Product: complement subcomponent Clq chain B #status predicted cMAT> F;31-114/Domain: collagenous, triple helix cCGDs F;31-114/Domain: complement Clq carboxyl-terminal homology cClQ> F;121-244/Domain: complement Clq carboxyl-terminal homology cClQ> F;32/Disulfide bonds: interchain #status experimental
                                                                                                                                                                                                                                                                                                                                 A;Molecule type: protein

A;Molecule type: protein

A;Residues: 29-56,'p',58-65,'K',67-71,'p',73-83,'K',85-86,'D',88-89,'N',91-122 <REI>
C;Comment: The first component of complement is a calcium-dependent complex of the three ivation of C1r (enzyme), C1s (proenzyme), and the other eight components of complement.

C;Comment: The C1q subcomponent is composed of nine subunits, six of which are disulfidedimers of the C chain. Equimolar amounts of the A, B, and C chains are found after reductions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT
C1HUQC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Biochem. J. 179, 367-371, 1979
A;Title: Complete amino acid sequences of the three collagen-like A;Reference number: A90304; MUID:80020137; PMID:486087
A;Accession: A03207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type:
A; Residues: 1-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Biochem. J. 274, 481-490, 1991
A;Title: Characterization and organization A;Reference number: S14350; MUID:91174759; A;Accession: S14351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Date: 22-May-1981 #sequence_revision 31-May-1996 C;Accession: S14351; A03207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement subcomponent Clq chain C precursor - human N;Alternate names: complement subcomponent Clq gamma
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                                                                                                                                                                                                    A; Introns: 60/3
                                                                                                                                                                                                                         A;Cross-references: GDB:128132; OMIM:120575
A;Map position: 'lp36.3-lp34.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R; Sellar, G.C.; Blake, D.J.; Reid, K.B.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C; Species: Homo sapiens (man)
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                                                                                                                                                                                                                                                                                   A;Gene: GDB:C1QG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R; Reid, K.B.M.
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;572-744/Region: carboxyl-terminal nonhelical
;617-743/Domain: complement C1q carboxyl-terminal homology
                                                                                                                                                                                                                                                                                                          ;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
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56; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -245 <SEL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LGIDGVKTPHAYAAKK-----GKNGGPAYEMPAFTAELTAPFPPVGAPIKFDRLLYNGRQ
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Pred. No. 2.1e-06
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PMID:1706597
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collagen alpha 1(VIII) chain precursor - human c;Species: Homo sapiens (man) C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 13-Aug-1999 C;Accession: S15435  
R;Muragaki, Y.; Mattei, M.G.; Yamaguchi, N.; Olsen, B.R.; Ninomiya, Y. Bur. J. Biochem. 197, 615-622, 1991  
A;Title: The complete primary structure of the human alpha-1(VIII) chain and A;Reference number: S15435; MUID:91231001; PMID:2029894  
A;Accession: S15435
                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Map position: 3q11.1-3q13.2 (;Superfamily: collagen alpha 1(VIII) chain; complement Clq carboxyl-terminal homology F;1-20/Domain: signal sequence #status predicted <SIG>F;21-744/Product: collagen alpha 1(VIII) chain #status predicted <MAT>F;21-117/Region: amino-terminal nonhelical
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                                                                                                                                                                                                                                                                                                                                                                                            F;118-571/Region: interrupted helical F;572-744/Region: carboxyl-terminal nonhelical F;617-743/Domain: complement Clq carboxyl-term
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Gene: GDB:COL8A1
A;Cross-references: GDB:128104; OMIM:120251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: EMBL:X57527; NID:g30081; PIDN:CAA40748.1; C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: mRNA
A; Residues: 1-744 < MUR>
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Best Local
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                                                                                                                                                                        162 -AFSAARTRSLVGSDAGP--GPRHQPLAFDTE----FVNIGG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     44 APGK--DGYDGLPGPKGEPGIPAIPGIRGPKGQKGEPGLPGHPGKNGPMGPPGMPGVPGP
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    LRRGDAVWLLSHDHDGYGAYSNHGKYITFSGFLVYP 297
                                            TGIFTCEVPGVYYFAYHV-HCKGGNVWVALFKNNEPVM-YTYDEYKKGFLDQASGSAVLL
                                                                                                                                LGIDGVKPPHATGAKKGKNGGPAYEMPAFTAELTAPFPPVGGPVKFNKLLYNGRQNYNPQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SVMLALRRGDAVWLLSHDHDGYGAYSNHGKYITFSGFLVYPD 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DYDTSTGKFTCKVPGLYYFVYHAS----HTANLCVLLYRSGVKVVTFCGHTSKTNQVNSG
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                                                                                       AGVFRCRLPGAYFFSFTLGKLPRKTLSVKLMKNRDEVQAMIYDDGASRRREMQSQSVMLA
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llarity 23.8%;
Conservative 33
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Pred. No. 6.4e-07;
                                                                                                                                                                                                                                                                                                                        Score 170; DB 2;
Pred. No. 3.7e-06;
                                                                                                                                                                                                                     -LGPQGQPGLPGPPGPPGPPAVMPPTPPPQGEYLPDMG
                                                                                                                                                                                                                                                                                                        Mismatches
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A; ACCESSANCE.

A; Molecule type: protein

A; Molecule type: protein

A; Molecule type: protein

A; Residues: 104-112, 'X', 114-117; 453-466 < NIN2>

A; Residues: 104-112, 'X', 114-117; 453-466 < NIN2>

C; Superfamily: collagen alpha 1 (VIII) chain; complement Clq carboxyl-terminal homology

C; Keywords: colled coll; extracellular matrix; glycoprotein; homotrimer; hydroxyproline

F; 11-18/Domain: signal sequence #status predicted <SIG>
F; 1-18/Domain: signal sequence (arroxyl-terminal homology <ClQ>
F; 547-673/Domain: complement Clq carboxyl-terminal homology <ClQ>
F; 453,456/Modified site: hydroxyproline (Pro) #status experimental

F; 611/Binding site: carbohydrate (Asn) (covalent) #status predicted
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N,Alternate names: type X collagen
C;Species: Gallum callum (--)
complement protein Clq beta chain precursor - rat C;Species: Rattus norvegicus (Norway rat) C;Date: 16-Feb-1995 #sequence_revision 12-May-1995 C;Accession: S49158
                                                                                                                                                                  RESULT
S49158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R;LuValle, P.; Ninomiya, Y.; Rosenblum, N.D.; Olsen, J. Biol. Chem. 263, 18378-18385, 1988
A;Title: The type X collagen gene. Intron sequences : A;Reference number: A31896; MUID:89054019; PMID:2461: A;Recession: A31896
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C;Date: 07-Oct-1994 #sequence_revision 10-Nov-1995 #text_change 13-Aug-1999
C;Accession: S21297; A31896; S65594; S77711; I50218
R;Ninomiya, Y.; Castagnola, P.; Gerecke, D.; Gordon, M.K.; Jacenko, O.; LuVall maguchi, N.; Olsen, B.R.
in Extracellular Matrix Genes, Sandell L.J. and Boyd C.D., eds., pp.79-114, Active Company of the control of the c
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R;Ninomiya, Y.; Gordon, M.; van der Rest, M.; Schmid, T.; Linsenmayer, J. Biol. Chem. 261, 5041-5050, 1986
J. Biol. Chem. 261, 5041-5050, 1986
A;Title: The developmentally regulated type X collagen gene contains a A;Reference number: I50218; MUID:86168227; PMID:3082876
A;Accession: S65594
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A;Accession: S77711
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A; Residues: 'T', 9, 'D', 11-12, 'EDQMKLYILFTM', 30-31, 'TCKSGRAFTTYMILQNVMADLVSSHT'
629, 'PQAVLSLISWRTIKCGSSCQIQNPMVSIPLNMFILLSQVSYLLKSNNIPLTMS' <NINL>
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A; Residues: 1-674 < NIN>
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A; Accession: S23297
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                129 GAPGATFSGYLVYADADADAPA------RGPPAPPEPR-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         708
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PPGPPGQSTIPEGYVKGESRELSGMSFMKAGANQALTGMPVSAFTVILSKAYPGAT-VPI
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Pred. No. 3.6e-06;
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9054019; PMID:2461368
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                                  12-May-1995 #text_change
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                                                   20-Aug-1999
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R;Apte, S.S.; Olsen, B.R.
Matrix 13, 165-179, 1993
A;Title: Characterization of the mouse type X collagen gene A;Reference number: S30127; MUID:93261348; PMID:8492743
A;Accession: S30127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    collagen alpha 1(X) chain precursor - mouse (;Species: Mus musculus (house mouse) (;Species: Mus musculus (house mouse) (;Date: 30-Sep-1993 #sequence revision 30-Sep-1993 #text_change 13-Aug-1999 (;Accession: S31216; S28807; S22215; S30127; I48299; S26397; S31830 R;Kong, R.Y.C.; Kwan, K.M.; Lau, E.T.; Thomas, J.T.; Boot-Handford, R.P.; Grant, Eur. J. Biochem. 213, 99-111, 1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: DNA
A; Residues: 1-285, A', 287-680 <ELI>
A; Residues: 1-285, A', 287-680 <ELI>
A; Cross-references: EMBL:X67348; NID:g50480; PIDN:CAA47763.1; PID:g50481
A; Elima, K.; Metsaeranta, M.; Kallio, J.; Peraelae, M.; Eerola, I.; Garo Biochim. Biophys. Acta 1130, 78-80, 1992
A; Title: Specific hybridization probes for mouse alpha-2(IX) and alpha-1 A; Reference number: S22215; MUID:92182017; PMID:1543751
A; Accession: S22215
A; Molecule type: mRNA A; Roeldues: 1-12, F. 14-26, 'S', 28-247, 'L', 249-285, 'A', 287-305, 'F', 307-416, 'S', 418-499, 'A; Residues: 1-12, F. 14-26, 'S', 418-499, 'A; R; Apte, S. S.; Seldin, M.F.; Hayashi, M.; Olsen, B.R. Bur. J. Biochem. 206, 217-224, 1992
Bur. J. Biochem. 206, 217-224, 1992
A; Title: Cloning of the human and mouse type X collagen genes and mapping of the mouse 'A; Reference number: I48299; MUID:92267014; PMID:1587271
A; Accession: I48299
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A; Residues: 1-253 <SCH>
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Titchem. J. 289, 247-253, 1993
Title: The mouse collagen. X gene: complete nucleotide; Reference number: S28807; MUID:93143676; PMID:8424763
                                                                                                                                                                                                                                                                                                                                                                        ;Molecule type: mRNA;Residues: 385-450,'X',452-627 <ELA>;Residues: 385-450,'X',452-627 <ELA>;Cross-references: EMBL:X63013; NID:g49795; PIDN:CAA44741.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Status: preliminary
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to the EMBL Data Library, March 1993
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29.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NID:g49793; PIDN:CAA79736.1; PID:g49794 R.; Metsaeranta, M.; Garofalo, S.; Pera
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Pred. No. 1.3e-06;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Peraelae, M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               217
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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 52-247,'L',249-285,'A',287-305,'F',307-416,'S',418-499,'L',501-566,'C',568,'I-A;Cross-references: BMBL:X65121; NID:g50482; PIDN:CAA46237.1; PID:g667031
B;Summers, T.A.; Irwin, M.H.; Mayne, R.; Balian, G.
J. Biol. Chem. 263, 581-587, 1988
A;Title: Monoclonal antibodies to type X collagen. Biosynthetic studies using an antibody A;Reference number: S26397; MUID:88087150; PMID:2826450
A;Accession: S26397
                                                                              A;Title: Cloning of human alpha-1(X) collagen DNA and localization A;Reference number: S15826; MUID:91243838; PMID:2037056 A;Accession: S15826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence revision 03-Nov-1995 #text_change 22-Jun-1999
C;Accession: S26396; S30086; S18826; S18249; A43901; I51870; S21856
C;Accession: S26396; S30086; S18826; S18249; A43901; I51870; S21856
R;Reichenberger, E.; Beier, F.; LuValle, P.; Olsen, B.R.; von der Mark, K.; Bertling, FEBS Lett. 311, 305-310, 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 12
CGHUID
collagen alpha 1(X) chain precursor - human
collagen alpha 1(X) chain precursor - human
N;Alternate names: procollagen alpha 1(X) chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Superfamily: collagen alpha 1(VIII) chain; complement C1q carboxyl-terminal homology C;Keywords: coiled coil; extracellular matrix; glycoprotein; homotrimer F;1-18/Domain: signal sequence #status predicted <SIG> F;19-680/Product: collagen alpha 1(X) chain #status predicted <MAT> F;553-679/Domain: complement C1q carboxyl-terminal homology <C1Q>
A;Molecule type: DNA
A;Residues: 561-647,'G', 649-666 <AP2>
A;Cross-references: EMBL:X58879; NID:g30013; PIDN:CAA41686.1; PID:g30014
                                                                                                                                                                   A;Cross-references: EMBL:X65120; NID:g23129
A;NOte: the initial difference is probably due to
R;Apte, S; Mattei, M.G.; Oleen, B.R.
FEBS Lett. 282; 393-396, 1991
                                                                                                                                                                                                                                                                                                                                                submitted to the EMBL Data A; Reference number: S30085 A; Accession: S30086
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A; Introns: 51/3
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A;Residues: 'SDGYFSQ',24-26,'KQ'
                                                                                                                                                                                                                                                                                      A; Molecule type: DNA
A; Residues: 'TIPFYGWVCWVCLL', 52-680 <APT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: DNA
A; Residues: 1-680 < REI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Title: Genomic organization and full-length cDNA sequence of human collagen A;Reference number: S26396; MUID:93012005; PMID:1397333
                                                                                                                                                                                                                                                                                                                                                                                                                                     R;Apte,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: EMBL:X68952; EMBL:X72578; EMBL:X72579; EMBL:X72580; GB:S47714; GB:S4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            470 GNPGA--PGPAGIATKGLNGPT-GPPGPPGPPGPR---GHSGEPGLPGPPGPPGPPGQAVMPD 523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   129 GAPGATFSGYLVYADADADAPARGPPAPPEPRSAFSAARTRSLVGSDAGPGPRHQ----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               260 LALRRGDAVWLLSHDHDGYGAYSNHGKYITFSGFLVYP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity 25.7 56; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAAGVFRCRLPGAYFFSFTLGKLPRKTLSVKLMKNRDEVQAMIYDDGASRRREMQSQSVM 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MELTENDOVWLQLPNAESNGLYSSEYVHSSFSGFLVAP
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Pred. No. 4.4e-06;
3; Mismatches 82;
                                                                                                                                                                                                                                                                                                                                                                                                             March 1992
                                                                                                                                                                                                                                   translation
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F;19-56/Domain: amino-terminal monhelical #status predicted <NCl>
F;57-519/Region: interrupted helical
F;57-619/Romain: amino-terminal nonhelical #status predicted <NCl>
F;520-680/Domain: complement Clq carboxyl-terminal homology <ClQ>
F;553-679/Domain: complement Clq carboxyl-terminal homology <ClQ>
F;553-679/Domain: complement Clq carboxyl-terminal homology <ClQ>
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A;Residues: 1-26, TT, 28-680 <THO>
A;Residues: 1-26, TT, 28-680 <THO>
A;Residues: 1-26, TT, 28-680 <THO>
A;Cross-references: EMBL:X60382; NID:g30094; PIDN:CAA42933.1; PID:g30095
A;Note: the sequence from Fig. 3 is inconsistent with that from Fig. 2 if
A;Note: the sequence from Fig. 3 is inconsistent with that from Fig. 2 if
R;Reichenberger, E.; Aigner, T.; von der Mark, K.; Stoss, H.; Bertling, W
Dev. Biol. 188, 562-572, 199;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                be important for skeletogenesis
C;Superfamily: collagen alpha l(VII) chain; complement Clq carboxyl-terminal homology
C;Keywords: coiled coil; extracellular matrix; glycoprotein; homotrimer; hydroxylysine;
F;1-18/Domain: signal sequence #status predicted <SIG>
F;19-680/Product: collagen alpha 1(X) chain #status predicted <MAT>
F;19-65/Domain: amino-terminal nonhelical #status predicted <NC2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Note: a defect in this gene may cause Schmid metaphyseal chondrodysplasia C;Complex: type X collagen may be a homotrimer C;Function:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: mRNA
A; Residues: 547-656 KRZ>
A; Cross-references: GB:M74050; GB:D57494; NID:g339884; PIDN:AAA61221.1; PID:g553796
A; Cross- references: GB:M74050; GB:D57494; NID:g339884; PID:AAA61221.1; PID:g553796
A; Cross- references: GB:M74050; GB:D57494; NID:g339884; PID:AAA61221.1; PID:g553796
A; Cross- references:
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A;Tille: The human collagen X gene. Complete primary translated sequence and chromosoma. A;Reference number: S18249; MUID:92109659; PMID:1764025
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A;Introns: 52/1
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A;Note: mutant sequence from patient with metaphyseal chondrodysplasia type
A;Note: a second mutant sequence with 614-Pro is also described
C;Comment: Prolines and lysines at the third position of the tripeptide repo
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A; Residues: 520-597, 'I
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Accession: S18249
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                                     642
                                                                                                                                                                                                                                                                                                                                                           524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           470
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                                     IDLTENDOVWLOLPNAESNGLYSSEYVHSSFSGFLVAP 679
                                                                                                                                                                                                     PRTGIFTCQIPGIYYFSYHV-HVKGTHVWVGLYKNGTPVM-YTYDEYTKGYLDQASGSAI
                                                                                                                                                                                                                                                       AAAGVFRCRLPGAYFFSFTLGKLPRKTLSVKLMKNRDEVQAMIYDDGASRRREMQSQSVM
                                                                                                                                                                                                                                                                                                                                                           GFIKAGQRPSLSGTPLVSANQGVTGMPVSAFTVILSKAYPAIGTPIPFDKILYNRQQHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GAPGATFSGYLVYADADADAPARGPPAPPEPRSAFSAARTRSLVGSDAGPGPRHQ-----
                                                                                                                 LALRRGDAVWLLSHDHDGYGAYSNHGKYITFSGFLVYP 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GSPGP--PGPAGIATKGLNGPT-GPPGPPGPR---GHSGEPGLPGPPGPPGPPGQAVMPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 166.5; DB 1
Pred. No. 6.4e-06;
2; Mismatches 83
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R;Muragaki, Y.; Shiota, C.; Inoue, M.; Ooshima, A.; Olsen, B.R.; Bur. J. Biochem. 207, 895-902, 1992
A;Title: Alpha-1(VIII)-collagen gene transcripts encode a short-characteric number: S23779; MUID:92362626; PMID:1499564
A;Accession: S23779
                                                                                                                                                                                                                                                                                      C;Superfamily: collagen alpha 1(VIII) chain; complement Clq carboxyl-terminal C;Keywords: coiled coil; extracellular matrix; glycoprotein; homotrimer F;1-18/Domain: signal sequence #status predicted <SIG> F;19-674/Product: collagen alpha 1(X) chain #status predicted <MAT> F;547-673/Domain: complement Clq carboxyl-terminal homology <ClQ>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: EMBL:X66976; NID:g50493; PIDN:CAA47387.1; PID:g1359953 C;Superfamily: collagen alpha 1(VIII) chain; complement Clq carboxyl-terminal homology F;616-742/Domain: complement Clq carboxyl-terminal homology <ClQ>
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C;Species: Mus musculus (house mouse)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 16-Jun-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R;Thomas, J.T.; Kwan, A.P.L.; Grant, M.E.; Boot-Handford, R.P. Biochem. J. 273, 141-148, 1991
A;Title: Isolation of cDMAs encoding the complete sequence of A;Reference number: S13301; MUID:91113131; PMID:1703407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 collagen alpha 1(X) chain precursor - bovine C;Species: Bos primigenius taurus (cattle) C;Date: 21-Nov-1993 #sequence_revision 23-Feb-1996 #text_change C;Accession: S13301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: DNA
A; Residues: 1-743 < MUR>
                                                                                                                                                                                                                                                                                                                                                                                                                      A; Gene: COL10A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: mRNA
A; Residues: 1-674 < THO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Accession: S13301
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: EMBL:X53556; NID:g263; PIDN:CAA37624.1; PID:g264
                                                                                                                                                                                                                                             Query Match
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                                                                                                                                                                                                                      Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAGVFRCRLPGAYFFSFTLGKLPRKTLSVKLMKNRDEVQAMIYDDGASRRREMQSQSVML
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                                                                                              VGTPGP--PGPAGIAVKGLNGPT-GPPGPPGPR---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LLRPGDQVFLQNPFEQAAGLYAGQYVHSSFSGYLLYP
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EDFVKAGQRPFVSANQGVTGMPVSAFTVILSKAYPAIGTPIPFDKILYNKQQHYDPRTGI
                                                                                                                                                                                               Conservative
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                                                                                                                                                                                          Score 163.5; DB 2;
Pred. No. 1.1e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 165.5; DB 1;
Pred. No. 8.7e-06;
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                                                                                                 -GNAGEPGLPGPPGPPGQVALP
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                                                -PLAFDTEFVNIGGDFDAAAGV
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                                                                                                                                                                                                                                             Length 674;
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RESULT 15
A60032
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C;Species: Rattus norvegicus (Norway rat)
C;Date: 03-Mar-1993 #sequence_revision 03-Mar-1993 #text_change 31-Mar-2000
Search completed: January 12, 2004, 08:16:43 Job time: 20.1178 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      32-49/Domain: transmembrane #status predicted <TMM>;50-224/Domain: extracellular #status predicted <EXT>;50-224/Domain: complement Clq carboxyl-terminal homology <ClQ>;53,110/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;Molecule type: mRNA
;Residues: 1-224 <WAD>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Superfamily: complement subcomponent Clq chain A; complement Clq carboxyl-terminal hon; Keywords: glycoprotein; transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Status: not compared with conceptual translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 9.9%;
Best Local Similarity 38.0%;
Matches 52; Conservative 1
                                                                                                                                                                                                                                                    152 VYNRQTIQVSLMQNGYPVISAFAGD-QDVTREAASNGVLLLMEREDKVHLKLERGNLMGG 210
                                                                                                                                                                                                                                                                                                              222 L-PRKTLSVKLMKNRDEVQAMIYDDGASRRREMQSQSVMLALRRGDAVWLLSHDHDGYGA 280
                                                                                                                                                                                                                                                                                                                                                                                                                 162 AFSAARTRSLVGSDAGPGPRHQPLAFDTEFVNIGGDFDAAAGVFRCRLPGAYFFSFTLGK 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  641 NDQVWLQLPNAGSNGLYSPEYVHSSFSGFLVAP 673
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         265 GDAVWLLSHDHDGYGAYSNHGKYITFSGFLVYP 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             583 FTCKIPGIYYFSYHI-HVKGTHAWVGLYKNGTPVM-YTYDEYIKGYLDQASGSAVIDLTE 640
                                                                                                                                                                                       281 YSNHGKYITFSGFLVYP 297
                                                                                                                                                                                                                                                                                                                                                                              94 AFSA--TRSTNHEPSEMSNRTMTIYFDQVLVNIGNHFDLASSIFVAPRKGIYSFSFHVVK 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FRCRLPGAYFFSFTLGKLPRKTLSVKLMKURDEVQAMIYDDGASRRREMQSQSVMLALRR 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 163; DB 2; Length 224; Pred. No. 3.2e-06; S; Mismatches 62; Indels
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Result
No.
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Perfect score:
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Maximum Match 100%
Listing first 45 summaries
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RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
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Kimura K., Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K.,
Wagatsuma M., Takahashi-Fujii A., Oshima A., Sugiyama A., Kawakami I
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99BXJI; Q96NP2; Q96ZR4;
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Complement-clq tumor necrosis factor-related protein 1 |
(G protein coupled receptor interacting protein) (GIP).
CLQTNF1 OR CTRP1.
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"GIP, a putative GPCR interacting protein.";
submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases
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Complement-clq tumor necrosis
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InterPro; IPR001087; Ccllagen.
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Pfam; PF01391; Ccllagen; 1.
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EMBL; AF239905; AAG44303.1; ALT_INIT.
EMBL; AF239840; AXK17964.1; -.
EMBL; BC021553; AAH21553.1; -.
EMBL; AK055541; BAB70947.1; -.
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modified and this statement is not removed. Usage by ar
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                                                                                                                                                                                                                                                            PRKTLSVKLMKNRDEVQAMIYDDGASRRREMQSQSVMLALRRGDAVWLLSHDHDGYGAYS
                                                                                                                                                                                                                                                                                   KK-----PMHSNHYYQTVIFDTBFVNLXDHFNMFTGKFYCYVFGLYFFSLNVHTW
                                                                                                                                                                                                                                                                                                             TRSLVGSDAGPGPRH-----QPLAFDTEFVNIGGDFDAAAGVFRCRLPGAYFFSFTLGKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    281 AA;
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147
22
241
                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               140
281
22
241
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281
            Chordata;
Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     license agreement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    31743 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                               13.1%;
30.2%;
                                                                        Last sequence update)
Last annotation updat
                                                                                                Created)
                                                                                                                                                                                                              295
                                                                                                                                                                                       275
                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 215; DE
Pred. No. 1.7e
26; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ₩...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CIQ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RELATED PROTEIN COLLAGEN-LIKE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          POTENTIAL.
COMPLEMENT-C1Q TUMOR NECROSIS FACTOR-
               Craniata; Vertebrata; Catarrhini; Hominidae
                                                             factor-related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -> P (IN REF. 1).
-> Q (IN REF. 1).
49E248CB88ACFB7C
                                                                                                                           243
                                                                           update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                              DB :
                                                                                                                           ₽
                                                             protein
                                                                                                                                                                                                                                                                                                                                                                                                                                     6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                          Euteleostomi;
                                                             ທ
                                                                                                                                                                                                                                                                                                                                                                                    -GDRG------LQGKY
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                                                             precursor
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Best Local
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DOMAIN
SEQUENCE
                    CQT2 HUMAN STANDARD; PRT; 285 AA.

Q9BXJ5;
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Complement-clq tumor necrosis factor-related clqTNF2 OR CTRP2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
Sheppard P.O., Humes J.M.;
"Homo sapiens complement-clq tumor necrosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRINTS; PRO0007; COMPLEMNTC1Q.
SMART; SM00110; C1Q; 1.
PROSITE; PS01113; C1Q; FALSE_NEG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00386; Clq; 1.
Pfam; PF01391; Collagen; 1.
PRINTS; PR00007; COMPLEMNTC1Q.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- SIMILARITY: Contains 1 collagenous domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Wiemann
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
            Homo sapiens (Human)
                                                                                                                  HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Genew; HGNC:14344; C1QTNF5.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AF329841; AAK17965.1; -. EMBL; AL110261; CAB53702.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (AUG-1999) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ottenwaelder B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE=Uterus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 25-243 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Collagen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR001073; Clq.
InterPro; IPR000087; Collagen.
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                                                                                                                                                                                                                                                                                                                                                      122 GAPHYALGAPGATFSG---YLVYADAD----ADAPARGPPAPP-----EPRSAFSAARTR 169
                                                                                                                                                                                                                                                                                                                                                                                 66;
                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                      KLMKNRDEVQAMIYDDGASRRREMQSQSVMLALRRGDAVWLLSHDHDGYGAYSNHGKYIT
                                                                                                                                                                                                                                                                           SRV----PPPSDAPLPFDRVLVNEQGHYDAVTGKFTCQVPGVYYFA-VHATVYRASLQF
                                                                                                                                                                                                                                                                                                  SLVGSDAGPGPRHQPLAFDTEFVNIGGDFDAAAGVFRCRLPGAYFFSFTLGKLPRKTLSV
                                                                                                                                                                                                                                                                                                                             GAP----GAPGEKGEGGRPGLPGPRGDPGPRGEAGPAGPTGPAGECSVPPRSAFSAKRSE
                                                                                                                                                                     FSGFLVYSD
                                                                                                                                                                                             FSGFLVYPD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Signal.
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97
243
                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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                                                                                                                                                                                                                                                                                                                                                                                              Score 213;
Pred. No. 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RELATED PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POTENTIAL.

COMPLEMENT-C1Q TUMOR NECROSIS FACTOR-
                                                                                                                                                                                                                                                                                                                                                                                                                                                              COLLAGEN-LIKE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mewes H.-W.,
                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                    7CCDA65CDA7EB784 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                          DB 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              factor-related protein.";
                                                                                                                                                                                                                                                                                                                                                                                 83;
                                   protein
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                                                                                                                                                                                                                                                                                                                                                                                                          Length 243;
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Euteleostomi;
                                      N
                                    precursor
                                                                                                                                                                                                                                                                                                                                                                                22;
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RX MEDLINE-2238957; PubMed=12477932;

RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Altschul S.F., Jordan H., Moore T., Max. Rubin G.M., Hong L.,

RA Hopkins R.F., Jordan H., Moore T., Max. Rubin G.M., Hong L.,

RA Hopkins R.F., Jordan H., Moore T., Max. Rubin G.M., Hong L.,

RA Hopkins R.F., Jordan H., Moore T., Max. Rubin G.M., Hong L.,

RA Hopkins R.F., Jordan R., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Hopkins R.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Raha S.S., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Rahas S.A., McEwan P.J., McKernan K.J., Makek J.A., Gunaratne P.H.,

RA Rahas S.A., McEwan P.J., McKernan M., Madan A., Rodrigues S., Sanchez A.,

RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Habey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

RA Habey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

RA Habey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

RA Habey J., Helton E., Schen J.W., Shevchenko Y., Bouffard G.G.,

RA Habey J., Helton E., Schmerz M.D., Dickson M.C.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

"Generation and initial analysis of more than 15,000 full-length

"Human and mouse cDNA sequences.";

Proc. Natl. Acad. Sci. U.S.A. 99:1699-16903(2002).
                                                                                                                                                                                                               Query Match
Best Local S
Matches 53
                                                                                                                                                                                                                                                                                                 DOMAIN
DOMAIN
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRINTS; PRO0007; COMPLE; SMART; SM00110; C1Q; 1. PROSITE; PS01113; C1Q;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR001073; Clq.
InterPro; IPR000087; Collagen.
Pfam; PF00386; Clq; 1.
Pfam; PF01391; Collagen; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Piddington C.S., Bishop P.; "Homo sapiens complement-clq tumor necrosis factor-related protein."; Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                       CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                           SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; BC011699; AAH11699.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AF329836; AAK17960.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Genew; HGNC:14325; C1QTNF2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- SIMILARITY: Contains 1 collagenous -!- SIMILARITY: Contains 1 ClQ domain.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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                                              195
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                                                                                                                                                                                                                    53;
                                                                                                                                                                                                                                       Similarity
                                            YYFTYDITLA-NKHLAIGLVHN-GQYRIRTFD--ANTGNHDVASGSTILALKQGDEVWLQ 250
                                                                                                                             PGPCSCGSGHTKSAFSVAVTKSYPRE---RLPIKFDKILMNEGGHYNASSGKFVCGVPGI 194
    LHGA----
                                                                                   YFFSFTAGKAPHKSLSVMLVRNRDEVQALAFDEQRRPGARRAASQSAMLQLDYGDTVWLR 119
                                                                                                                                                                                                                                                                                                                                                                                                                               Signal..
                                                                                                                                                                                                                                                                                                   40
143
285 l
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                                                                                                                                                                                                                                                                                                     AΑ;
                                                                                                                                                                       GSSELRSAFSAA--RTTPLEGTSEMAVTFDKVYVNIGGDFDVATGQFRCRVPGA 59
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      ----PHYALGAPGATFSGYLVYADAD 145
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285
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285
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                                                                                                                                                                                                               12.3%; Score 201; DB 1; 34.4%; Pred. No. 2.4e-09; bive 30; Mismatches 47
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                                                                                                                                                                                                                                                                                                 POTENTIAL.

COMPLEMENT-C1Q TUMOR NECROSIS FACTOR-
RELATED PROTEIN 2.

COLLAGEN-LIKE.

C10.

7E31FF9868D4EDFA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    domain.
                                                                                                                                                                                                                    47;
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251

IFYSEQNGLFYDPYWT----DSLFTGFLIYADQD 280

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RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altechul S.F., Zeeberg B., Buerow K.H., Schaefer C.F., Bhat N.K.,
RA Altechul S.F., Zeeberg B., Buerow K.H., Schaefer C.F., Bhat N.K.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Browmstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
"Generation and initial analysis of more than 15,000 full-length
ruman and mouse cDNA sequences."
"Generation and initial analysis of more than 15,000 full-length
ruman and mouse CDNA sequences."
"Generation and initial analysis of more than 15,000 full-length
ruman and mouse CDNA sequences."
"Generation and initial analysis of more than 15,000 full-length
ruman and mouse CDNA sequences."
"Generation and initial analysis of more than 15,000 full-length
ruman and mouse CDNA sequences."
"Generation and initial analysis of more than 15,000 full-length
ruman and mouse CDNA sequences."
                     DOMAIN
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28-FEB-2003 (Rel. 41, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Complement-clq tumor necrosis factor-related protein 6 precursor.
C1QTNF6 OR CTRP6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CQT6_HC
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                                                                                                                                                                                      Pfam; PF00386; Clq; 1.
Pfam; PF01391; Collagen; 1.
                                                                                                                                                                                                                                                                                          EMBL; AF329842; AAK17966.1; -. EMBL; BC020551; AAH20551.1; -.
                                                                                                                                                                                                                                                                                                                                                      use by non-profit institutions as long modified and this statement is not removed entitles requires a license agreement (See or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Piddington C.S., Sheppard P.O.; "Homo sapiens complement-clq tumor necrosis factor-related Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa;
Mammalia; Eutheria;
    CARBOHYD
                                                                                     CHAIN
                                                                                                        SIGNAL
                                                                                                                            Collagen;
                                                                                                                                               PRINTS; PR00007; COMPL
PROSITE; PS01113; C1Q;
                                                                                                                                                                                                                                                                           Genew; HGNC
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IPR000087; Collagen.
                                                                                                                            Signal
    97
139
91
                                                                                                                                                                                                                                                                       :14343; C1QTNF6.
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                                                                                                                                                                       COMPLEMNTC1Q
    138
278
91
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                                                                                                                                             FALSE_NEG
COMPLEMENT-C1Q TUMOR NECROSIS
RELATED PROTEIN 6.
COLLAGEN-LIKE.
C1Q.
N-LINKED (GLCNAC. . .) (POTENT
                                                                                                      POTENTIAL.
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(See http://www.isb-sib.ch/announce)
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Best Local S
Matches 87
                                             MGD; MGI:1344400; Clqrf.
GO; GO:0005737; C:cytoplasm; IDA.
InterPro; IPR001073; Clq.
InterPro; IPR0001073; Collagen.
Pfam; PF00386; Clq; 1.
Pfam; PF01391; Collagen; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Berube N.G., Swanson X.H., Bertram M.J., Kittle J.D., Didenko V., Baskin D.S., Smith J.R., Pereira-Smith O.M., Baskin D.S., Smith J.R., Pereira-Smith O.M., "Cloning and characterization of CRF, a novel Clq-related factor, expressed in areas of the brain involved in motor function."; Brain Res. Mol. Brain Res. 63:233-240(1999)

--- TISSUE SPECIFICITY: EXPRESSED IN BRAINSTEM. MORE ABUNDANT IN OF THE DERVOUS SYSTEM INVOLVED IN MOTOR FUNCTION, SUCH AS THE PURKINJE CELLS OF THE CEREBELLUM, THE ACCESSORY OLIVARY NUCLE THE PONS AND THE RED NUCLEUS.
PRINTS; PR00007; COM
SMART; SM00110; C1Q;
                                                                                                                                                                                                                                                          the European Bioinformatics Institute. There are no rest
use by non-profit institutions as long as its content
modified and this statement is not removed. Usage by an
entitles requires a license agreement (See http://www.isb-
or send an email to license@isb-sib.ch).
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Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                SWISS-PROT entry is copyright. It is produced through a collable the Swiss Institute of Bioinformatics and the EMBL outst European Bioinformatics Institute. There are no restrictions
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Collagen;
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APM1 OR ACRP30 OR GBP28.
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01-NOV-1997 (Rel. 35, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Adiponectin precursor (30 kDa adipocyte complement-related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIGNAL
                                                                      MEDLINE=99196984; PubMed=10095105; Saito K., Tobe T., Minoshima S., A Nakano Y., Shimizu N., Tomita M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE=Adipose tissue; MEDLINE=96224171; PubMed=8619847;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Butheria; Primates; Catarrhini; Hominidae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAMOH
"The human apM-1, an adipocyte-specific gene linked TNF's and to genes expressed in activated T cells, ichromosome 1921.3-q23, a susceptibility locus identicombined hyperlipidemia (FCH).";
                                                                                                                                                                                                    Saito K., Tobe T., Minoshima S., Asakawa S., (Nakano Y., Shimizu N., Tomita M.;
"Organization of the gene for gelatin-binding Gene 229:67-73(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q15848;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Maeda K.,
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                                                                                                                                                                                                                                                                                                                    SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                        "cDNA cloning and expression of a novel adipose specific
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                                                                                                                                                                                                                                                                                                                                                                                   apM1
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Pred. No. 3.1e-09;
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C1Q-RELATED FACTOR
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                                                                                                                Buechler C.,
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                       linked to the family of sells, is mapped to identified for familial
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Hara K., Boutin P., Mori Y., Tobe K., Dina C., Yasuda K., Yamauchi T., Otabe S., Okada T., Eto K., Kadowaki H., Hagura R., Akanuma Y., Yazaki Y., Nagai R., Taniyama M., Matsubara K., Yoda M., Nakano Y., Ximura S., Tomita M., Kimura S., Ito C., Froguel P., Kadowaki T., "Genetic variation in the gene encoding adiponectin is associated with an increased risk of type 2 diabetes in the Japanese population."; Diabetes 51:536-540(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-20440368; PubMed=10982546;
Ouchi N., Kihara S., Arita Y., Okamoto Y., Maeda K., Kuriyama Hotta K., Nishida M., Takahashi M., Muraguchi M., Ohmoto Y., Nakamura T., Yamashita S., Funahashi T., Matsuzawa Y.; "Adiponectin, an adipocyte-derived plasma protein, inhibits endothelial NF-kappaB signaling through a cAMP-dependent pathw Circulation 102:1296-1301(2000).
                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Adiponectin, a new member of the family of soluble defense collagens, negatively regulates the growth of myelomonocytic progenitors and the functions of macrophages."; Blood 96:1723-1732(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Genomic structure and mutations adiponectin.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "The fat-derived hormone adiponectin reverses insulin resistance associated with both lipoatrophy and obesity.";
Nat. Med. 7:941-946(2001).
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Mori Y., Ide T., Murakami K., Tsuboyama-Kasaoka N., Ezaki O.,
Akanuma Y., Gavrilova O., Vinson C., Reitman M.L., Kagechika
Shudo K., Yoda M., Nakano Y., Tobe K., Nagai R., Kimura S., 1
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Yokota T., Oritani K., Takahashi I
Ouchi N., Kihara S., Funahashi T.,
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Horie M., Shimomura I., Hotta K., Kuriyama H., Kihara S., I
Yamashita S., Funahashi T., Matsuzawa Y.;
"Genomic structure and mutations in adipose-specific gene,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VARIANT ADIPONECTIN DEFICIENCY CYS-112.
MEDLINE=20378830; PubMed=10918532;
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                                                                                         [MIM:605441], resulting in very low concentration of adiponectin. Decreased adiponectin plasma levels are with obesity insulin resistance, and diabetes type 2. PHARMACEUTICAL: Adiponectin might be used in the treadiabetes type 2 and insulin resistance. SIMILARITY: Contains 1 collagenous domain. SIMILARITY: Contains 1 C1Q domain.
                                                                                                                                                                                                                                                                                     FUNCTION: IMPORTANT NEGATIVE REGULATOR IN HEMATOPOIESIS AND IMMUNE SYSTEMS; MAY BE INVOLVED IN ENDING INFLAMATORY RESPONSES THROUGH ITS INHIBITORY FUNCTIONS. INHIBITS ENDOTHELIAL MP-KAPPAB SIGNALING THROUGH A CAMP-DEPENDENT PATHWAY. INHIBITS INF-ALPHA-INDUCED EXPRESSION OF ENDOTHELIAL ADHESION MOLECULES. INVOLVED IN THE CONTROL OF FAT METABOLISM AND INSULIN SENSITIVITY. SUBUNIT: HOMOOLIGOMER (POTENTIAL).
                                                                                                                                                                                                                                TISSUE SPECIFICITY: Synthesized e secreted into plasma.
DISEASE: Defects in APM1 are the
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., Tenner A.J., Tomiyama
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ProDom; PD000007; C1g helix; 1.
SMART; SM00110; C1Q; 1.
PROSITE; PS01113; C1Q; 1.
Hormone; Collagen; Signal; Repeat; Hydroxylation;
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EMBL; AB012165; BAA867;
EMBL; AB012164; BAA867;
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AJ131461; CAB52413.1; JOINED
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47; Conserv
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                                                                                                                                                                                                                                                          /FTId=VAR_013278.
64D8C6C1204B1018 CRC64;
                                                                                                                                                                                                                                                                                                                                                    /FTId=VAR_013273.
R -> C (in adiponectin deficiency)
/FTId=VAR_013274.
                                                                                                                                                                                                                                                                                                                                                                                                 HYDROXYLATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COLLAGEN-LIKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADIPONECTIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POTENTIAL
                                                                                                                                                                                                                                                                                        FTId=VAR_013277
                                                                                                                                                                                                                                                                                                          /FTId=VAR_013276
                                                                                                                                                                                                                                                                                                                                FTId=VAR_013275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INTERCHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Obesity; Diabetes
                                                                                                                                                                                                                 Mismatches
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(BY SIMILARITY).
                                                                                                                                                                                                                                    Length 244;
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mellitus.
                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                 18;
                                                                                                                                                                                                                 Gaps
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                                                                                                                                                   119
                                                                                                                                                                                             64
                                                                                                                               214
                                            Collagen;
SIGNAL
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Submitted
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STITTE REPRESENTATION OF THE PROPERTY OF THE P
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RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.D., Collins F.S., Magner L., Shenmen C.M., Schuler G.D.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Heiseh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
RA Schnerch A., Schein J.S.A. 99:16899-16903(2002).

C. -- TISSUE SPECIFICITY: Expressed DIN BRAINSTEM.

C. -- SIMILARITY: Contains 1 Cl0 domain.

C. -- SIMILARITY: Contains 1 Cl0 domain.
                                                                                                                                                                                                PRINTS; PR00007; COMPLEMN
SMART; SM00110; C10; 1.
PROSITE; PS01113; C10; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AF410771; AAK95248.1; -.
EMBL; BC008798; AAH08798.1; -.
GO; GO:0007626; P:locomotory behavior; NAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboratic between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it use by non-profit institutions as long as its content is in no we modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Berube N.G., Swanson X.H., Bertram M.J., Kittle J.D., Didenko V., Baskin D.S., Smith J.R., Pereira-Smith O.M. novel Clq-related factor, "Cloning and characterization of CRF, a novel Clq-related factor, expressed in areas of the brain involved in motor function.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-SEP-2003 (Rel. 42, Last annotation update)
Clq-related factor precursor
ClQRF OR CRF.
                                                                                                                                                                                                                                                                                                           InterPro; IPR001073; C1q.
InterPro; IPR000087; Collagen.
Pfam; PF00386; C1q; 1.
Pfam; PF01391; Collagen; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AF095154; AAC64186.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. MEDLINE=99097006;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                   Signal.
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67
123
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   A.
                                                                                                                                                                                                                                                                              COMPLEMNTCIQ
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       26452
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   MW;
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POTENTIAL.
C10-RELATED FACTOR.
COLLAGEN-LIKE.
C10.
C10.
W; 52C51CDF59CAE2BF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chung M.-W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (See http://www.isb-sib.ch/announce,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Х.Ľ.,
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RAPARAL RAPARA RAPARAL RAPARA RAPA
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APM1_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            δ
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APM1 MOUSE
Q60994; Q62400; Q9DC68;
Q60994; Q62400; Q9DC68;
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Adiponectin precursor (30 kDa adipocyte complement-related
Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Arakawa T., Hara A., Pukunishi Y., Konno H., Adachi J., Fukuda Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE=Adipocyte;
MEDLINE=96070757; PubMe
Scherer P.E., Williams
"A novel serum protein
                                                                                                                                                                                                                                                                                                                                                    PubMed=11162643;
Das K., Lin Y., Widen E., '
"Chromosomal localization,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=96209999; PubMed=8631877;
Hu E., Liang P., Spiegelman B.M.;
"AdipoQ is a novel adipose-specific gene dysregulated in obesity.";
J. Biol. Chem. 271:10697-10703(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=Fibroblast;
                                                                                                                                                                                                                                                                                                                         of the mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                STRAIN=C57BL/6J; TISSUE=Heart;
MEDLINE=21085660; PubMed=11217851;
                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      adipocytes
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            139
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chem. 270:26746-26749(1995).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NRDEVQAMIYDDGASRRREMQSQSVMLALRRGDAVWLLSHDHDGYGAYSNHGKYITFSGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GPPGPPGDPGPPGPVGPPGEKGEPGKPGPPGLPGAGGSGAISTATYTTVPRVAFYAGLKN
                                                                                                                                                                                                                                                                         Biophys.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ----HQPLAFDTEFVNIGGDFDAAAGVFRCRLPGAYFFSFTLGKLPR----KTLSVKLMK
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                                                                                                                                                                                                                                                                                                                           gene
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                                                                                                                                                                                                                                                                                                                         iden E., Zhang Y., Scherer P.)
lization, expression pattern,
encoding adipocyte-specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PubMed=7592907;
                                                                                                                                                                                                                                                                            Res.
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27.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            S., Fogliano M. similar to Clq,
                                                                                                                                                                                                                                                                            Commun.
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Pred. No. 1.2e-
26; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                         280:1120-1129(2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               M., Baldini G., Lodish H.F.; 1q, produced exclusively in
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vant T.,
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RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J., RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T., RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., A Blake J.; Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Barsh G., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P., A Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Byzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L., Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S., Wangtional annotation of a full-length mouse cDNA collection."; II. Nature 409:685-690(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SMART; SM00110; C1Q; 1.
PROSITE; PS01113; C1Q;
                                                                                                                                               888
                                                                                                                                                                                                          EMBL; U37222; AAA80543.1; -.
EMBL; U49915; AAB06706.1; -.
EMBL; AA804466; AAK13417.1; -.
EMBL; AK003118; BAB22597.1; -.
EMBL; AK003118; BAB22597.1; -.
EMBL; AK003118; BAB22597.1; -.
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Berg A.H., Combs T.P., Du X., Brownlee
"The adipocyte-secreted protein Acrp30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Froguel P., Kadowaki T.;
"The fat-derived hormone adiponectin
associated with both lipoatrophy and
Nat. Med. 7:941-946(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=21372498; PubMed=11479627;
Yamauchi T., Kamon J., Waki H., Terauchi Y., Kubota N., Hara K.,
Yamauchi T., Kamon J., Waki H., Tsuboyama-Kasaoka N., Ezaki O.,
Mori Y., Ide T., Murakami K., Tsuboyama-Kasaoka N., Ezaki O.,
Akanuma Y., Gavrilova O., Vinson C., Reitman M.L., Kagechika H.,
Akanuma Y., Gavrilova O., Vinson K., Nagai R., Kimura S., Tomi
                                              PRINTS; PR00007; COMPLEMNTC1Q. ProDom; PD000007; Clg_helix; 1.
                                                                             InterPro; IPR001073; Ciq.
InterPro; IPR0010087; Collagen.
Pfam; PF00386; Clq; 1.
Pfam; PF01391; Collagen; 1.
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                                                                                                                                            GO:0005576; C:extracellular; IDA.
GO:0005515; F:protein binding activity; I
GO:0006635; P:fatty acid beta-oxidation;
                                                                                                                                                                                                                                                                                                                                                                         s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its
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Collagen; Signal;
Repeat;
                                                                                                                                                               activity; IPI
Hydroxylation; Plasma;
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enhances hepatic insulin
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KOide T., Aso A., Yorihuzi T., Nagata K.;
"Conformational requirements of collagenous peptiby the chaperone procein HSP47.";
J. Biol. Chem. 275:27957-27963 (2000).
-1- TISSUE SPECIFICITY: EXPRESSED IN GLIAL CELLS.
-1- SIMILARITY: Contains 1 collagenous domain.
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                                                  the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed entities requires a license agreement (See or send an email to license@isb-sib.ch).
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                     MGD;
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                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                         16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Gliacolin precursor (Clq-like protein).
                                                                                                                                                                                                                                                                                                                                          Q9ESN4;
16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Polymorphism;
SIGNAL
                                 EMBL;
                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                   NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                     Mus musculus (Mouse)
            GO:0005515;
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                                 AB044560; BAB15806.1;
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1.2387350; Clq1.
nnn5515; F:protein binding
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                                                                                                                                                                                                                                                                                                                                                                                                                     LEVGDQVWLQVYGDGDHNGLYADNVNDSTFTGFLLYHD 245
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G -> N (IN REF
Y -> F (IN REF
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ed. No. 2.3e-08;
Mismatches 73
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           activity;
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01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1995 (Rel. 32, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Hibernation-associated plasma protein HP-25 precursor specific blood complex, 25 kDa subunit).
Tamias sibiricus (Siberian chipmunk) (Asian chipmunk).
Tamias sibiricus (Chordata; Craniata; Vertebrata; Eu
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SEQUENCE
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SMART; SM00110; C1Q; 1.
PROSITE; PS01113; C1Q; 1.
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DOMAIN
                                                                    J. Biol. Chem. 267:473-478(1992).
-i- FUNCTION: PLASMA PROTEINS HP-20, HP-
140 kDa COMPLEX VIA DISULFIDE BONDS
                                                                                                                                                                                                   Takamatsu N., Ohba K., Kondo J., Kondo N., Shiba T. "Hibernation-associated gene regulation of plasma p collagen-like domain in mammalian hibernators.";
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Pfam; PF01391; Collagen;
                                                                                                         Kondo N., Kondo J.;
"Identification of novel blood proteins
                                                                                                                                         MEDLINE=92112696;
                                                                                                                                                                                                                                                                                   NCBI_TaxID=64680;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Collagen;
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                                                                                                                                                       TISSUE=Plasma;
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InterPro; IPR000087; Collagen.
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              HIBERNATION SPECIFIC.

HIBERNATION SPECIFIC:
SUBCELLULAR LOCATION: Extracellular.
SUBCELLULAR LOCATION: Extracellular.
TISSUE SPECIFICITY: PLASNA; SYNTHESIZED IN THE LIVER.
TISSUE SPECIFICITY: PLASNA; SYNTHESIZED IN THE LIVER.
DEVELOPMENTAL STAGE: THE PROTEIN COMPLEX DISAPPEARS AS HIBER
PLASMA AT CEASES.
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             HIBERNATION
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Pred. No. 3.2e
13; Mismatches
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GLIACOLIN.
COLLAGEN-LIKE.
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             AND
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                                                                       THE PLASMA
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RESULT 12
C1QB_HUMAI
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                    CIQB_HUMAN STANDARD; PRT; 251 AA. P02746; Q96H17; 21-JUL-1986 (Rel. 01, Created) 01-JUL-1993 (Rel. 26, Last sequence update) 15-SEP-2003 (Rel. 42, Last annotation update) Complement CIq subcomponent, B chain precursor.
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CARBOHYD
SEQUENCE
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SMART; SM00110; C1Q; 1.

PROSITE; PS01113; C1Q; 1.

Signal; Collagen; Glycoprotein; Plasma; Multigene family.

SIGNAL 1 28
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                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                               "Molecular cloning and characte
gene coding for the B-chain of
complement system.";
Biochem. J. 231:729-735(1985).
                                                                                                                                                                                  MEDLINE=86076906; PubMed=3000358
                                                                                                                                                                                                                                                                                                                                             Homo sapiens (Human)
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Pfam; PF01391; Collagen; 1.
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InterPro; IPR000087; Collagen
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SEQUENCE FROM N.A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LFQSSVKIRLM--RDGIQV------REKEAQANDSYKHAMGSVIMALGKGDKVWLESK 192
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22664 MW;
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                                                                                                    characterization of the complementary DNA chain of subcomponent Clq of the human
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Pred. No. 4.2e-08;
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COLLAGEN-LIKE.
C1Q.
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RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., RA Alfschui S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., RA Alfschui S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Ra Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Ra Stapleton M.J., Ugdin T.B., Bonaldo M.F., Carninci P., Prange C., Ra Stapleton M., Ugdin T.B., Bonaldo M.F., Carrinci P., Prange C., Ra Stapleton M.J., Ugdin T.B., Bonaldo M.F., Carrinci P., Prange C., Ra Stapleton M.J., Worley K.C., Hale S., Carrinci P., Prange C., Mullahy S.J., Mosea S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Ra Bosak S.A., McEwan P.J., McKernan K.J., Lu X., Gibbs R.A., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Ra Pahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Ra Hakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Ra Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Ra Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Ra Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

"Generation and initial analysis of more than 15,000 full-length but and mouse CDNA sequences."
Immunobiology 199:286-294(1998).

C. I-FUNCTION: C1Q ASSOCIATES WITH THE PROENZYMES CIR AND C1S TO YIELD C1-FUNCTION: C1Q ASSOCIATES WITH THE SERUM COMPLEMENT SYSTEM. THE C1-FUNCTION: C1Q ASSOCIATES WITH THE CA(2+)-DEPENDENT C1C C1R(2)(21) PROENZYME COMPLEX, AND EFFICIENT ACTIVATION OF C1 TAKES PLACE ON INTERACTION OF THE GLOBULAR HEADS OF C1Q WITH THE C1 FC REGIONS OF IGG OR IGM ANTIBODY PRESENT IN IMMUNE COMPLEXES.

C. -!- SUBUNIT: C1 IS A CALCIUM-DEPENDENT TRIMOLECULAR COMPLEX OF C1Q, R AND S IN THE MOLAR RATION OF 1:2:2. C1Q SUBCOMPONENT IS COMPOSED OF NINE SUBUNITS, SIX OF WHICH ARE DISULFIDE-LINKED DIMERS OF THE C OF NINE SUBUNITS, SIX OF WHICH ARE DISULFIDE-LINKED DIMERS OF THE C CHAIN.

C. -!- DISEASE: Defects in C1QB are a cause of C1Q deficiency
                                                                                                                                                                                                                                                                                                                                                                                                                                          "Cloning and characterization of the complementary DNA for the chain of normal human serum Clq."; Philos. Trans. R. Soc. Lond., B, Biol. Sci. 306:345-354(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIINE=82283890; PubMed=6981411; Reid K.B.M., Gagnon J., Frampton J.; Completion of the amino acid sequences of the A and B chains of subcomponent C1q of the first component of human complement."; Biochem. J. 203:559-569(1982).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=79041552; PubMed=708376;
Reid K.B.W., Thompson E.O.P.;
Reid K.B.W., Thompson E.O.P.;
B. Chain of subcomponent Clq of the first component of
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present in subcomponent Clq of the
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                                                                                                                                                                                                                                                                                                                                  "Molecular basis of hereditary Clq deficiency.";
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EMBL; M36278; AAC41692.1; -.
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                                                                                                                                                                                                                                                                                                                               DOMAIN
                                                                                                                                                                                                                                                                                                                                                         SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                  PRINTS;
                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00386; Clq; 1.
Pfam; PF01391; Collagen; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                  GO; GO:0005602; C:complement component C1q complex; GO; GO:0003811; F:complement activity activity; TAS InterPro; IPR001073; C1q.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; X03084; CAA26880.1; -
                                                                                                            VARIANT
                                                                                                                                               MOD_RES
                                                                                                                                                        MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS01113; C1Q;
                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 [MIM:120570]. It is a rare genetic disorder which is associated with recurrent infections and a high prevalence of lupus erythematosus-like symptoms. It is characterized by a loss of activation of the complement classical pathway. SIMILARITY: Contains 1 collagenous domain.
                 149
                                                                                                                                                                                                                                                                                                                                                                                         ; PR00007; COMPLE
SM00110; C1Q; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HGNC:1242; C1QB.
                                          Similarity
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                 PARGPPAPPEP----
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                                                                                                                                                                                                                                                                                                                                                                 Disease mutation;
                                                                                                                                                                                                                                                                                                                                                                                                   COMPLEMNTC1Q.
                                                                                                            Plasma;
                                                                   26
83
98
26459
                                        11.1%;
                                                                   Μ¥.
                                 32;
                                                                          O-LINKED (GAL...).
G -> D (in ClQ deficiency).
/FTId=VAR_008541.
Q -> E (IN REF. 3).
N -> D (IN REF. 3).
G -> P (IN REF. 3 AND 4).
                                                                                                                                                                                                                                                                                                                                                                         Hydroxylation;
                ----RSAFSAARTRSLVGSDAGPGPRHQPLAFDTEFVNIG
                                Score 182; DB
Pred. No. 7.3e
32; Mismatches
                                                                                                                                                               HYDROXYLATION. O-LINKED (GAL.
                                                                                                                                                                                       HYDROXYLATION.
HYDROXYLATION.
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                                                                                                                                                                                                                          O-LINKED (GAL.
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                                                                                                                                                                                                                                                                                                                                                COMPLEMENT C1Q
                                                                  -> P (IN REF. 3 . 78C5752E267A0EF7
                                                                                                                                                                                                                                                                                                                                                                 Pyrrolidone
                                                           00853.

N REF. 3).

IN REF. 3).

(IN REF. 3 AND 4).
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                           DB 1,
7.3e-08;
7.61;
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                                                                                                                                                                                                                                                                                                                                                                Glycoprotein; one carboxylic
                                                                                                                                                                                                                                                                                                                                               SUBCOMPONENT,
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:
                                                Length 251;
                                 Indels
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                 195
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95

PKGGPGAPGAPGPKGESGDYKATQKIAFSATRTINV----PLRRDQTIRFDHVITNMN

148

PRINTS; PR00007; COMPLEMNTC1Q. SMART; SM00110; C1Q; 1. Pfam; PF00386; Clq; 1. Pfam; PF01391; Collagen; 2.

CIQ;

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RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeebeerg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Zeebeerg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Raha S.S., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M.,
                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HUMAN
                                                                                                                                                            EMBL; AF329839; AAK17963.1; -.
EMBL; BC022187; AAH22187.1; -.
Genew; HGNC:14342; C1QTNF7.
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SEQUENCE FROM N.A.
Sheppard P.O.,
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Complement-clq tumor necrosis factor-related protein 7 precursor. C1QTNF7 OR CTRP7.
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28-FEB-2003 (Rel.
15-SEP-2003 (Rel.
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                                                                                                                                                                                                                                                          or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted
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                                                                                                               InterPro; IPR001073; Clq.
InterPro; IPR000087; Collagen.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIMILARITY: Contains 1 collagenous domain. SIMILARITY: Contains 1 C1Q domain.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HUMAN
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         D., Bishop P., Lasser G.W.;
tumor necrosis factor-related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Craniata; Vertebrata; Catarrhini; Hominidae;
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Best Local
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DOMAIN
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                    "The cloning and sequencing of alpha 1(VIII) collagen cDNAs demonstrate that type VIII collagen is a short chain collagen and contains triple-helical and carboxyl-terminal non-triple-helical domains similar to those of type X collagen.";

J. Biol. Chem. 264:16022-16029(1989).
-!- FUNCTION: MAJOR COMPONENT OF THE DESCEMET'S MEMERANE (BASEMENT MEMBRANE) OF CORNEAL ENDOTHELIAL CELLS.
-!- SUBUNIT: MAY FORM HOMOTRIMERS, OR HETEROTRIMERS IN ASSOCIATION WITH ALPHA 2(VIII) TYPE COLLAGENS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JAN-1990 (Rel.
01-JAN-1990 (Rel.
15-SEP-2003 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JAN-1990 (Rel. 13, Created)
01-JAN-1990 (Rel. 13, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Collagen alpha 1(VIII) Chain precursor (Endothelial collagen)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RABIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CHAIN
                                                                  EMBL; J05042; AAA31204.1; -. PIR; A34246; A34246.
                                                                                                                  use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way
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InterPro; IPR001073; C1q.
InterPro; IPR000087; Collagen.
Pfam; PP00386; C1q; 1.
Pfam; PP01391; Collagen; 8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=89380199; PubMed=2476437;
Yamaguchi N., Benya P.D., van der Rest M., Ninomiya Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=9986
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                  PTW: Prolines at the third position of the tripeptide repeating unit (G-X-Y) are hydroxylated in some or all of the chains. MISCELLANEOUS: 4 consecutive G-P-P tripeptides are present at the C-terminus of the triple-helical region. These may provide high thermal stability of this region.

SIMILARITY: STRONG, TO ALPHA 2 TYPES VIII AND X COLLAGENS.
                                                                                                                                                                                                                                                       SIMILARITY: Contains 1 C1Q domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         174
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IGGDFDVATGQFRCRVPGAYFFSFTAGKAPHKSLSVMLVRNRDEVQALAFDEQRRPGARR 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VASGSTVIYLQPEDEVWLEIFFTDQNGLFSDPGWADSLFSGFLLYVDTD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                289
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              139
276
30683
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289
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 181; DB 1; Length 289; Pred. No. 1e-07;
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COMPLEMENT-C1Q TUMOR NECROSIS FACTOR-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COLLAGEN-LIKE
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P88085; Q91080;

01-NOV-1995 (Rel. 32, Created)

01-NOV-1995 (Rel. 32, Last sequence update)

15-JUL-1998 (Rel. 36, Last annotation update)

15-JUL-1998 (Rel. 36, Last annotation update)

15-DUL-1998 (Rel. 36, Last annotation update)

15-DUL-1998 (Rel. 36, Last annotation update)

15-JUL-1998 (Rel. 36, Last annotation update)

15-JUL-1998 (Rel. 36, Last annotation update)

15-JUL-1998 (Rel. 36, Last sequence update)

15-JUL-1998 (Rel. 32, Created)

16-JUL-1998 (Rel. 32, Created)

16-JUL-1998
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                                                                                                                                                                                                                                                                                                                                                                                          Science 267:1031-1034(1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=13106;
                                                                                                                                           TISSUE SPECIFICITY: SPECIALIZED SECRETORY SUPPORTING CEL-
OUTER PERIMETER OF THE SACCULAR EPITHELIUM.
SIMILARITY: CONCENTED FOR POSITIONS TRANSLATION; A FRAMESHIFT
CAUTION: THIS IS A CONCEPTUAL TRANSLATION; A FRAMESHIFT
INTRODUCED FOR POSITIONS 391-419 SO AS TO MAXIMIZE THE S
                                                         SWISS-PROT entry is copyright. It is produced through a collaboration en the Swiss Institute of Bioinformatics and the EMBL outstation -
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ITH OTHER SHORT-CHAIN COLLAGENS.
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Pred. No. 1.4e-06;
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Q9Y6C2	Q9UG76	Q96G58	Q96IH6	P83425	Q8BZS3	Q8BME9	Q8BMF0	Q99K41	Q8TEJ5	Q81UU4	Q9JHG0	Q920N0	Q9DCM6	062789	Q9ES30	Q8BGU2	Q8IUK8	Q9Z1K4	26.5560	Q9N178	Q8BGL6	Q921S8	Q8BVD7	Q8CHX9	Q8R1Z2	Q8BKR0	Q8K3R4	Q95MQ4
homo	homo	homo	Q96ih6 homo sapien	P83425 mytilus edu	3 mus mu	Q8bme9 mus musculu	Bru	Bnm	Q8tej5 homo sapien	OMO	8 mus			062789 sus scrofa	0 mus	Bru	Q8iuk8 homo sapien	4 ratt	Q95j95 canis famil	Q9n178 sus scrofa	Q8bg16 mus musculu	mus	Bru	Bru	Q8rlz2 mus musculu	Bnw	Q8k3r4 rattus norv	Q95mq4 bos taurus

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Best Local Simi
Matches 312;
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OBIV25;
O1-MAR-2003 (TrEMBLrel. 23, Created)
O1-MAR-2003 (TrEMBLrel. 23, Last sequence update)
O1-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Similar to C1q and tumor necrosis factor related protein 4.
Homo sapiens (Human).

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                         Strausberg R.;
Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases EMBL; BC035628; AAH35628.1; -.
SEQUENCE 329 AA; 35256 MW; 16064DA8182A6732 CRC64;
                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9606;
                                                        137
                          181
197
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                                                                                                                   77
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                                                                                                                                                                                                                                                     Similarity
                                                      HGAPHYALGAPGATFSGYLVYADADADAPARGPPAPPEPRSAFSAARTRSLVGSDAGPGP 180
                                                                                                                                   FFSFTAGKAPHKSLSVMLVRNRDEVQALAFDEQRRPGARRAASQSAMLQLDYGDTVWLRL 120
                 RHQPLAFDTEFVNIGGDFDAAAGVFRCRLPGAYFFSFTLGKLPRKTLSVKLMKNRDEVQA
                                                                                                                                                                                             LGPTPGPGSSELRSAFSAARTTPLEGTSEMAVTFDKVYVNIGGDFDVATGQFRCRVPGAY 60
                                                                                                                                                                               LGPTPGPGSSELRSAFSAARTTPLEGTSEMAVTFDKVYVNIGGDFDVATGQFRCRVPGAY
 RHQPLAFDTEFVNIGGDFDAAAGVFRCRLPGAYFFSFTLGKLPRKTLSVKLMKNRDEVQA
                                                                                                                  FFSFTAGKAPHKSLSVMLVRNRDEVQALAFDEQRRPGARRAASQSAMLQLDYGDTVWLRL
                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                    99.5%;
                                                                                                                                                                                                                                       Score 1631; DB 4;
Pred. No. 5e-132;
0; Mismatches 1;
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                                                                                                                                                                                                                                                                     Length 329;
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 256
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Best Local S
Matches 295
O9DOW2
Q9DOW2;
Q9DOW2;
O1-JUN-2001 (TrEMBLrel.
O1-JUN-2001 (TrEMBLrel.
O1-CCT-2002 (TrEMBLrel.
O710001E10Rik protein.
O710001E10RIK.
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Q8R066;
01-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Strausberg R.;
Submitted (ARP-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC027315; AAH27315.1; -.
MGD; MGI:1914695; 0710001E10Rik.
InterPro; IRR001073; C1q.
Pfam; PF00386; C1q; 2.
SMART; SM00110; C1Q; 2.
PROSITE; PS01113; C1Q; 2.
PROSITE; PS01113; C1Q; 2.
SEQUENCE 326 AA; 35057 MW; 72339172B7B1051A CRC64;
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01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Similar to Clq and tumor necrosis factor related protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;
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Pred. No. 5.6e-122;
2; Mismatches 13;
                                                  Created)
Last sequence update)
Last annotation update)
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RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pescole G., Quackenbush J.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pescole G., Quackenbush J.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pescole G., Quackenbush J.,
RA Schriml I.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
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                                                                                                                                                                                       Q9DCB6 PRELIMINARY;
Q9DCB6;
01-JUN-2001 (TrEMBLrel. 17, C
01-JUN-2001 (TrEMBLrel. 17, L
01-OCT-2002 (TrEMBLrel. 22, L
0710001E10Rik protein.
                                                                                 Mus musculus (Mouse)
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Functional annotation of a full-length mouse cDNA collection.";
"Functional annotation of a full-length mouse cDNA collection.";
Nature 409:685-690(2001).
EMBL; AK004340; BAB33268.1;
MGD; MGI:1914695; 0710001E10Rik.
InterPro; IPR001073; C1q;
Pfam; PF00386; C1q; 1.
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TISSUE=Embryo;

TISSUE=Embryo;
                                 NCBI_TaxID=10090;
                                                                                                                                                                              0710001E10RIK.
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Mammalia; Eutheria;
   SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RTRSLVGSDAGPGPRHQPLAFDTEFVNIGGDFDAAAGVFRCRLPGAYFFSFTLGKLPRKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MIQLDYGDTVMLRLHGAPQYALGAPGATFSGYLVYADADADAPARG-PAAPEPRSAFSAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   YITESGELVYPDLAAAGPPALKPPEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LSVKLMKNRDEVQAMIYDDGASRRREMQSQSVMLPLRRGDAVWLLSHDHDGYGAYSNHGK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   205 AA;
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; 22190 MW;
                                                                                       Chordata;
Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chordata; Craniata; Vertebrata; E
Rodentia; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61.2%; Score 1003.5;
93.7%; Pred. No. 2.2e
                                                                                                                                                                                                                                 Last
Last
                                                                                    Craniata; Vertebrata;
Sciurognathi; Muridae;
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annotation update)
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; Murinae; Mus.
                                                                                                                     Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1;
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STRAIN=C57BL/6J; TISSUE=Brain;

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Q9H667
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RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Peeole G., Quackenbush J.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Peole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Schriml L., Moilla D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Suruki H., Sato K., Schoenbach C., Seya T., Sakamoto N.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wunshaw-Roris A Yoshida W. Hasenawa Y. Kawaji H. Yohrenbi S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
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Best Local 9
TISSUE-Small intestine;
TISSUE-Small intestine;
Watanabe K., Kumagai A., Itakura S., Yamazaki M., Tasnı
Suzuki Y., Obayashi M., Nishi T., Shibahara T., Tanaka
Nakamura Y., Isogai T., Sugano S.;
"NEDO human cDNA sequencing project.";
"NEDO human cDNA sequencing project.";
                                                                                                                                                                                                                          O9H667;
01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence up
01-CCT-2002 (TrEMBLrel. 22, Last annotation
Hypothetical protein FLJ22569.
Homo sapiens (Human)
                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
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Wynshaw-Boris A., Yoshida
                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                      NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                          Q9H667
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SEQUENCE 205 AA; 22215 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                    YITFSGFLVYPDLAAAGPPALKPPEL
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                       project.";
EMBL/GenBank/DDBJ databases
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                                                                                                                                                                                                                                                                                  Last sequence update)
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Pred. No. 7.4e-78;
                                                                                                                                                                                         Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            56AD37793C437300 CRC64;
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                                                                                              Tashiro H.,
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EMBL; BC007520; AAH07520.1; --
InterPro; IPR001073; Clq.
Pfam; PF00386; Clq; 1.
PRINTS; PR00007; COMPLEMNTC1Q.
                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR001073; C1q.
Pfam; PF00386; C1q; 1.
SMART; SM00110; C1Q; 1.
PROSITE; PS01113; C1Q; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Aerbajinai W., Miller J.L.; Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases EMBL; AY074490; AAL71549.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q8TE71
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Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
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01-MAR-2003
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01-JUN-2002
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  1038
                                                                                                                                                                                                                                               147 DAPARGP-----PAPPEPRSAFSAARTRSLVGSDAGPGPRHQPLAFDTEFVNIGG 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                147 DAPARGP------PAPPEPRSAFSAARTKSLVGSDAGPGPRHQPLAFDTEFVNIGG 196
                                                                                                                                                       197 DFDAAAGVFRCRLPGAYFFSFTLGKLP-RKTLSVKLMKNRDEVQAMIYDDGASRRREMQS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             119 NHAILQLFQGDQIWLRLH----RGAIYGSSWKYSTFSGYLLYQD 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        197 DFDAAAGVFRCRLPGAYFFSFTLGKLP-RKTLSVKLMKNRDEVQAMIYDDGASRRREMQS 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        63;
                                                                                                                                                                                                                                                                                                                                                Similarity
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     NHAILQLFQGDQIWLRLH
                                                                                                                                                                                                                 DVPVTNPAATILPVHVYPLPQQMRVAFSAART----SNLAPGTLDQPIVFDLLLNNLGE 978
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QSVMLALRRGDAVWLLSHDHDGYGA-YSNHGKYITFSGFLVYPD
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                                                 QSVMLALRRGDAVWLLSHDHDGYGA-YSNHGKYITFSGFLVYPD
                                                                                                        TFDLQLGRENCPVNGTYVF1FHMLKLAVNVPLYVNLMKNEEVLVSAYANDGAP-DHETAS
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158 AA; 1
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38.4%;
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                                                                                                                                                                                                                                                                                                                    16; Mismatches
                                                                                                                                                                                                                                                                                                                                           Score 230; DB 4;
Pred. No. 5.9e-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Last sequence up
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 230; DB 4; Length 158. Pred. No. 4.7e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
  -RGAIYGSSWKYSTFSGYLLYQD 1077
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 47DB10EDD6DC9760 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                             2B88BF3C47D032D6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1077
                                                                                                                                                                                                                                                                                                                                                                      DB 4; Length 1077;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    update)
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                                                                                                                                                                                                                                                                                                                    Indels
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                                                                                                                                                             255
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RESULT 7

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RESULT 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q8R1P2
Q8R1P2;
Q8R1P2;
01-JUN-2002 (TrEMBLrel. 21, Cr
01-JUN-2002 (TrEMBLrel. 21, Lr
01-JUN-2003 (TrEMBLrel. 23, I
                                                 Query Match
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Best Local
       Matches
                                                                                                                                         Strausberg R;
Submitted (FEB-2002) to the EMBL/GenBank/DDBJ
EMBL; BC023468; AAH23468.1; -
MGD; MGI:1919254; 1600017K21Rik.
InterPro; IPR001073; C1q.
InterPro; IPR001073; C1q.
InterPro; IPR000087; C01lagen.
Pfam; P700386; C1q; 1.
SMART; SM00110; C1Q; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Similar to hypothetical protein FLJ22569.
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRINTS; PRO0007; COMPLEMNTC1Q.
SMART; SM00110; C1Q; 1.
PROSITE; PS01113; C1Q; 1.
Hypothetical protein.
SEQUENCE 158 AA; 17533 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q8K1IO;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Similar to RIKEN cDNA 1600017K21 gene (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (APR-2002) to the EMBL/GenBank/DDBJ EMBL; BC027523; AAH27523.1; -. IRR001073; Clq. Pfam; PF00386; Clq; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Strausberg R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                            TISSUE=Liver;
                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE=Uterus;
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                             Local
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       56;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAAGVFRCRLPGAYFFSFTLGKLP-RKTLSVKLMKURDEVQAMIYDDGASRRREMQSQSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VTSPAAAILPVHIYPLPQQMRVAFSAART----SNLAPGTLDQPIVFDLLLNNLGETFN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VLQLLQGDQIWLRLH----RGAIYGSSWKYSTFSGYLLYQD
                                                                                                   182 AA;
       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13.8%;
ilarity 39.1%;
Conservative 10
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Rodentia;
                                                                                                   20863 MW;
                             13.5%;
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       20;
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                             Score 220.5; DB 11; Length 182; Pred. No. 3.7e-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 226;
Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                   559C73DE9517882F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    86E9321C99225FCB CRC64;
         Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    æ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 158;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               298
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    9
Gaps
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QRESULTY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fhudda S.,
RA Arakawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shabata Y., Storch K.-F.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shabata Y., Storch K.-F.,
RA Hayashizaki Y.,
Hanga K., Kaniya M., Lee N., Kohtsuki S.,
RA Hayashizaki Y.,
Hanga K., Kaniya M., Lee N., Kohtsuki S.,
Hanga K., Kaniya M., Lee N., Kaniya M., Lee N.H., Kaniya M
   Query Match
Best Local S
Matches 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q9QXP7
Q9QXP7;
01-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sheppard P., Deisher T., Whitmore T., O'Hara P.; "Mus musculus putative se Submitted (OCT-1999) to t
                                                                                                                                                pfam; PF00386; Clq; 1.
pfam; PF01391; Collagen; 1.
PRINTS; PR00007; COMPLEMNTC1Q.
SMART; SM00110; ClQ; 1.
SEQUENCE 281 AA; 32009 MW;
                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AF192499; AAF06664.1; -.
EMBL; AK005484; BAB24070.1; -.
MGD; MGI:1919254; 1600017K21Rik.
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UNN-2002 (TrEMBLrel. 21, Last annotation update)
Putative secreted protein 2SIG37 (1600017K21RIK pro
ZSIG37 OR 1600017K21RIK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=C57BL/6J; TISSUE=Placenta; MEDLINE=21085660; PubMed=11217851
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nature 409:685-690(2001)
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                                                                                                                                                                                                                                                                                                                                       InterPro; IPR001073; Clq.
InterPro; IPR000087; Collagen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               161 SAFSAARTRSLVGSDAGFGFRHQFLAFDTEFVNIGGDFDAAAGVFRCRLFGAYFFSFTLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             47
                                          Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KLPRKTLSVKLMKNRDEVQAMIYDDGASRRREMQSQSVMLALRRGDAVW--LLSHDHDGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAFSVGRKKALHSND-----YFQPVVFDTEFVNLYKHFNMFTGKFYCYVPGIYFFSLNVH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GAYSNHGKYITFSGFLVYPDLAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ulus putative secreted protein."; (OCT-1999) to the EMBL/GenBank/DDBJ databases
       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PubMed=11217851;
13.5%; Score 220.5; DB 11 39.2%; Pred. No. 6.5e-11; tive 20; Mismatches 58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Grant F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                        C9816216DB6419E2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chen
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                                                                              DB 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Haldeman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          protein)
       Indels
                                                                              Length
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   9;
       Gaps
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RESULT 11
QBRO02
ID QBRO02
AC QBRO02
DT 01-JU
DT 01-JU
DT 01-MA
DE Simil
GN CLOTH
OS MUS T
OC ELUKAI
OC Mammas
OX NCBI-
RN [1]
RP SEQUE
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local
                                                                                                 Q8R002;
01-JUN-2002 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
01-MAR-2003 (TrEMBLrel.
                                  Mus musculus (Mouse).
Eukaryota; Metazoa; (
Mammalia; Eutheria; F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; BC029485; AAH29485.1; -...
InterPro; IPR001073; C1q.
InterPro; IPR001087; Collagen.
Pfam; PF00386; C1q; 1.
Pfam; PF01391; Collagen; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q8N6P2;
01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Clq and tumor necrosis factor related protein 5.
            NCBI_TaxID=10090;
[1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Strausberg R.;
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ
                                                                            CIQTNF5.
                                                                                        Similar to DKFZP586B0621 protein
                                                                                                                                                          Q8R002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRINTS; PRO0007; COMPLEMNTC1Q.
SMART; SM00110; C1Q; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QBN6P2
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                              167
                                                                                                                                                                                                                                                                                                       230
                                                                                                                                                                                                                                                                                                                                  113
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                                                                                                                                                                                                                                                                                                                                                                                       57
                                                                                                                                                                                                                                                                                                                                                                                                                                           66;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                       KLMKNRDEVQAMIYDDGASRRREMQSQSVMLALRRGDAVWLLSHDHDGYGAYSNHGKYIT
                                                                                                                                                                                                                                                                                                                                  SRV----PPPSDAPLPFDRVLVNEQGHYDAVTGKFTCQVPGVYYFA-VHATVYRASLQF
                                                                                                                                                                                                                                                                                                                                                           SLVGSDAGPGPRHQPLAFDTEFVNIGGDFDAAAGVFRCRLPGAYFFSFTLGKLPRKTLSV 229
                                                                                                                                                                                                                                                                                                                                                                                       GAP----GAPGEKGEGGRPGLPGPRGDPGPRGEAGPAGPTGPAGECSVPPRSAFSAKRSE
                                                                                                                                                                                                                                                                                                                                                                                                                GAPHYALGAPGATFSG---YLVYADAD----ADAPARGPPAPP-----EPRSAFSAARTR 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IFSDEFDTYITFSGYLVKPASEP 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GAYSNHGKYITFSGFLVYPDLAP 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KLPRKTLSVKLMKNRDEVQAMIYDDGASRRREMQSQSVMLALRRGDAVW--LLSHDHDGY 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAFSVGRKKALHSND----YFQPVVFDTEFVNLYKHFNMFTGKFYCYVPGIYFFSLNVH
                                                                                                                                                                                                                                                    FSGFLVYPD
                                                                                                                                                                                                                                                                             DLVKNGESIASFFQFFGGWPKPASLSGGAMVRLEPEDQVWVQVGVGDYIGIYASIKTDST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TWNQKETYLHIMKNEEEV-VILYAQ-VSDRSIMQSQSLMMELREEDEVWVRLFKGERENA
                                                                                                                                                                                                                           FSGFLVYSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               243 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                          235
                                                                                                                                                                                                                                                    298
                                    Chordata;
Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25326 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       13.0%; Score 213; DB 4; 34.9%; Pred. No. 2.4e-10;
                                                                                                    21,
21,
23,
                                                                                                                                                                                                                                                                                                                                                                                                                                           18;
                                                                                    Last sequence update)
Last annotation update)
otein (Hypothetical 25.4
                                                                                                                                 Created)
                                    Sciurognathi;
                                                                                                                                                          PRT;
                                                  Craniata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6D9306A0EB21B44A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             243
                                                                                                                                                           243
                                     Vertebrata; Euteleostomi;
thi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 4; Length 243;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A
                                                                                                                                                                                                                                                                                                                                                                                                                                           83;
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                          kDa
                                                                                        protein)
                                                                                                                                                                                                                                                                                                                                                                                                                                           22;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                  166
                                                                                                                                                                                                                                                                                                                                                                                       112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   258
                                                                                                                                                                                                                                                                              226
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RESULT 12
Q8K479
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                                                                                                                                                 ACCOUNT DESCRIPTION OF THE PROPERTY OF THE PRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      밁
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Query Match
Best Local S
Matches 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                  MGD; MGI:2385958; Clqtnf5.
InterPro; IPRO01073; Clq.
InterPro; IPRO00087; Collagen.
Pfam; PF01391; Collagen; 2.
PRINTS; PR00007; COMPLEMNTC1Q.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR001073; C1q.
InterPro; IPR000087; Collagen.
Pfam; PF00386; C1q; 1.
Pfam; PF01391; Collagen; 1.
SMART; SM00110; C1Q; 1.
Hypothetical protein.
SEQUENCE 243 AA; 25420 MW; 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Complement-clq tumor necrosis factor-related protein.
ClqTNF5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Strausberg R.;
Submitted (MAR-2002) to the
EMBL; BC023068; AAH23068.1;
EMBL; BC025174; AAH25174.1;
MGD; MGI:2385958; Clqtnf5.
                                                                                                                                                                                                                                                                                                                                                                                                                                     "Mfrp, a gene encoding a frizzled related protein, mouse retinal degeneration 6.";
Hum. Mol. Genet. 11:1879-1886(2002).
EMBL; AF469650; AAM89217.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q8K479
                                                                                                                                                 SEQUENCE
                                                                                                                                                                                    PRINTS; PR00007; COMPLE SMART; SM00110; C1Q; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q8K479;
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Submitted (FEB-2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=C57BL/6J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kameya S., Hawes N.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=22135657;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nishina P.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      221
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     122 GAPHYALGAPGATFSGYLVYADADADAPA-RGPPAP------PEPRSAF 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                57 GAP----GAPGEKGEG-----GRPGLPGPRGEPGPRGEAGPMGAIGPAGECSVPPRSAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          64;
1 Similarity 63; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IKTDSTFSGFLVYSD 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SAARTRSLVGSDAGFGFRHQPLAFDTBFVNIGGDFDAAAGVFRÇRLFGAYFFSFTLGKLF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HGKYITFSGFLVYPD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RASLQFDLVKNGQSIASFFQYFGGWPKPASLSGGAMVRLEPEDQVWVQVGVGDYIGIYAS
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                                                                                                                                                 243 AA;
   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PubMed=12140190;
N.L., Chang B., Heckenlively J.R.,
                                                                                                                                                     25436 MW;
   12.3%; Score 202; DB 11; 32.3%; Pred. No. 2.1e-09; tive 17; Mismatches 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12.5%; Score 205; DB 11; 32.8%; Pred. No. 1.2e-09; tive 16; Mismatches 81
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                                                                                                                                                     CRC64;
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                                                                        Length 243;
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       Indels
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       34;
   Gaps
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RESULT 13
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RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Arakawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashina J., Mazazarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Seya T., Shibata Y., Storch K.-F.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Kohtsuki S.,
RA Hayashizaki Y., Soshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
Query Match
Best Local Similarity
Matches 53; Conserv
                                                                                                                                                                       Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases. EMBL; AK007683; BAB25187.1; -. EMBL; BC030324; AAAJ30324.1; -. MGD; MGI:1916433; 1810033KOSRik. InterPro; IPR001073; C1q. InterPro; IPR001073; C1q. InterPro; IPR001087; Collagen.
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Q9D8U4; PRELIMINARY;
Q1-BU42; O1-JUN-2001 (TrEMBLrel. 17,
01-JUN-2001 (TrEMBLrel. 17,
01-MAR-2003 (TrEMBLrel. 23,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=C57BL/6J; TISSUE=Pancreas; MEDLINE=21085660; PubMed=11217851;
                                                                               SEQUENCE
                                                                                                                Pfam; PF00386; Clq; 1.
Pfam; PF01391; Collagen; 2.
PRINTS; PR00007; COMPLEMNTC1Q.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus (Mouse).
                                                           PROSITE; PS01113; C1Q; 1.
                                                                                                                                                                                                                                                                                             Strausberg
                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                        Nature 409:685-690(2001).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
1810033K05Rik protein (RIKEN cDNA 1810033K05 gene).
                                                                                                                                                                                                                                                                                                                                                                       "Functional annotation of a full-length mouse cDNA collection.";
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    Conservative
                    12.2%; Score 200; DB 1 34.9%; Pred. No. 4e-09;
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    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 294
                                    DB 11;
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    45;
                                      Length 294;
    Indels
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  24;
    Gaps
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RESULT 15
Q8BRW2
ID Q8BRW
AC Q8BRW
DT 01-MA
DT 01-MA
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Best Local Similarity
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InterPro; IPR000087; Collagen.
Pfam; PP00386; C1q; 1.
Pfam; PF01391; Collagen; 1.
PRLNTS; PR00007; COMPLEMNTC1Q.
ProDom; PD000007; Collagen; 1.
SMART; SM00110; C1Q; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (1)
SEQUENCE FROM N.A.
TISSUE=Adipose tissue;
MEDLINE=21232234; PubMed=11334417;
MEDLINE=21232234 T., Bodkin N.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q95JD7;
01-DEC-2001 (TrEMBLrel. 19,
01-DEC-2001 (TrEMBLrel. 19,
01-MAR-2003 (TrEMBLrel. 23,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Circulating concentrations of the adipocyte protein adiponectin are decreased in parallel with reduced insulin sensitivity during the progression to type 2 diabetes in rhesus monkeys."; Diabetes 50:1126-1133(2001).
EMBL, AF404407; ARK92202.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Macaca mulatta (Rhesus macaque).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
Cercopithecinae; Macaca.
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                                                                         Q8BRW2
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                                                                                                                                                                                                                                                                                                                                                    TAGKAPH-----KSLSVMLVRNRDEVQALAFDEQRRPGARRAASQSAMLQLDYGDTVWLR
                                                                                                                                                                                                                                                                                                                                                                                                      PGEGAYVYRSAFSVGLETYVT-VPNMPIRFTKIFYNQQNHYDGSTGKFHCNIPGLYYFAY
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                                                                                                                                                                                                                                                                                                  ----HITVYMKDVKVSLFK-KDKAMLFTYDQYQENNVDQ-ASGSVLLHLEVGDQVWLQ
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                                                                           PRELIMINARY;
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31.3%; Pred. No. 1.2e-08;
tive 30; Mismatches 55
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Q8BRW2; 01-MAR-2003 01-MAR-2003

(TrEMBLrel.

23,

Created) Last seq

sequence update)

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SORRITARY RANGES
Search completed: January 12, 2004, 08:19:08 Job time: 44.1078 secs
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                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.

STRAIN-C57BL/6J; TISSUB-AORTA and vein;
MEDLINE-22354683; PubMed-12466851;
The FANTOM Consortium,
the RIKEN Genome Exploration Research Group Phase I & II Team;
"Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";
Nature 420:563-573(2002).
EMBL; AK041214; BAC30866.1; -.
SEQUENCE 247 AA; 26751 MW; 0D3FA64C789CAEF3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Adipocyte complement related protein of 30 kDa.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Metazoa; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=10090;
                                                                                                                                                                  150 TGKFYCNIPGLYYFSYHI-TVYMKDVKVSLFK-KDKAVLFTYDQYQEKNVDQASGSVLLH 207
                                                                                202 AGVFRCRLPGAYFFSFTLGKLPRKTLSVKLMKNRDEVQAMIYDDGASRRREMQSQSVMLA 261
                                                                                                                                                                                                                                                                                         146 ADAPARGPPAPP----EPRSAFSAARTRSLYGSDAGPGPRHQPLAFDTEFVNIGGDFDAA 201
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Maximum Match 100%
Listing first 45 summaries
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1476
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      AAB61423
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Human novel secret Monkey MANGO 245 pp Human MANGO 245 ma Adipocyte compleme Adipocyte compleme Murine MANGO 245 phuman MANGO 245 phuman MANGO 245 cy
                                                                                                                                                                                                                        Description
                                                                                                                                                                             Human ZACRP4.
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o acid sequen	AAB08428	21	ന	•	20
e adipocyte-s	$\vdash$	20	281		220.5
Novel human protei	84	22	12	•	230
Novel human protei	84	22	12		230
l human prote		22	20	٠	230
l human prote	AAE09840	22	00	•	230
l human prote	AAE09844	22	1043	•	230
l human prote	AAE09838	22	2	•	230
1 human	AAE09849	22	993	•	230
1 human prote	AAE09843	22	992	•	230
l human prote	AAE09847	22	958	•	230
1 human prote	AAE09841	22	957	14.0	230
l human prote	AAE09845	22	909	•	230
₽	AAE09839	22	908	•	230
lung	AAE13802	22	.746	•	230
lung	AAB44461	21	746	•	230
Human lung tumour	AAY29512	20	746		230
Human genset metab	AA015420	23	710	•	230
Human pancreatic c	ABB08645	23	709	•	230
Human polypeptide	AAM99927	22	202	14.0	230
Human protein SEQ	AAM78334	22	800		231
Human polypeptide	ABB53292	23	252	•	3
Novel secreted pro	AAU83100	23	252	•	3
Human molecule for	AA019412	23	252	14.5	237.5
Human zacrp5. Hom	AAB49590	22	252	٠	ω
Adipocyte compleme	ABG70386	23	133		507
Mature monkey MANG	AAB61468	22	130		552
Human MANGO 245 Cl	AAB61470	22	117		609
Human ORFX ORF1953	AAB42189	21	123		618
Monkey MANGO 245 C	AAB61472	22	126	37.9	622
Human MANGO 245 ex	AAB61477	22	125	•	635
Murine MANGO 245 C	AAB61489	22	126	•	639
Human MANGO 245 Cl	AAB61469	22	126	٠	646
Human secreted pro	ABB11578	22	127	40.5	664
Ž	AAB61473	22	134	٠	683
Adipocyte compleme	ABG70383	23	221	•	707.5

## ALIGNMENTS

RESULT 1 AAB61606

AAB61606;

AAB61606 standard; Protein; 329 AA

Peptide Human; zacrp4; complement factor Clq domain; chromosome liqil; energy balance; cellular metabolic reaction; autocrine factor; development; cell proliferation; differentiation; cell surviva Domain WO200102565-A2 Domain Key Homo sapiens Human ZACRP4. 05-APR-2001 (first entry) /label= C1q\_domain\_#1 160..328 /label= Clq\_domain\_#2 /label= Signal\_peptide Location/Qualifiers

01-JUL-1999;

99US-0346502

28-JUN-2000; 2000WO-US17692

11-JAN-2001.

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RESULT 2
ABG79643
ID 79643
AC ABG7
XX ABG7
XX ABG7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present sequence is human ZACRP4 protein. ZACRP4 protein has two complement factor C1q domains. The ZACRP4 gene is located on human chromosome 11q11. The ZACRP4 coding sequence and protein have a number of uses described in the specification, including, modulatation of energy balance and cellular metabolic reactions in mammals. In addition, ZACRP4 protein is useful as an autocrine factor, particularly during development, in mediating the processes of an organism, in regulating cellular processes such as cell proliferation and/or differentiation, cell survival and energy balance.
                                        Human; SECP; secreted protein; cell proliferative disorder; actinic keratosis; arteriosclerosis; bursitis; hepatitis; cancer; autoimmune disorder; inflammatory disorder; AIDS; asthma; allergy; acquired immunodeficiency syndrome; anaemia; atopic dermatitis; cardiovascular disorder; congestive heart failure; vascular tumour; ischaemic heart disease; moucardial infarction; epilepsy; stroke; hypertensive heart disease; moucardial infarction; epilepsy; stroke; hypertensive heart disease; moucardial disorder; renal tubular acidosis; Alzheimer's disease; developmental disorder; renal tubular acidosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1;
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Cushing's syndrome;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABG79643 standard; Protein;
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DB; AAF28672.
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Pred. No. 4e-152;
0; Mismatches 0;
                    muscular
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                 dystrophy; hypothyroidism;
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                                                                                                                                                                                                                                                                                   CC anti-SECP antibody, and screening for antiagonists and modulators of CC SECP function or expression. The SECP proteins and nucleic acids are CC useful in the diagnosis, treatment and prevention of cell proliferative CC (e.g. actinic keratosis, arteriosclerosis, burstis, hepatitis or CC cancer), autoimmune/inflammatory (e.g. AIDS (acquired immunodeficiency CC syndrome), asthma, anaemia, allergies or atopic dermatitis), CC cardiovascular (e.g. congestive heart failure, ischaemic heart disease, CC myocardial infarction, hypertensive heart disease, or Alzheimer's CC meurological (e.g. epilepsy, stroke, cerebral meoplasms, or Alzheimer's CC disease), and developmental (e.g. renal tubular acidosis, Cushing's CC disease), and developmental (e.g. renal tubular acidosis, Cushing's CC specification. These may also be used in assessing the effects of CC exogenous compounds on the expression of nucleic acid and amino acid CC sequences of the secreted proteins. The present sequence represents a compounds of the invention of the invention
                                                                                                                                              Query Match
Best Local S
Matches 311
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26-FEB-2001;
07-SEP-2001;
21-DEC-2001;
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08-FEB-2001;
09-FEB-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (SECP1-24), proteins 90% identical to them and active fragments of them. Also included are nucleic acids encoding the SECP proteins, a recombinant polynucleotide comprising a promoter sequence operably linked to the nucleic acid, a cell transformed with the recombinant polynucleotide, an a transgenic organism comprising the recombinant polynucleotide, an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New human secreted proteins and nucleic acids useful in diagnosing, treating and preventing cell proliferative, autoimmune/inflammatory, cardiovascular, neurological, and developmental disorders -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lee
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                                                                                                                                                                                                                                 Sequence
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Yang .
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Tang J, Than
Richardson
                                                                                                                                                                      Similarity
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FFSFTAGKAPHKSLSVMLVRNRDEVQALAFDEQRRPGARRAASQSAMLQLDYGDTVWLRL
                                                             LGPTPGPGSSELRSAFSAARTTPLEGTSEMAVTFDKVYVNIGGDFDVATGQFRCRVPGAY
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2001US-271639P.
2001US-317818P.
2001US-343553P.
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2001US-267924P.
2001US-267816P.
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K, Lal PG, Honche.
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                                                                                                                                              Score 1620; DB 23;
Pred. No. 2.9e-150;
0; Mismatches 2;
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Blliott VS;
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NK, Lee S;
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                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                  Isolated cDNAs encoding TANGO 244, TANGO 246, TANGO 275, TANGO 300 and MANGO 245 proteins, useful in the treatment of inflammatory diseases (e.g. idiopathic ulcerative colitis), tumors, renal disorders and lived disorders (e.g. jaundice) -
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                                                                                                        Local Similarity
hes 302; Conserv
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mmune; allergy; c
eatic; skeletal;
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                                                                                                                                                                                                                                                                                                     Fig 25; 262pp; English.
                                                                LGPTPGPGSSELRSAFSAARTTPLEGTSEMAVTFDKVYVNIGGDFDVATGQFRCRVPGAY
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FFSFTVGKAPHKSLSVMLVRNHDEVQALAFDEQRRPSARRAASQSAMLQLDYGDTVWLRL
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                        FFSFTAGKAPHKSLSVMLVRNRDEVQALAFDEQRRPGARRAASQSAMLQLDYGDTVWLRL 120
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                                                                                                      Conservative
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96.5%;
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cardiovascular; brain; degenerative; placental;
; muscle.
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                                                                                                                   Score 1579; DB 22; Pred. No. 3.1e-146;
                                                                                                      Mismatches
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LGPTPGPGSSELRSAFSAARTTPLEGTSEMAVTFDKVYVNIGGDFDVATGQFRCRVPGAY

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LGPTPGPGSSELRSAFSAARTTPLEGTSEMAVTFDKVYVNIGGDFDVATGQFRCRVPGAY

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                                                                                             The present invention relates to cDNAs encoding TANGO 244, TANGO 246, TANGO 275, TANGO 300 and MANGO 245 proteins. The nucleic acids, proteins and protein modulators useful treating colonic disorders, inflammatory diseases, tumors, renal disorders, liver disorders, lung disorders, autoimmune dallergic diseases, cardiovascular diseases, brain disorders,
                                                                                                                                                                                                                    Isolated cDNAs encoding TANGO 244, TANGO 246, TANGO 275, TANGO 300 and MANGO 245 proteins, useful in the treatment of inflammatory diseases (e.g. idiopathic ulcerative colitis), tumors, renal disorders and liver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TANGO; MANGO; colon; inflammation; tumor; renal; liver; lung; autoimmune; allergy; cardiovascular; brain; degenerative; placental; pancreatic; skeletal; muscle.
                                                 Sequence
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                                                                                   degenerative diseases placental,
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human MANGO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAB61423
                                                                                                                                                                                                                                                                                                                      (MILL-) MILLENNIUM PHARM INC.
            Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         317
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      257
  283;
             Similarity
                                                                                                                                                                                  Fig 23; 262pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MIYDDGASRRREMQSQSVMLALRRGDAVWLLSHDHDGYGAYSNHGKYITFSGFLVYPDLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RHQPLAFDTEFVNIGGDFDAAAGVFRCRLPGAYFFSFTLGKLPRKTLSVKLMKNRDEVQA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HGAPQYALGAPGATFSGYLVYADADADAPARGPPAPPEPRSAFSAARTRSLVGSDAGSGP 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PAAPPGLGAPELL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MIYDDGASRRREMQSQSVMLALRRGDAVWLLSHDHDGYGAYSNHGKYITFSGFLVYPDLA
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                                                                                                                                                                                                         (e.g.
                                                 348 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     245
  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                             Barnes
                                                                                                                                                                                                                                                                                                                                              99US-0342687.
                                                                                                                                                                                                          jaundice)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protein;
           90.3%;
                                                                                                                                                                                                                                                                                              Σ̈́
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              313
                                                                                                                                                                                                                                                                                              Fraser
Pred. No. 1.7e
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            348
                                                                                   pancreatic, skeletal and
                                                                                                                                                                                                                                                                                              3
                                                                                                                                                                                                                                                                                             Sharp
 1.7e-136;
hes 1;
                          멾
                      Length
  Indels
                         348;
                                                                                    muscle
 0
                                                                                                                                     for
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RESULT 5
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  밁
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                      S
                                              Query Match
Best Local S
Matches 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TANGO; MANGO; colon; 
autoimmune; allergy; 
pancreatic; skeletal;
                                                                                                                                        The present invention relates to cDNAs encoding TANGO 244, TANGO 245, TANGO 300 and MANGO 245 proteins. TANGO 275, TANGO 300 and MANGO 245 proteins and protein modulators are useful for The nucleic acids, proteins and protein modulators are useful for treating colonic disorders, inflammatory diseases, tumors, renal disorders, liver disorders, lung disorders, autoimmune diseases, allergic diseases, cardiovascular diseases, brain disorders, allergic diseases, cardiovascular diseases, brain disorders,
                                                                                                                                                                                                                                                          Isolated cDNAs encoding TANGO 244, TANGO 246, TANGO 275, TANGO 300 MANGO 245 proteins, useful in the treatment of inflammatory disease (e.g. idiopathic ulcerative colitis), tumors, renal disorders and l
                                                                                                                                                                                                                                                                                                                                                                                                                               04-JAN-2001.
                                                                                            Sequence
                                                                                                                                                                                                                            Disclosure;
                                                                                                                                                                                                                                                                                                                                   Holtzman
                                                                                                                                                                                                                                                                                                                                                                                29-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                        29-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200100672-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         04-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAB61466
                                                                                                                                                                                                                                                                                                                                                         (MILL-) MILLENNIUM PHARM INC
                                                                                                                               degenerative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           137
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MANGO 245 mature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          77
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                                               282;
                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RHQPLAFDTEFVNIGGDFDAAAGVFRCRLPGAYFFSFTLGKLPRKTLSVKLMKNRDEVQA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RHOPLAFDTEFVNIGGDFDAAAGVFRCRLEGAYFFSFTLGKLPRKTLSVKLMKNRDEVQA
LGPTPGPGSSELRSAFSAARTTPLEGTSEMAVTFDKVYVNIGGDFDVATGQFRCRVPGAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MIYDDGASRRREMQSQSVMLALRRGDAVWLLSHDHDGYGAYSNH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HGAPQYALGAPGATFSGYLVYADADADAPARGPPAPPEPRSAFSAARTRSLVGSDAGPGP
                                                                                                                                                                                                                                                 (e.g. jaundice)
                                                                                            334
                                                                                                                                                                                                                            Page 242; 262pp;
                                              90.1%;
ilarity 99.3%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                        2000WO-US18184.
                                                                                                                               diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first
                                                                                                                                                                                                                                                                                                                                   Barnes
                                                                                            Ą,
                                                                                                                                                                                                                                                                                                                                                                               99US-0342687.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              inflammation; tumor; renal; liver; lung;
cardiovascular; brain; degenerative; placental;
                                                                                                                                                                                                                                                                                                                                   M,
                                                                                                                             placental, pancreatic,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    muscle.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                protein
                                                                                                                                                                                                                                                                                                                                   Fraser
                                             Score 1476; Di
Pred. No. 3.9e
0; Mismatches
                                              0
                                                                                                                                                                                                                          English
                                                                                                                                                                                                                                                                                                                                  3
                                                                                                                                                                                                                                                                                                                                  Sharp
                                            DB 22;
1.9e-136;
1es 2;
                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                               skeletal
                                               Indels
                                                                    Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      284
                                                                                                                               and muscle
                                                                      334;
                                                                                                                                                                                                                                                             diseases
rs and liver
                                              0
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  62
                         60
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Gangolli E*I* Stone DJ, Spytek KA,

J, Anderson

'n, o,

Shimkets RA Boldog FL,

Vernet CAM, Malya kets RA, Burgess C og FL, Smithson G,

Malyankar UM, LT.

Zerhusen Bl i L, Ji W;

Kekuda sen BD,

. R; Liu

×

Patturajan

N-PSDB;

ABS52097

WPI; 2002-590744/63.

Novel isolated NOVX polypeptide useful atherosclerosis, metabolic disorders,

l for treating diabetes, ober

sity, infectious

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RESULT 6
ABG70385
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20-DEC-2000;
02-MAY-2001;
29-MAY-2001;
24-JUL-2001;
10-AUG-2001;
10-AUG-2001;
29-AUG-2001;
14-SEP-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Alzheimer's disease; Parkinson's disease; immune disorder; cancer; haematopoietic disorder; cirrhosis; pancreatitits; learning defect; memory defect; infertility; congenital heart defect; hair growth; pigmentation disorder; endocrine disorder; respiratory disease; health; pigmentation disorder; endocrine disorder; respiratory disease; bone marrow transplantation; endocrine disease; allergy; inflammation; nephrological disorder; reindocrine disease; allergy; inflammation; nephrological disorder; reindocrine disease; age-related disorder; neuropsychiatric disorder; system disorder; age-related disorder; neuropsychiatric disorder; EGF-related protein; SCUBEI; TEN-M4; nadipocyte complement_related Clq tumour necrosis factor; out at first; beta adrenergic receptor kinase; EphA6/ehk-2; glucose transporter; type 1a membrane sushi-containing domain; butyrophilin; type 1a membrane-sushi domain containing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; NOVX; NOVX-associated disorder; cardiomyopathy; atherosclerosis; cell signal processing; metabolic pathway modulation; metabolic disorder; obesity; diabetes; infectious disease; neurodegenerative disorder; acne;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Adipocyte complement-related
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                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
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                                                                                                                                                      (CURA-)
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                                                                                                                                                    CURAGEN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RHOPLAFDTEFVNIGGDFDAAAGVFRCRLPGAYFFSFTLGKLPRKTLSVKLMKURDEVQA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         standard;
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                                                                                                                                                                                 ; 2000US-265704P.

2000US-257314P.

2001US-288153P.

2001US-294075P.

2001US-307506P.

2001US-311500P.

2001US-311613P.

2001US-315617P.

2001US-322358P.
                                                                                                                                                                                                                                                                                                                                        2001WO-US50331
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RESULT 7
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AC ABG77
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XX ABG77
XX D5 -N
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      disorders (e.g. obesity), diabetes, infectious disease, neurodegenerative disorders (e.g. Alzheimer's disease, Parkinson's disease), immune disorders, haematopoietic disorders and various cancers. The molecules of the invention are also useful for treating or preventing cirrhosis, pancreatitis, learning and memory defects, infertility, congenital heart defects, acne, hair growth, pigmentation disorders, endocrine disorders, respiratory diseases, gastro-intestinal diseases, reproductive, health, neurological diseases, bone marrow transplantation, endocrine diseases, allergy and inflammation, nephrological disorders, neuropsychiatric disorders and age-related disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention relates to new NOVX polypeptides. The invention is useful for treating or preventing a NOVX-associated disorder such as cardiomyopathy or atherosclerosis, where the disorder is related to cell
                                 gastro-intestinal
                                                      memory defect; infertility; congenital heart defect; hair growth pigmentation disorder; endocrine disorder; respiratory disease; h
                                                                                                                                                                       Human; NOVX; NOVX-associated disorder; cardiomyopathy; atherosclerosis; cell signal processing; metabolic pathway modulation; metabolic disorde cobesity; diabetes; infectious disease; neurodegenerative disorder; acne
                                                                                                                                                                                                                                                                                                                                                           05-NOV-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABG70384
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             disease,
                                                                                     haematopoietic disorder; cirrhosis; pancreatitis; learning memory defect; infertility; congenital heart defect; hair c
                                                                                                                                                                                                                                                                                           Adipocyte complement-related Clq
                                                                                                                                            Alzheimer's disease; Parkinson's disease; immune disorder; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             present amino acid sequence represents a NOVX protein of the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           standard; Protein;
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                                                                                                                                                                                                                                                                                                                                                        (first entry
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                              disease; reproductive;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                              Tumour Necrosis Factor-like protein
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      disease;
                                 neurological
allergy;
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                              disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              299;
                                                                                                                   defect;
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FFSFTAGKAPHKSLSVMLVRNRDEVQALAFDEQRRPGARRAASQSAMLQLDYGDTVWLRL

FFSFTAGKAPHKSLSVMLVRNRDEVQALAFDEQRRPGARRAASQSAMLQLDYGDTVWLRL

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20-DEC-2000;
02-MAY-2001;
29-MAY-2001;
24-JUL-2001;
10-AUG-2001;
29-AUG-2001;
                                                                                                                                                                                               The present invention relates to new NOVX polypeptides. The invention is useful for treating or preventing a NOVX-associated disorder such as cardiomyopathy or atherosclerosis, where the disorder is related to cell signal processing and metabolic pathway modulation in a subject, preferably human. The invention is also useful for treating metabolic disorders (e.g. obesity), diabetes, infectious disease, neurodegenerative disorders, haematopoietic disorders and various cancers. The molecules of the invention are also useful for treating cirrhosis, pancreatitis, learning and menory defects, infertility, congenital heart defects, anne, hair growth, pigmentation disorders, endocrine disorders, respiratory disease, gastro-intestinal diseases, reproductive, health, neurological diseases, bone marrow transplantation, endocrine diseases,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gangolli
Stone DJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel isolated NOVX polypeptide useful for treating cardiomyopathy, atherosclerosis, metabolic disorders, diabetes, obesity, infectious disease, anorexia, neurodegenerative disorders, Alzheimer's disease
                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; Page 30; 318pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        nephrological disorder; urinary system disorder; age-related disorneuropsychiatric disorder; EGF-related protein; SCUBE1; TEN-M4; adipocyte complement-related Clq tunour necrosis factor; out at fix beta adrenergic receptor kinase; EphA6/ehk-2; glucose transporter; type la membrane sushi-containing domain; butyrophilin; type la membrane-sushi domain containing.
                                                                                                                                                                                        allergy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (CURA-)
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                                                          Local Sin
hes 267;
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  17
                                                                                                                                                                                        and inflammation,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURAGEN
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                   LGPTPGPGSSELRSAFSAARTTPLEGTSEMAVTFDKVYVNIGGDFDVATGQFRCRVPGAY
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  LGPTPGPGSSELRSAFSAARTTPLEGTSEMAVTFDKVYVNIGGDFDVATGQFRCRVPGAY
                                                                                                                                                           neuropsychiatric
t amino acid sequ
                                                                                                                   284
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7 2001US-288153P.

7 2001US-294075P.

7 2001US-307506P.

7 2001US-311590P.

7 2001US-315617P.

7 2001US-312358P.
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                                                          Conservative
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                                                                       82.9%;
                                                                                                                                                           sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Shimkets RA, Buryer, Smithson G,
                                                                                                                                                                                        nephrological
                                                                                                                                                          ephrological disorders, urinary system disorders and age-related disorders. ence represents a NOVX protein of the
                                                          <u>.</u>.
                                                        Score 1358.5; DB
Pred. No. 1e-124;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Vernet CAM,
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                                                                                     DB
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                                                                                     Length
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                                    Query Match
Best Local S
Matches 163
                                                                                                The present invention relates to cDNAs encoding TANGO 244, TANGO 246, TANGO 275, TANGO 300 and MANGO 245 proteins.
The nucleic acids, proteins and protein modulators are useful for treating colonic disorders, inflammatory diseases, tumors, renal disorders, liver disorders, lung disorders, autoimmune diseases, allergic diseases, cardiovascular diseases, brain disorders, degenerative diseases placental, pancreatic, skeletal and muscle
                                                                                                                                                                                                               Isolated
MANGO 245
                                                                                                                                                                                                                                                                                                                                                                                         TANGO; MANGO; colon; inflammation; tumor; renal; liver; lung; autoimmune; allergy; cardiovascular; brain; degenerative; placental; pancreatic; skeletal; muscle.
                                                                        Sequence
                                                                                          disorders.
                                                                                                                                                                                                                                                                                               29-JUN-1999;
                                                                                                                                                                                                                                                                                                                                    04-JAN-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                              Murine MANGO
                                                                                                                                                                                           disorders (e.g. jaundice)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            181
                                                                                                                                                                                                    ted cDNAs encoding TANGO 244, TANGO 246, TANGO 275, TANGO 300 and 245 proteins, useful in the treatment of inflammatory diseases idiopathic ulcerative colitis), tumors, renal disorders and lives
 17
                                              Similarity
                                                                                                                                                                                                                                                            DA,
         LGPTPGPGSSELRSAFSAARTTPLEGTSEMAVTFDKVYVNIGGDFDVATGQFRCRVPGAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PAAPPGLGASELL 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MIYDDGASRRREMQSQSVMLALRRGDAVWLLSHDHDGYGAYSNHGKYITFSGFLVYPDLA
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                                                                                                                                                                                                                                                                                                                                                                                                                              245 protein.
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-GPGSSELRSAFSAARTTPLEGTSEMAVTFDKVYVNIGGDFDAATGRFRCRVPGAY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein; 199
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87.2%;
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                                  Score 809; DB 22;
Pred. No. 4.7e-71;
4; Mismatches 16;
                                                                                                                                                                                                                                                            Sharp
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                                                    Length
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ID AABC
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Matches 144
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The nucleic acide, proteins and protein modulators are useful for treating colonic disorders, inflammatory diseases, tumors, renal disorders, liver disorders, lung disorders, autoimmune diseases, allergic diseases, cardiovascular diseases, brain disorders, degenerative diseases placental, pancreatic, skeletal and muscle
                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Page 247; 262pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                               Isolated cDNAs encoding TANGO 244, TANGO 246, TANGO 275, TANGO MANGO 245 proteins, useful in the treatment of inflammatory di (e.g. idiopathic ulcerative colitis), tumors, renal disorders disorders (e.g. jaundice) -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Holtzman
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pancreatic; skeletal;
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autoimmune; allergy; cardiovascular; brain; degenerative; pl
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                                                                                                                46.4%; S llarity 100.0%; Conservative 0;
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                                                                                                                Score 760; DB 22;
; Pred. No. 2.9e-66;
0; Mismatches 0;
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02-MAY-2001; 2001US-288153P.
29-MAY-2001; 2001US-294075P.
24-JUL-2001; 2001US-307566P.
10-AUG-2001; 2001US-31159P.
10-AUG-2001; 2001US-311613P.
29-AUG-2001; 2001US-315617P.
14-SEP-2001; 2001US-322358P.
useful for treating or preventing a NOVX-associated disorder such as cardiomyopathy or atherosclerosis, where the disorder is related to cell signal processing and metabolic pathway modulation in a subject, preferably human. The invention is also useful for treating metabolic disorders (e.g. ablesity), diabetes, infectious disease, neurone disorders (e.g. Alzheimer's disease, parkingon's disease), immune disorders, haematopoietic disorders and various cancers. The molecules of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       haematopoietic disorder; cirrhosis; pancreatitis; learning defect; memory defect; infertility; congenital heart defect; hair growth; pigmentation disorder; endocrine disorder; respiratory disease; health; gastro-intestinal disease; reproductive; neurological disease; bone marrow transplantation; endocrine disease; allergy; inflammation; nephrological disorder; urinary system disorder; age-related disorder; neuropsychiatric disorder; EGF-related procein; SCUBEI; TEN-M4; adipocyte complement-related C1q tumour necrosis factor; out at first; beta adrenergic receptor kinase; EphA6/ehk-2; glucose transporter; type la membrane sushi-containing domain; butyrophilin;
                                                                                                                                                                                               Novel isolated NOVX polypeptide useful for treating cardiomyopathy, atherosclerosis, metabolic disorders, diabetes, obesity, infectious disease, anorexia, neurodegenerative disorders, Alzheimer's disease
                                                                                                               The present invention relates to new NOVX polypeptides. The invention
                                                                                                                                                 Claim 1;
                                                                                                                                                                                                                                                                                                                                              Gangolli EA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cell signal processing; metabolic obesity; diabetes; infectious disc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; NOVX; NOVX-associated disorder; cardiomyopathy; atherosclerosis;
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                                                                                                                                                                                                                                                                                                                                              Patturajan M,
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                                                                                                                                                                                                                                                                                                             Shimkets RA, Burgess C
Boldog FL, Smithson G,
                                                                                                                                               English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             autoimmune; allergy; cardiova pancreatic; skeletal; muscle.
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                                                                                                                                                                                                                                                                                                                                                                                         WO200100672-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TANGO; MANGO; colon; inflammation; tumor; renal; liver; lung; autoimmune; allergy; cardiovascular; brain; degenerative; pla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Monkey MANGO
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                                                                           WPI; 2001-050127/06
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-----VNIGGDFDAAAGVFRCRLPGAYFFSFTLGKLPRKTLSVKLMKNRDEVQAMIYD
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                                                                                                                              Barnes
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                                                                                                                            Sharp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       152
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Isolated cDNAs encoding TANGO MANGO 245 proteins, useful in

244, TANGO the treatme

246; TANGO 275, TANGO 300 a ent of inflammatory diseases

treatment

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RESULT 12
ABB11578
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches 131;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention relates to cDNAs encoding TANGO 244, TANGO 246, TANGO 275, TANGO 300 and MANGO 245 proteins. The nucleic acids, proteins and protein modulators are useful for treating colonic disorders, inflammatory diseases, tumors, renal disorders, liver disorders, lung disorders, autoimmune diseases, allergic diseases, cardiovascular diseases, brain disorders, degenerative diseases placental, pancreatic, skeletal and muscle
                                                                                                                                                                                                                                                                                                            Human; cytokine; cell proliferation; cell differentiation; growth factor; haematopoiesis regulation; tissue growth; immunomodulator; activin; inhibin; chemotaxis; chemokinesis; thrombolysis; oncogenesis; proliferation; metastasis; cancer; tumour; haematopoietic disorder; myeloid cell disorder; lymphoid cell disorder; asthma; arthritis; chronic inflammatory condition; proliferative retinopathy; atherosclerosis; coronary heart disease; arterial ischaemia; bone disorder; osteoporosis; vascular growth disorder; tissue regeneration; wound healing; infection; immune disorder; cell culture drow wound healing; infection; immune disorder;
                                                                                                                                                                                                                                                                       cell culture; drug screening; gene therapy; antiinflammatory; antiasthmatic; antiarthritic; haemostatic; antiarteriosclerotic; cardiant; virucide; antibacterial;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (e.g. idiopathic ulcerative colitis), tumors, renal disorders and liver
                            Tang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABB11578 standard; peptide; 127 AA
WPI; 2001-457740/49
                                                                                       03-FEB-2000; 2000US-0496914.
27-APR-2000; 2000US-0560875.
                                                                                                                                   05-FEB-2001; 2001WO-US03800
                                                                                                                                                               09-AUG-2001
                                                                                                                                                                                                                                                        antifungal; vulnerary;
                                                                                                                                                                                               WO200157188-A2
                                                                                                                                                                                                                            Homo sapiens
                             ΤY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   282
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      secreted protein homologue, SEQ ID NO:1948
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ш
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                                                         HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AFSAARTRSLVGSDAGPGPRHQPLAFDTEFVNIGGDFDAAAGVFRCRLPGAYFFSFTLGK 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SNHGKYITFSGFLV 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AFSAARTRSLVGSDAGSGPRHRPLAFDTELVNIGGDFDAAAGVFRCRLPGAYFFSFTLGK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SNHGKYITFSGFLV 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (e.g.
                            Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  134 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28; 262pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               jaundice)
                               Drmanac
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97.8%;
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Pred. No. 6.3e-59;
1; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 134;
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N-PSDB; ABA08822
                                                                                                                                            treating
                                                                                                                                        .g. arthritis and cancer
                                                                                                                                           proteins and DNA encoding sequences useful for preventing, ing or ameliorating a medical condition in a mammalian subject
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Claim 20; Page 214-215; 1963pp; English

CC haematopoiesis regulatory activity; tissue growth activity; chemotactic or chemokinetic activity: activity is haematopoiesis; concert chemotactic or chemokinetic activities; haemostatic, thrombotic or chemotactic or conditions on their biological activities, polypeptides and nucleotides of conditions, e.g., by protein or gene therapy. Such conditions include conditions, e.g., by protein or gene therapy. Such conditions include conditions, e.g., by protein or gene therapy. Such conditions include conditions, e.g., by protein or gene therapy. Such conditions include conditions, e.g., by protein or gene therapy. Such conditions include conditions, e.g., asthematory conditions (e.g., myeloid or lymphoid cell conditions), chronic inflammatory conditions (e.g., asthma or arthritis), cronic inflammatory conditions (e.g., asthma or arthritis), confict ative retinopathy, atherosclerosis, coronary heart disease, coronary heart or activities may be used to promote wound conditions (e.g., of burns, incisions and ulcers), while those with conditions (e.g., of burns, incisions and ulcers), while those with conditions of the same to promote wound conditions and the promote wound conditions and ulcers), while those with conditions and ulcers) and another to replace cell such as the conditions of the can be used to augment or replace cells damaged by illness, and in the diagnosis of the above conditions, and in drug also be used in the diagnosis of the above conditions, and in man or the processor expenses a novel human conditions. or polypeptides in a sample, and methods of identifying compounds which bind to polypeptides of the invention. Although novel, many of the polypeptides of the invention have homology to known proteins, thereby giving an insight into their probable biological activities, and hence potential therapeutic applications. The polypeptides of the invention in have various activities, including cytokine, cell proliferation or cell differentiation activities; stem cell growth factor activity. Sequences ABB10981-ABB12330 represent 1350 novel human polypeptides, and sequences ABA08225-ABA09574 represent nucleic acids encoding them. The invention also relates to vectors and recombinant host cells comprising a nucleotide of the invention, methods of producing the novel polypeptides, antibodies against the polypeptides, methods of detecting the nucleotides or polypeptides in a sample, and methods of identifying compounds which bind to not produced the first sample, and methods of identifying compounds which bind to not produced the novel polypeptides. Sequence polypeptide techniques. The present sequence represents a novel human 127 of the invention Ŗ cell may

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RESULT 13
AAB61469
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Best Local S
                                                                                                                                                                            Matches
       04-APR-2001
                      AAB61469;
                                      AAB61469
                                                                                                                                                           187
                                                                                             307
                                                                                                                             247
                                                                             121
                                                                                                                                                                             126;
                                                                                                             61
                                                                                                                                             <u>بــ</u>
                                                                                                                                                                                   Similarity
                                                                                                                      ASRRREMOSOSYMLALRRGDAVWLLSHDHDGYGAYSNHGKYITFSGFLVYPDLAPAAPPG
                                                                                                                                                       standard;
                                                                             LGASELL
                                                                                             LGASELL 313
                                                                                                             SSRRREMQSQSVMLALRRGDAVWLLSHDHDGYGA
                                                                                                                                             FDTEFVNIGGDFDAAAGVFRCRLPGAYFFSFTLGKLPRKTLSVKLMKNRDEVQAMIYDDG
                                                                                                                                                                            Conservative
       (first entry)
                                                                             127
                                     protein;
                                                                                                                                                                                   40.5%;
                                       126
                                                                                                                                                                            Score 664; DB 22.
Pred. No. 4.3e-57
1; Mismatches
                                       ₹
                                                                                                                                                                                             22;
                                                                                                                                                                              <u>,</u>
                                                                                                                                                                                            Length
                                                                                                                                                                              Indels
                                                                                                                                                                                              127;
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                                                                                                                                                                              Gaps
                                                                                                                               306
                                                                                                                                               60
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RESULT 14
AAB61489
ID AAB61
XX AAB61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention relates to cDNAs encoding TANGO 244, TANGO 245, TANGO 300 and MANGO 245 proteins. TANGO 245, TANGO 275, TANGO 300 and MANGO 245 proteins are useful for The nucleic acids, proteins and protein modulators are useful for treating colonic disorders, inflammatory diseases, tumors, renal disorders, liver disorders, lung disorders, autoimmune diseases, allergic diseases, cardiovascular diseases, brain disorders, degenerative diseases placental, pancreatic, skeletal and muscle
                                                                        pancreatic;
                                                                                                                        TANGO;
                                                                                                                                                                              Murine
                                                                                                                                                                                                                                 04-APR-2001
                                                                                                                                                                                                                                                                                                                                  AAB61489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Fig 26; 262pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Isolated cDNAs encoding TANGO 244, TANGO 246, TANGO 275, TANGO 300 and MANGO 245 proteins, useful in the treatment of inflammatory diseases (e.g. idiopathic ulcerative colitis), tumors, renal disorders and liver disorders (e.g. jaundice)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      04-JAN-2001
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pancreatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Holtzman DA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                29-JUN-2000; 2000WO-US18184.
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autoimmune; allergy; cardiovascular; brain; degenerative; placental;
pancreatic; skeletal; muscle.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-050127/06.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (MILL-) MILLENNIUM PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121
                                                                     mmune; allergy; c
eatic; skeletal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                125;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61
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                                                                                                                                                                              MANGO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                  standard; protein; 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AFSAARTTPLEGTSEMAVTFDKVYVNIGGDFDVATGQFRCRVPGAYFFSFTAGKAPHKSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FSGYLV 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SVMLVRNRDEVQALAFDEQRRPGARRAASQSAMLQLDYGDTVWLRLHGAPQYALGAPGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SVMLVRNRDEVQALAFDEQRRPGARRAASQSAMLQLDYGDTVWLRLHGAPHYALGAPGAT 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                FSGYLV 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AFSAARTTPLEGTSEMAVTFDKVYVNIGGDFDVATGQFRCRVPGAYFFSFTAGKAPHKSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (e.g. jaundice)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 126 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                              245
                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Barnes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99US-0342687.
                                                                                                                                                                           Clq
                                                                                        inflammation; tumor; renal; liver; lung; cardiovascular; brain; degenerative; pla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   39.4%;
                                                                                                                                                                           domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Σ,
                                                                        muscle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fraser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  #1
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Pred. No. 2.5e-55;
D; Mismatches 1
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                                                                                              brain; degenerative; placental;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sharp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 126;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
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RESULT 15
AAB61477
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local S
Matches 122
                                                                                                                     autoimmune; allergy; cardiova
pancreatic; skeletal; muscle.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      renal disorders, liver disorders, lung disorders, autoimmune allergic diseases, cardiovascular diseases, brain disorders, degenerative diseases placental, pancreatic, skeletal and mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TANGO 246, TANGO 275, TANGO 300 and MANGO 245 proteins. The nucleic acids, proteins and protein modulators are useful treating colonic disorders, inflammatory diseases, tumors,
                                                                                                                                               TANGO; MANGO; colon;
         29-JUN-1999;
                              29-JUN-2000; 2000WO-US18184
                                                     04-JAN-2001
                                                                                                  Homo sapiens
                                                                                                                                                                       Human MANGO 245
                                                                                                                                                                                             04-APR-2001
                                                                                                                                                                                                                                         AAB61477 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Isolated cDNAs encoding TANGO 244, TANGO 246, TANGO 275, TANGO 300 and MANGO 245 proteins, useful in the treatment of inflammatory diseases (e.g. idiopathic ulcerative colitis), tumors, renal disorders and liver disorders (e.g. jaundice) -
                                                                           WO200100672-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Page 260-261; 262pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Holtzman DA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29-JUN-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               present invention relates to cDNAs encoding TANGO 244,
                                                                                                                                                                                                                                                                                                     121
                                                                                                                                                                                                                                                                                                                          135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2001-050127/06
                                                                                                                                                                                                                                                                                                                                                                                                                                            122;
                                                                                                                                                                                                                                                                                                                                                 61
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                                                                                                                                                                                                                                                                                                                                                 SVMLVRNRDEVQALAFDKQRRPGARRAASQSAMLQLDYGDTVWLRLHGAPHYALGAPGAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          126 AA;
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         99US-0342687
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                                                                                                                                                                      extracellular
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MT
                                                                                                                                   cardiovascular;
                                                                                                                                                inflammation;
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 639; DB 22;
Pred. No. 1.2e-54;
3; Mismatches 1
                                                                                                                                                                       domain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      English.
                                                                                                                                                tumor; renal; liver;
                                                                                                                                    brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sharp JD
                                                                                                                                   degenerative;
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Search completed: January 12, 2004, 08:15:35 Job time : 48.1687 secs
                                                                                                                                                                                                                                                                                                                                                                                              Query Match 38.7%; Something 100.0%; I Best Local Similarity 100.0%; I Matches 123; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention relates to cDNAs encoding TANGO 244, TANGO 246, TANGO 275, TANGO 300 and MANGO 245 proteins. The nucleic acids, proteins and protein modulators are useful for treating colonic disorders, inflammatory diseases, tumors, renal disorders, liver disorders, lung disorders, autoimmune diseases, allergic diseases, cardiovascular diseases, brain disorders, degenerative diseases placental, pancreatic, skeletal and muscle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Isolated cDNAs encoding TANGO 244, TANGO 246, TANGO 275, TANGO 300 and MANGO 245 proteins, useful in the treatment of inflammatory diseases (e.g. idiopathic ulcerative colitis), tumors, renal disorders and liver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 246; 262pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 disorders (e.g. jaundice) -
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                                                                                                                                                                                                                                                                                                LGPTPGPGSSELRSAPSAARTTPLEGTSEMAVTFDKVYVNIGGDFDVATGQFRCRVPGAY
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; Pred. No. 2.9e-54;
0; Mismatches 0;
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Title:
Perfect score:
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Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                       Score
                                                                                                                                                                                                                                                                                                                                                                                                         18
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/cgn2_6/ptodata/1/pubpaa
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Copyright (c) 1993 - 2004 Compugen Ltd.
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/cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
/cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
/cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
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/cgn2_6/ptodata/1/pubpaa/US100_PUBCOMB.pep:*
/cgn2_6/ptodata/1/pubpaa/US10_Rum_PUB.pep:*
/cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
/cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*
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/cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep:*
/cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
/cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
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US-09-893-737-52

US-10-091-458-43

US-10-205-055A-2

US-09-738-973-185

US-09-854-133-185

US-10-144-649A-185

US-10-309-422-10

US-10-309-422-14

US-10-309-422-14

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US-10-236-055A-14
US-10-236-055A-16
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PUBCOMB.pep:*
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                               Sequence 2, Appli
Sequence 16, Appl
Sequence 16, Appl
Sequence 52, Appl
Sequence 2, Appl
Sequence 2, Appl
Sequence 185, App
Sequence 185, App
Sequence 10, Appl
Sequence 10, Appl
Sequence 22, Appl
Sequence 22, Appl
Sequence 7, Appl
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-085-167-2
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Publication No. US20030170781A1
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## ALIGNMENTS

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Sequence 2, Application NS/10085167

Publication N. US20030170781A1

GENERAL INFORMATION:
APPLICANT: HOLLOWAY, James L.
APPLIC
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US-10-236-055A-14
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Sequence 16, Application US/10236055A
Publication No. US20030134328A1
GENERAL INFORMATION:
APPLICANT: Basham, Beth E.
APPLICANT: Forsythe, Ian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 14, Application US/10236055A Publication No. US20030134328A1 GENERAL INFORMATION:
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SOFTWARE: PatentIn version 3.1
SEQ ID NO 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches 312;
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APPLICANT: Moshrefi, Mehrdad
APPLICANT: Moshrefi, Mehrdad
APPLICANT: Parham, Christi
TITLE OF INVENTION: MAMMALIAN GENES; RELATED REAGENTS
FILE REFERENCE: DX01343K
CURRENT APPLICATION NUMBER: US/10/236,055A
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/317,988
PRIOR APPLICATION NUMBER: US 60/317,988
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TYPE: PRT
ORGANISM: Homo sapiens
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Pred. No. 2.3e-148;
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APPLICANT: Gorman, Daniel M.
APPLICANT: Mattson, Jeanine
APPLICANT: Mattson, Jeanine
APPLICANT: Moshrefi, Mehrdad
APPLICANT: Parham, Christi
TITLE OF INVENTION: MAMMALIAN GENES; RELATED REAGENTS
FILE REFERENCE: DX01343K
CURRENT APPLICATION NUMBER: US/10/236,055A
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/317,988
PRIOR APPLICATION NUMBER: US 60/317,988
PRIOR FILING DATE: 2001-09-06
NUMBER OF SEQ ID NOS: 36
SOFTWARE: PatentIn version 3.1
SEQ ID NO 16
                                                                                          ; TYPE: PRT
; ORGANISM: Homo
US-09-893-737-52
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                                                                                                                                                     PRIOR APPLICATION NUMBER: US 60/215,446
PRIOR FILING DATE: 2000-06-30
NUMBER OF SEQ ID NOS: 329
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 52
LENGTH: 252
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Matches
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Patent No. US20020110855A1
Best Local Similarity 43.0 Matches 65; Conservative
                                             Query Match
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TYPE: PRT
ORGANISM: Mus r
                                                                                                                                                                                                                                                                                                                                            APPLICANT: Sheppard, Paul O.
APPLICANT: Presnell, Scott R.
TITLE OF INVENTION: MAMMALIAN SECRETED PROTEINS
FILE REFERENCE: 00-41
                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/893,737
CURRENT FILING DATE: 2001-06-28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 FFSFTAGKAPHKSLSVMLVRNRDEVQALAFDEQRRPGARRAASQSAMLQLDYGDTVWLRL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17 LGPA-GPGSSELRSAFSAARTTPLEGTSEMAVTFDKVYVNIGGDFDAATGRFRCRVPGAY 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 LGPTPGPGSSELRSAFSAARTTPLEGTSEMAVTFDKVYVNIGGDFDVATGOFRCRVPGAY 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RHQPLAFDTEFVNIGGDFDAAAGVFRCRLPGAYFFSFTLGKLPRKTLSVKLMKNRDEVQA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAGPPALKPPEL 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PAAPPGLGASEL 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MIYDDGASRRREMQSQSVMLPLRRGDAVWLLSHDHDGYGAYSNHGKYITFSGFLVYPDLA 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MIYDDGASRRREMQSQSVMLALRRGDAVWLLSHDHDGYGAYSNHGKYITFSGFLVYPDLA 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RHRPLAFDTELVNIGGDFDAAAGVFRCRLPGAYFFSFTLGKLPRKTLSVKLMKNRDEVQA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FFSFTAGKAPHKSLSVMLVRNRDEVQALAFDEQRRPGARRAASQSAMLQLDYGDTVWLRL
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                          14.5%; Score 237.5; DB 10; Length 252; 43.0%; Pred. No. 1.4e-14;
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  12; Mismatches
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Pred. No. 6.1e-137;
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       Indels
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    13;
    Gaps
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152 GPPAPPEPR--SAFSAARTRSLVGSDAGPGPRHQPLAFDTEFVNIGGDFDAAAGVFRCRL 209

; PRIOR FILING DATE: 2000-08-14	PRIOR APPLICATION NUMBER: 60/241.809	יי יי קים
FILING DATE	APPLICATION NUMBER	; PR
; PRIOR FILING DATE: 2000-08-14 : PRIOR APPLICATION NUMBER: 60/227,182	PRIOR FILING DATE: 2000-08-14	יי יי על על
APPLICATION N	FILING DATE: 2000-09-29	; PR
FILING DATE: 2000-08-14	APPLICATION NUMBER: 60	; PR
; PRIOR FILING DATE: 2000-08-22	PRIOR FILING DATE: 2000-08-14	
APPLICATION N	FILING DATE: 2000-08-30	, PR
; PRIOR FILING DATE: 2000-11-17	APPLICATION NUMBER	, pg
FILING DATE: 2000-11-17		, , , , , , , , , , , , , , , , , , ,
APPLICATION N	FILING DATE: 2000-09-21	; PR
FILING DATE: 2000-11-08	APPLICATION NUMBER	; PR
; PRIOR FILING DATE: 2000-11-08	PRIOR APPLICATION NUMBER: 60/235,834	 D. P. R.
APPLICATION N	FILING DATE: 2000-12-08	; PR
	APPLICATION N	, PR
7241	ATION NUMBER	. ,. PR
APPLICATION N	FILING DATE: 2000-07-07	; PR
; PRIOR FILING DATE: 2000-10-13	PRIOR APPLICATION NUMBER: 60/216,880	. PR
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APPLICATION N	FILING DATE: 2000-07-07	; PR
FILING DATE: 2000-1	APPLICATION N	; PR
; PRIOR FILING DATE: 2000-10-02	DRIOR APPLICATION NUMBER: 60/226,868	. ;
APPLICATION N	FILING DATE: 2000-08-14	; PR
FILING DATE:	APPLICATION NUMBER: 60	; PR
; PRIOR FILING DATE: 2000-09-29	DRIOR FILING DATE: 00/0718,290	
APPLICATION N	FILING DATE: 2000-08-14	; PR
	APPLICATION N	; PR
; PRIOR APPLICATION NUMBER: 60/237,038	PRIOR FILING DATE: 2000-07-11	אַק
APPLICATION N	FILING DATE: 2000-07-2	; PR
FILING DATE:	APPLICATION NUMBER: 60	; PR
; PRIOR APPLICATION NUMBER: 60/236,367	PRIOR FILING DATE: 2000-08-14	 קים
APPLICATION N	FILING DATE: 2000-07-11	
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; PRIOR ELLING DATE: 2000-09-05	PRIOR FILING DATE: 2000-166-28	. י. על
APPLICATION N	FILING DATE: 2000-02-04	, PR
FILING DATE: 2000-09-01	APPLICATION N	; PR
; PRIOR FILING DATE: 2000-09-01	DRICK REFLICATION NUMBER: 60/179,065	
APPLICATION N	FILING DATE: 2001-01-17	, PR
: PRIOR FILING DATE: 2000-09-01	PRIOR APPLICATION NUMBER: 09/764, 900	, ,
FILING DATE: 2000-09	APPLICATION NU	
z	REFE	; FI
APPLICATION N	NT: Rosen et al.	. ; AF
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; PRIOR FILING DATE: 2000-12-08	Sequence 43, Application US/10091458 Publication No. US200100646677A1	. Seg
APPLICATION N	091-458-4	US-10
; PRIOR APPLICATION NUMBER: 60/236,368 ; PRIOR FILING DATE: 2000-09-29	17.5	RESULT
FILING DATE: 2000-08		;
; PRIOR FILING DATE: 2000-11-01	219 VRMFORDRUN-AIYGRHGDIV-TPSGHTUKD 248	D b
APPLICATION N	270LLSHDHDGYGAYSNHGK-YITFSGFLYYP 297	Ş
; PRIOR APPLICATION NUMBER: 60/241,785 : PRIOR FILING DATE: 2000-10-20	161 PGVYFLSLNVHTWNYKETYLHIMLNR-RPAAVLYAQ-PSERSVMQAQSLMLLLAAGDAVW 218	Дb
FILING DATE: 2000-09	- CATTLE SET LEGALETA LEGA PARTITUD A STATE CONTROL OF A STATE CONTROL	5
FILING DATE: 2000-11		?
<pre>; PRIOR FILING DATE: 2000-10-20 ; PRIOR APPLICATION NUMBER: 60/249,299</pre>	106 GPPGAACRRAYAAFSVGRREGLHSSDHFQAVPFDTELVNLDGAFDLAAGRFLCTV 160	Дb

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Matches
                                       Query Match
                                                                                                                                                                                                                                                                                                 OR FILING DATE: 2000-09-08
OR APPLICATION NUMBER: 60/233,064
OR FILING DATE: 2000-09-14
OR APPLICATION NUMBER: 60/232,397
OR APPLICATION NUMBER: 60/232,397
OR FILING DATE: 2000-09-14
OR APPLICATION NUMBER: 60/232,397
OR APPLICATION NUMBER: 60/232,399
OR FILING DATE: 2000-09-14
OR APPLICATION NUMBER: 60/232,401
OR APPLICATION NUMBER: 60/232,401
OR APPLICATION NUMBER: 60/232,401
OR APPLICATION NUMBER: 60/234,808
OR APPLICATION NUMBER: 60/241,808
Local Similarity nes 63; Conserv
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APPLICATION NUMBER: 60/232,080
FILING DATE: 2000-09-08
APPLICATION NUMBER: 60/231,414
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APPLICATION NUMBER: 60/241,221
FILING DATE: 2000-10-20
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FILING DATE: 2000-09-08
APPLICATION NUMBER: 60/232,081
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APPLICATION NUMBER: 60/249,215
FILING DATE: 2000-11-17
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FILING DATE: 2000-11-17
APPLICATION NUMBER: 60/249,211
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FILING DATE: 2000-11-17
APPLICATION NUMBER: 60/249,244
FILING DATE: 2000-11-17
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APPLICATION NUMBER: 60/249,207
FILING DATE: 2000-11-17
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APPLICATION NUMBER: 60/249,213
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APPLICATION NUMBER: 60/249,218
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                                                                               APPLICATION NUMBER: 60/246,475
FILING DATE: 2000-11-08
APPLICATION NUMBER: 60/231,243
FILING DATE: 2000-09-08
                                                                                                                                                                                                                          APPLICATION NUMBER: 60/241,786
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APPLICATION NUMBER: 60/241,826
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APPLICATION NUMBER: 60/249,214
FILING DATE: 2000-11-17
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APPLICATION NUMBER: 60/249,208
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                       14.0%; Score 230; DB 15; 38.4%; Pred. No. 5.5e-14;
16;
  Mismatches
                                         Length 202;
    Indels
    22;
  Gaps
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; LENGTH: 420
; TYPE: PRT
; ORGANISM: Homo s
US-10-236-055A-2
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; Sequence 185, Application US/09738973
; Patent No. US20020110563A1
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US-10-236-055A-2
                                                                                                                                                                                                                                                GENERAL INFORMATION
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Best Local Similarity
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CURRENT APPLICATION NUMBER: US/10/236,055A
CURRENT FILING DATE: 2003-02-28
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TITLE OF INVENTION: MAMMALIAN GENES; RELATED REAGENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
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                                    APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn version 3.1
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                  PPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                    381 NHAILQLFQGDQIWLRLH----RGAIYGSSWKYSTFSGYLLYQD 420
                                                                                                                                                                                                                                                                                                                                                                                                          256 QSVMLALRRGDAVWLLSHDHDGYGA-YSNHGKYITFSGFLVYPD 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                322 TFDLQLGRFNCPVNGTYVFIFHMLKLAVNVPLYVNLMKNEEVLVSAYANDGAP-DHETAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      197 DFDAAAGVFRCRLPGAYFFSFTLGKLP-RKTLSVKLMKNRDEVQAMIYDDGASRRREMQS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      267 DVPVTNPAATILPVHVYPLPQQMRVAFSAART----SNLAPGTLDQPIVFDLLLNNLGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      147 DAPARGP------PAPPEPRSAFSAARTRSLVGSDAGPGPRHQPLAFDTEFVNIGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             256 QSVMLALRRGDAVWLLSHDHDGYGA-YSNHGKYITFSGFLVYPD 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 104 TFDLQLGRFNCPVNGTYVFIFHMLKLAVNVPLYVNLMKNEEVLVSAYANDGAP-DHETAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         147 DAPARGP-----PAPPEPRSAFSAARTRSLVGSDAGPGPRHQPLAFDTEFVNIGG 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2, Application US/10236055A ion No. US20030134328A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      63;
INVENTION:
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                                  Secrist, Heather
Indirias, Carol Y
Benson, Darin R.
Elliot, Mark
Mannion, Jane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DFDAAAGVFRCRLPGAYFFSFTLGKLP-RKTLSVKLMKNRDEVQAMIYDDGASRRREMQS 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DVPVTNPAATILPVHVYPLPQQMRVAFSAART----SNLAPGTLDQPIVFDLLLNNLGE 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mattson, Jeanine
Moshrefi, Mehrdad
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Forsythe, Ian
Gorman, Daniel M.
                Mannion, Jane
Kalos, Michael D
                                                                                                                                Mohamath, Raodoh
Algate, Paul A.
                                                                                                                                                                                          Henderson, Robert
Lodes, Michael J.
                                                                                                                                                                      Fling,
                                                                                                                                                                                                                            Reed, Steven G.
                                                                                                                                                                                      Lodes,
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                                                                                                                                                                      Steven P.
COMPOSITIONS AND METHODS FOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14.0%; Score 230; DB 12; 38.4%; Pred. No. 1.5e-13;
                                                                                            Yoseph
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16; Mismatches
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US-09-854-133-185; Sequence 185, Application US/09854133; Publication No. US20020183499A1
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                                       RESULT 9
US-10-144-649A-185
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NUMBER OF SEQ ID NOS: 735
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 185
LENGTH: 746
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Best Local Similarity
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APPLICANT: Secrist, Heather
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: THE THERAPY AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.475C10
CURRENT APPLICATION NUMBER: US/09/854,133
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CURRENT APPLICATION NUMBER: US/09/738,973
CURRENT FILING DATE: 2000-12-14
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SOFTWARE: FastSEQ for
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APPLICANT: Mohamath, Raodoh
APPLICANT: Henderson, Rober
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LENGTH: 746
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es 63; Conser
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                                                                                                                                                                                                                                                                                                           593 DVPVTNPAATILPVHVYPLPQQMRVAFSAART----SNLAPGTLDQPIVFDLLLNNLGE
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185, Application US/10144649A ion No. US20030118599A1
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                                                                                                                              NHAILQLFQGDQIWLRLH----RGAIYGSSWKYSTFSGYLLYQD 746
                                                                                                                                                                                                                        TFDLQLGRFNCPVNGTYVF1FHMLKLAVNVPLYVNLMKNEEVLVSAYANDGAP-DHETAS
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; Pred. No. 3.2e-13;
16; Mismatches 63;
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Pred. No. 3.2e-13;
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Best Local :
                                                                                                                                                                                                                  Matches
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CURRENT FILING DATE: 2002-12-03
PRIOR APPLICATION NUMBER: US/09/798,771
PRIOR FILING DATE: 2001-03-02
PRIOR FILING DATE: 2001-03-02
PRIOR APPLICATION NUMBER: US 60/186,557
PRIOR FILING DATE: 2000-03-02
NUMBER OF SEQ ID NOS: 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/10/144,649A CURRENT FILING DATE: 2002-08-21 NUMBER OF SEQ ID NOS: 749
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APPLICANT: McNeill, Patricia D.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FO
TITLE OF INVENTION: THE THERAPY AND DIAGNOSIS
FILE REFERENCE: 210121.475C11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Wilganowski, Nathaniel L. APPLICANT: Turner, C. Alexander Jr. TITLE OF INVENTION: NO. US20030139587A1el Human FILE REFERENCE: LEX-0142-USA
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ORGANISM: Homo sapien
                                                                                                                                                                                                                                                                                                                     ORGANISM: homo sapiens
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                                                                                    197 DFDAAAGVFRCRLPGAYFFSFTLGKLP-RKTLSVKLMKNRDEVQAMIYDDGASRRREMQS
                                                                                                                              755 DVPVTNPAATILPVHVYPLPQQMRVAFSAART----SNLAPGTLDQPIVFDLLLNNLGE 809
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  256 QSVMLALRRGDAVWLLSHDHDGYGA-YSNHGKYITFSGFLVYPD 298
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38.4%; Pred. No. 4.2e-13;
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; Pred. No. 3.2e-13;
16; Mismatches 63;
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6; Mismatches
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                                                                                                                                                                                                                                                       Length 908;
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147 DAPARGP-----PAPPEPRSAFSAARTRSLVGSDAGPGPRHQPLAFDTEFVNIGG 196

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RESULT 12
US-10-309-422-14
; Sequence 14, Application US/10309422
; Publication No. US20030139587A1
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Warches 63; Conserve
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                                                                                           ORGANISM: homo sapiens
US-10-309-422-14
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; ORGANISM: homo
US-10-309-422-22
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CURRENT APPLICATION NUMBER: US/10/309,422
CURRENT FILING DATE: 2002-12-03
PRIOR APPLICATION NUMBER: US/09/798,771
PRIOR FILING DATE: 2001-03-02
PRIOR APPLICATION NUMBER: US 60/186,557
PRIOR FILING DATE: 2000-03-02
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       Matches
                                                    Query Match
                                                                                                                                                                                         SEQ ID NO 14
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                                                                                                                                                                                                                                                               APPLICANT: Walke, D. Wade
APPLICANT: Wilganowski, Nathaniel L.
APPLICANT: Wilganowski, Nathaniel L.
APPLICANT: Turner, C. Alexander Jr.
APPLICANT: TURNERTION: No. US20030139587A1el Human Proteins and Polynucleotides Encoding
FILE REFERENCE: LEX-0142-USA
CURRENT APPLICATION NUMBER: US/10/309,422
CURRENT APPLICATION NUMBER: US/09/798,771
PRIOR APPLICATION NUMBER: US/09/798,771
PRIOR PRIOR PILING DATE: 2001-03-02
PRIOR PILING DATE: 2001-03-02
PRIOR APPLICATION NUMBER: US/09/798,757
                                                                                                                                                                                                               NUMBER OF SEQ ID NOS: 43
SOFTWARE: FastSEQ for Windows Version 4.0
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APPLICANT: Wilganowski, Nathaniel L.
APPLICANT: Turner, C. Alexander Jr.
TITLE OF INVENTION. NO. US20030139587A1el Human Proteins and Polynucleotides Encoding
                                                                                                                                                                                                                                                          PRIOR FILING DATE: 2000-03-02
                                                                                                                                              LENGTH: 957
TYPE: PRT
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    Local Similarity
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       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sapiens
14.0%; Score 230; DB 12; 38.4%; Pred. No. 4.5e-13; 16: Mismatches 63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14.0%;
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Pred. No. 4.2e-13;
6; Mismatches 63;
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                                                Length 957;
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    Indels
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Sequence 18, Application US/10309422

Publication No. US20030139587A1

GENERAL INFORMATION:
APPLICANT: Walke, D. Wade
APPLICANT: Wilganowski, Nathaniel L.
APPLICANT: Turner, C. Alexander Jr.
TITLE OF INVENTION: No. US20030139587A1el Human Pro
FILE REFERENCE: LEX-0142-USA
CURRENT APPLICATION NUMBER: US/10/309,422
CURRENT FILING DATE: 2002-12-03
PRIOR APPLICATION NUMBER: US/9/798,771
PRIOR APPLICATION NUMBER: US 60/186,557
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; TYPE: PRT
; ORGANISM: homo sapiens
US-10-309-422-26
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US-10-309-422-26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
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NUMBER OF SEQ ID NOS: 43
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Wilganowski, Nathaniel L.
APPLICANT: Turner, C. Alexander Jr.
TITLE OF TURENTION. NO. US20030139587A1el Human Proteins and Polynucleotides Encoding
FILE REFERENCE: LEX:-0142-USA
CURRENT APPLICATION NUMBER: US/10/309,422
CURRENT FILING DATE: 2002-12-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: US 60/186,557
PRIOR FILING DATE: 2000-03-02
NUMBER OF SEQ ID NOS: 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Walke, D. Wade APPLICANT: Wilganowski, I
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         805 DVPVTNPAATILPVHVYPLPQQMRVAFSAART----SNLAPGTLDQPIVFDLLLNNLGE 859
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      197 DFDAAAGVFRCRLPGAYFFSFTLGKLP-RKTLSVKLMKNRDEVQAMIYDDGASRRREMQS 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            147 DAPARGP-----PAPPEPRSAFSAARTRSLVGSDAGPGPRHQPLAFDTEFVNIGG 196
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   256 QSVMLALRRGDAVWLLSHDHDGYGA-YSNHGKYITFSGFLVYPD 298
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SEQ ID

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FILE REFERENCE: LEX-0142-USA
CURRENT APPLICATION NUMBER: US/10/309,422
CURRENT FILING DATE: 2002-12-03
PRIOR APPLICATION NUMBER: US/09/798,771
PRIOR FILING DATE: 2001-03-02
PRIOR APPLICATION NUMBER: US 60/186,557
PRIOR FILING DATE: 2000-03-02
NUMBER OF SEQ ID NOS: 43
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 30
LENGTH: 993
TYPE: PRT
ORGANISM: homo sapiens
US-10-309-422-30
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US-10-309-422-30
US-10-309-422-30
JOS-10-309-422-30
Sequence 30, Application US/10309422
Sequence 30, Application US/20030139587A1
GENERAL INFORMATION:
GENERAL INFORMATION:
Wilganowski, Nathaniel L.
APPLICANT: Wilganowski, Nathaniel L.
APPLICANT: Turner, C. Alexander Jr.
APPLICANT: Turner, C. Alexander Jr.
TITLE OF INVENTION: No. US20030139587A1el Human Proteins and Polynucleotides Encoding
Search completed: January 12, 2004, 08:33:36 Job time: 39.1098 secs
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; TYPE: PRT
; ORGANISM: homo sapiens
US-10-309-422-18
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 63; Conserv
                                                                                                                                                                                                                  895 TFDLQLGRFNCPVNGTYVFIFHMLKLAVNVPLYVNLMKNEEVLVSAYANDGAP-DHETAS 953
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                                                                                                                                                      256 QSVMLALRRGDAVWLLSHDHDGYGA-YSNHGKYITFSGFLVYPD 298
                                                                                                                                                                                                                                                                   197 DFDAAAGVFRCRLPGAYFFSFTLGKLP-RKTLSVKLMKURDEVQAMIYDDGASRRREMQS 255
                                                                                                                                                                                                                                                                                                                              840 DVPVTNPAATILPVHVYPLPQQMRVAFSAART----SNLAPGTLDQPIVFDLLLNNLGE 894
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                                                                                                         954 NHAILQLFQGDQIWLRLH----RGAIYGSSWKYSTFSGYLLYQD 993
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                                                                                                                                                                                                                                                                                                                                                                                                                                     14.0%; Score 230; DB 12; Length 993;
38.4%; Pred. No. 4.7e-13;
ative 16; Mismatches 63; Indels 2
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Result
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Maximum Match 100%
Listing first 45 summaries
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        Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed,
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        Score
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seq length:
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Sequence 2, Appli
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Sequence 295, App
Sequence 11, Appl
Sequence 10, Appl
Sequence 294, App
Sequence 198, App
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Sequence 44, Application US/09118408A
Patent No. 626544
GENERAL INFORMATION:
APPLICANT: Sheppard, Paul O.
TITLE OF INVENTION: ADIPOCYTE-SPECIFIC PROTEIN HOMOLOGS
FILE REFERENCE: 97-30
CURRENT APPLICATION NUMBER: US/09/118,408A

RESULT 2 US-09-118-408-44

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RESULT 3
US-09-506-855-44
; Sequence 44, Application US/09506855
; Patent No. 6448221
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                  GENERAL INFORMATION: APPLICANT: Sheppard
                                                      Sequence 44, Application US/09911176B
Patent No. 6518403
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SEQ ID NO 44
LENGTH: 281
TYPE: PRT
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LENGTH: 281
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ORGANISM: Mus musculus
-09-118-408-44
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EARLIER APPLICATION NUMBER: 60/053,154
EARLIER FILING DATE: 1997-07-18
NUMBER OF SEQ ID NOS: 47
SOFTWARE: FastSEQ for Windows Version 3.0
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CURRENT APPLICATION NUMBER: US/09/506,855
CURRENT FILING DATE: 2000-02-17
NUMBER OF SEQ ID NOS: 50
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APPLICANT: Lasser, Gerald W.
APPLICANT: Bishop, Paul D.
TITLE OF INVENTION: INHIBITORS FOR USE IN HEMOSTASIS
TITLE OF INVENTION: IMMUNE FUNCTION
APPLICANT: Sheppard, Paul O. TITLE OF INVENTION: ANTIBODIES THAT BIND
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nes 56; Conservative
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                                                                                                                                                                            TWNQKETYLHIMKNEEEV-VILYAQ-VSDRSIMQSQSLMMELREEDEVWVRLFKGERENA 258
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39.2%; Pred. No. 1.8e-14;
ative 20; Mismatches 58; Indels 9
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LENGTH: 281
TYPE: PRT
ORGANISM: Mus musculus
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CURRENT FILING DATE: 2000-07-19
PRIOR APPLICATION NUMBER: 09/253,604
PRIOR FILING DATE: 1999-02-19
PRIOR APPLICATION NUMBER: 09/444,794
PRIOR FILING DATE: 1999-11-22
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PRIOR FILING DATE: 1997-07-18
NUMBER OF SEQ ID NOS: 52
SOFTWARE: FastSEQ for Windows Version 3.0
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CURRENT APPLICATION NUMBER: US/09/911,176B
CURRENT FILING DATE: 2001-07-23
PRIOR APPLICATION NUMBER: 09/118,408
PRIOR FILING DATE: 1998-07-17
PRIOR FILING DATE: 1998-07-17
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TYPE: PRT
ORGANISM: Mus (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: 09/506,855
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILE REFERENCE: 99-12C3
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                                                                                                      221 KLPRKTLSVKLMKNRDEVQAMIYDDGASRRREMQSQSVMLALRRGDAVW--LLSHDHDGY 278
                                                                                                                                            146 AAFSVGRKKALHSND-----YFQPVVFDTEFVNLYKHFNMFTGKFYCYVPGIYFFSLNVH
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Similarity 39.2%; Pred. No. 1.8e-14;
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                                                             TWNOKETYLHIMKNEEEV-VILYAQ-VSDRSIMOSOSLMMELREEDEVWVRLFKGERENA 258
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FastSEQ for Windows Version 3.0
GAYSNHGKYITFSGFLVYPDLAP 301
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US-09-506-852-44
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APPLICANT: Sheppard, Paul O.
TITLE OF INVENTION: ADIPOCYTE-SPECIFIC PROTEIN HOMOLOGS
FILE REFERENCE: 97-30
CURRENT APPLICATION NUMBER: US/09/118,408A
CURRENT FILING DATE: 1998-07-17
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APPLICANT: Sheppard, Paul O.
TITLE OF INVENTION: ADIPOCYTE-SPECIFIC PROTEIN HOMOLOGS
FILE REFERENCE: 97-30
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LENGTH: 281
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                                                                                                                                                                                                                                                                                                                                                                                SEQ ID NO 2
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NUMBER OF SEQ ID NOS: 44
SOFTWARE: FastSEQ for Windows Version
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CURRENT FILING DATE: 2000-02-17
EARLIER APPLICATION NUMBER: 60/053,154
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                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                  LENGTH: 281
TYPE: PRT
ORGANISM: Homo sapien
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            279 GAYSNHGKYITFSGFLVYPDLAP 301
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 161 SAFSAARTRSLVGSDAGFGFRHQFLAFDTEFVNIGGDFDAAAGVFRCRLFGAYFFSFTLG 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      259 IFSDEFDTYITFSGYLVKPASEP 281
                                                                                                                                                                   53 RCRVPGAYFFSFTAGKAPHKSLSVMLVRNRDEVQALAFDEQRRPGARRAASQSAMIQLDY 112
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TRSLVGSDAGPGPRH-----QPLAFDTEFVNIGGDFDAAAGVFRCRLPGAYFFSFTLGKL
                                            GKTGSAGARGHTGPKGQKGSMGAPGERCKSH--YA-
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                                                                                   GDT--VWLRLHGAP---HYALGAPGATFSGYLVYADADADAPARGPPAPPEPRSAFSAAR 167
                                                                                                                           RCCDPGTSMYPATA--VPQINITILKGEKGDR------GDRG-----LQGKY 113
                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                             13.1%; Score 215; DB 3; Length 281; 30.2%; Pred. No. 6.6e-14; tive 26; Mismatches 86; Indels
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Pred. No. 1.8e-14;
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; TYPE: PRT
; ORGANISM: Homo sapien
US-09-506-855-2
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US-09-911-176B-2
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 2
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APPLICANT: Sheppard, Paul O.
APPLICANT: Lasser, Gerald W.
APPLICANT: Bishop, Paul D.
                                                                                                                                                                                                     Sequence 2, Application US/09911176B Patent No. 6518403
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TITLE OF INVENTION: IMMUNE FUNCTION
FILE REFERENCE: 99-12
CURRENT APPLICATION NUMBER: US/09/506,855
CURRENT FILING DATE: 2000-02-17
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CURRENT APPLICATION NUMBER: US/09/911,176B
CURRENT FILING DATE: 2001-07-23
PRIOR APPLICATION NUMBER: 09/118,408
PRIOR FILING DATE: 1998-07-17
PRIOR APPLICATION NUMBER: 60/053,154
                                                                                                BENERAL INFORMATION:

APPLICANT: Sheppard, Paul O.

TITLE OF INVENTION: ANTIBODIES THAT BIND AN

TITLE OF INVENTION: ADIPOCYTE-SPECIFIC PROF

FILE REFERENCE: 97-3001
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Similarity 30.2%;
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Pred. No. 6.6e-14;
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; SEQ ID NO 2
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-911-176B-2
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US-09-619-740-2
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APPLICANT: Sheppard;
APPLICANT: Lasser, G
APPLICANT: Bishop, P
TITLE OF INVENTION:
                                                                                                                                                                                                         13.1%; Score 215; DB 4; Length 281; Best Local Similarity 30.2%; Pred. No. 6.6e-14; Matches 77; Conservative 26. Minor 1
                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE:
SEQ ID NO 2
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Best Local S
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PRIOR FILING DATE: 2000-02-17
NUMBER OF COLUMBER 2000-02-17
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SOFTWARE: FastSEQ for Windows Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILE REFERENCE: 99-12C3
CURRENT APPLICATION NUMBER: US/09/619,740
CURRENT FILING DATE: 2000-07-19
PRIOR APPLICATION NUMBER: 09/253,604
PRIOR FILING DATE: 1999-02-19
PRIOR APPLICATION NUMBER: 09/444,794
PRIOR FILING DATE: 1999-11-22
PRIOR FILING DATE: 1999-11-22
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                                                                                                                                                                                                                                                                                                                  LENGTH: 281
TYPE: PRT
ORGANISM: Homo sapien
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FastSEQ for Windows Version
TRSLVGSDAGPGPRH-----QPLAFDTEFVNIGGDFDAAAGVFRCRLPGAYFFSFTLGKL 222
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                                                         GKTGSAGARGHTGPKGOKGSMGAPGERCKSH--YA--
                                                                                                  GDT--VWLRLHGAP---HYALGAPGATFSGYLVYADADADAPARGPPAPPEPRSAFSAAR 167
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Lasser, Gerald W.
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US-09-506-852-2
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US-09-336-536-4
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CURRENT APPLICATION NUMBER: US/09/336,536
CURRENT FILING DATE: 1999-06-18
NUMBER OF SEQ ID NOS: 75
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 4
LENGTH: 228
TYPE: PRT
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Best Local S
Matches 77
                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Leiby, K.
APPLICANT: McKay, C.
APPLICANT: BOSSONE, S.
APPLICANT: BOSSONE, S.
APPLICANT: BOSSONE, S.
APPLICANT: BOSSONE, S.
APPLICANT: MCKay, C.
A
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APPLICANT: Sheppard, Paul O.
TITLE OF INVENTION: ADIPOCYTE-SPECIFIC PROTEIN HOMOLOGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 2, Application US/09506852
Patent No. 6566499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 4, Application US/09336536 Patent No. 6406884
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CURRENT APPLICATION NUMBER: US/09/506,852
CURRENT FILING DATE: 2000-02-17
CURRENT PILING DATE: 2000-02-17
EARLIER APPLICATION NUMBER: 60/053,154
EARLIER FILING DATE: 1997-07-18
NUMBER OF SEQ ID NOS: 44
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TYPE: PRT
ORGANISM: Homo sapien
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les 77; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           113 GDT--VWLRLHGAP---HYALGAPGATFSGYLVYADADADAPARGPPAPPEPRSAFSAAR 167
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30.2%; Pred. No. 6.6e-14;
1tive 26; Mismatches 86;
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APPLICANT: Sheppard, Paul O.

APPLICANT: Humes, Jacqueline M.

TITLE OF INVENTION. ADIPOCYTE-SPECIFIC PROTEIN HOMOLOGS

FILE REFERENCE: 97-49

CURRENT APPLICATION NUMBER: US/09/140,804

CURRENT FILING DATE: 1998-08-26

EARLIER APPLICATION NUMBER: 60/056,983

EARLIER APPLICATION NUMBER: 50/056,983

EARLIER FILING DATE: 1997-08-26

NUMBER OF SEQ ID NOS: 47

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 2

LENGTH: 243
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; ORGANISM: Homo sapiens
US-09-140-804-2
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                                                                                                                                   RESULT 14
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US-09-140-804-2
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GENERAL INFORMATION:
APPLICANT: Leiby, K.
APPLICANT: McKay, C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 13.0%; Score 213; DB 3; Length 243; Best Local Similarity 34.9%; Pred. No. 8.6e-14; Matches 66; Conservative 18; Mismatches 83; Indels
                                                                 Sequence 3, Application US/09336536 Patent No. 6406884
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Patent No. 6197930
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les 66; Conserv
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                                                                                                                                                                                                                              FSGFLVYPD 298
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                                                                                                                                                                                                     FSGFLVYSD 235
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              GAP----GAPGEKGEGGRPGLPGPRGDPGPRGEAGPAGPTGPAGECSVPPRSAFSAKRSE 112
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SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 3
; LENGTH: 243
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-336-536-3
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                                                                                                                                                                                                                                                                                   Query Match 13.0%; Score 213; DB 4; Length 243; Best Local Similarity 34.9%; Pred. No. 8.6e-14; Matches 66; Conservative 18; Mismatches 83; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 2, Application US/09686838B Patent No. 6482612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/686,838B CURRENT FILING DATE: 2000-10-10 PRIOR APPLICATION NUMBER: US 09/140,804 PRIOR FILING DATE: 1998-08-26 PRIOR APPLICATION NUMBER: US 60/056,983 PRIOR FILING DATE: 1997-08-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Sheppard, Paul O.
APPLICANT: Humes, Jacqueline M.
TITLE OF INVENTION: Adipocyte-Specific Protein
FILE REFERENCE: 97-49D1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/336,536
CURRENT FILING DATE: 1999-06-18
NUMBER OF SEQ ID NOS: 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Bossone, S. TITLE OF INVENTION: SECRETED PROTEINS AND USES FILE REFERENCE: 7853-144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 50
                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 243
TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              y Match 13.0%; Score 213; DB 4; Length 243;
Local Similarity 34.9%; Pred. No. 8.6e-14;
hes 66; Conservative 18; Mismatches 83; Indels
  167
                                            230 KLMKNRDEVQAMIYDDGASRRREMQSQSVMLALRRGDAVWLLSHDHDGYGAYSNHGKYIT 289
                                                                                                                                          170 SLVGSDAGPGPRHQPLAFDTEFVNIGGDFDAAAGVFRCRLPGAYFFSFTLGKLPRKTLSV 229
                                                                                                                                                                                                                                      122 GAPHYALGAPGATFSG---YLVYADAD----ADAPARGPPAPP----EPRSAFSAARTR 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              290 FSGFLVYPD 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                167 DLVKNGESIASFFQFFGGWPKPASLSGGAMVRLEPEDQVWVQVGVGDYIGIYASIKTDST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          230 KLMKNRDEVQAMIYDDGASRRREMQSQSVMLALRRGDAVWLLSHDHDGYGAYSNHGKYIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            113 ŚRV----PPPSDAPLPFDRVLVNEQGHYDAVTGKFTCQVPGVYYFA-VHATVYRASLQF 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      170 SLVGSDAGPGPRHQPLAFDTEFVNIGGDFDAAAGVFRCRLPGAYFFSFTLGKLPRKTLSV 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    122 GAPHYALGAPGATFSG---YLVYADAD----ADAPARGPPAPP-----EPRSAFSAARTR 169
                                                                                                                                                                                            57 GAP----GAPGEKGEGGRPGLPGPRGDPGPRGEAGPAGPTGPAGECSVPPRSAFSAKRSE 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       57 GAP----GAPGEKGEGGRPGLPGPRGDPGPRGEAGPAGPTGPAGECSVPPRSAFSAKRSE 112
  DLVKNGESIASFFQFFGGWPKPASLSGGAMVRLEPEDQVWVQVGVGDYIGIYASIKTDST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FSGFLVYSD 235
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Qy 290 FSGFLVYPD 298
|||||||
|Db 227 FSGFLVYSD 235

Search completed: January 12, 2004, 08:20:04
Job time: 16.9311 secs

GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 12, 2004, 08:12:09; Search time 9.84032 Seconds (without alignments) 1661.397 Million cell updates/sec

Title: Perfect score: US-10-085-167-2\_COPY\_160\_358 894

1 ADADAPARGPPAPPEPRSAF.....LVYPDLAPAAPPGLGASELL 170

Scoring table:

Searched:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters: 283308

283308 seqs, 96168682 residues

Minimum DB Maximum DB seq length: 0
seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

pir1:\*
pir2:\*
pir3:\*
pir4:\*

Database

PIR\_76:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

29	28	27	26	20	24	23	22	21	20	19	18	17	16	15	. 14	13	12	11	10	9	80	7	9,	່ທ	4	w	2	_	Result No.	
82.5	85	85	123.5	129	•	•	134	135.5	143	144	150.5	153	154.5	155.5	160.5	163	163	163.5	164	164	165.5	165.5	166.5	170	175	177.5	182	0	Score	
9.2	9.5	9.5	٠	14.4	14.5	14.8		15.2			16.8	17.1	17.3	٠	18.0	18.2	18.2	18.3	٠	•	18.5	•	8	•	19.6	19.9	20.4	23.3	Query	4
472	1228	589	423	992	170	635	245	245	196	215	253	193	743	246	744	674	224	744	680	680	744	253	674	245	244	215	253	219	Length	
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E98020	A57384	H83085	A55797	T08772	B57131	A57131	819018	C1HUQA	A48150	C48150	I49560	A37873	S23779	S29328	S15435	S13301	A60032	A34246	\$31216	CGHU1D	S23298	\$49158	S23297	C1HUQC	JC4708	B48150	СІНООВ	T14782	ID	
_		conserved hypothet	collagen precursor	н	alpha	$\mathbf{L}$	complement subcomp	complement subcomp	hibernation-relate	n-relat		n precu	collagen alpha 1(V	t subc	collagen alpha 1(V	n alpha 1 (	in-like c	alpha 1	lagen alpha 1	alpha 1	pha 1	complement protein	collagen alpha 1(x	얼	gelatin-binding 28	3	вирсош	hypothetical prote	tion	

RESULT 2 C1HUQB

complement subcomponent Clq chain B precursor [validated] - human N;Alternate names: complement subcomponent Clq beta chain C;Species: Homo sapiens (man) C;Date: 22-May-1981 #sequence revision 31-May-1996 #text\_change 08-Dec-2000 C;Accession: B23422; A3422; B90304; A90301; B90315; A03206 R;Reid, K.B.M. B3422; A3422; B90304; A90301; B90315; A03206 R;Reid, K.B.M. Molecular cloning and characterization of the complementary DNA and gene codin: A;Reference number: A23422; MUID:86076906; PMID:3000358

A;Molecule type: DNA A;Residues: 'HS',1-32 <REI> A;Note: the authors translated the codon AGT for the second position as Arg; they were u

A; Accession: A23422

## ALIGNMENTS

T14782 T14782 C;Bpecies: Homo sapiens (man) R;Gpecies: Homo sapiens (man) R;Gpecies: Homo sapiens (man) A;Grosserie (man) A;Grosseri	TI14782 Typothetical protein DKFZp586B062 C;Species: Homo sagiens (man) C;Date: 20-Sep-1999 #sequence_rev C;Accession: T14782 R;Ottenwaelder, B.; Obermaier, B. submitted to the Protein Sequence A;Reference number: Z18184 A;Recession: T14782 A;Coession: T14782 A;Coession: T1219 <ott> A;Coession: T219 <ott> A;Cross-references: EMBL:AL110261 C;Generics: 1-219 <ott> A;Cross-references: EMBL:AL110261 C;Generids: 1-219 <ott> A;Cross-references: EMBL:AL110261 C;Generids: 1-219 <ott> A;Cross-references: EMBL:AL10261 C;Generids: 1-219 <ott> A;Note: DKFZp586B0621.1 C;Superfamily: complement C1q car C;Generids: 1-219 <ott> A;Note: DKFZp586B0621.1 C;Superfamily: complement C1q car Query Match Best Local Similarity 35.7%; Matches 56; Conservative 1 Db 61 EAGPAGPTGPAGECSVPPR Qy 4 DAPARGPPAPPEPR Db 61 EAGPAGPTGPAGECSVPPR Qy 59 AGVERCRLPGAYFFSFTLG Db 116 TGKFTCQVPGVYYFA-VHA Qy 119 LRRGDAVWLLSHDHDYGA Qy 119 LRRGDAVWLUSHDHDYGA Db 175 LEPEDQVWVQVGVGDYIGI</ott></ott></ott></ott></ott></ott></ott>
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A; Map position: 1
C; Superfamily: cc
C; Keywords: compl
F; 1-27/Domain: si
F; 28-253/Product:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C.Superfamily: Complement subcomponent Clq chain A; complement Clq carboxyl-terminal how C; Keywords: complement pathway; glycoprotein; heterodimer; hydroxylysine; hydroxyproline; F;1-27/Domain: signal sequence #status predicted «SIG»
F;28-253/Product: complement subcomponent Clq chain B #status experimental <MAT»
F;33-116/Domain: collagenous, triple helix cCOL»
F;28/Modified site: gyrrolidone (arboxyl-terminal homology <ClO»
F;28/Modified site: pyrrolidone carboxylic acid (Gin) (in mature form) #status experiment F;31/Dsaulfide bonds: interchain (to chain A-26) #status experimental F;35,38,41,53,56,65,83,86,101,104,107/Modified site: 4-hydroxyproline (Pro) #status experimental F;35,38,41,53,56,65,83,86,101,104,107/Modified site: (Lys) #status experimental F;59,62,77,92,98,110/Modified site: S-hydroxylysine (Lys) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Molecule type: protein
A;Molecule type: protein
A;Roesidues: 136-253 <RE4>
A;Residues: 136-253 <RE4>
A;Note: 176-Glx may also be present
C;Comment: The first component of complement is a calcium-dependent complex of the three ivation of Clr (enzyme), Cls (proenzyme), and the other eight components of complement.
C;Comment: The Clq subcomponent is composed of nine subunits, six of which are disulfide (see pIR:C1HUQC) chain. Equimolar amounts of the A, B, and C chains are found after redu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: protein
A; Residues: 28-99, 'P', 101-195
R; Reid, K.B.M.; Gagnon, J.; Fx
Biochem, J. 203, 559-569, 1982
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: mRNA
A; Residues: 28-253 <RI
A; Cross-references: EN
                                                              RESULT 3
B48150
Libernation-related protein HP-25 precursor - Siberian chipmunk
C;Species: Eutamias sibiricus (Siberian chipmunk)
C;Date: 16-Feb-1994 #sequence_revision 25-Apr-1997 #text_change
C;Accession: B48150; B41752
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Biochem. J. 203, 559-569, 1982
A;Title: Completion of the amino acid sequences of the A
A;Reference number: A90315; MUID:82283890; PMID:6981411
A;Accession: B90315
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A; Residues: 'E', 29-84, 'D', 86-99, 'P', 101-135
Mol. Cell. Biol. 13, 1516-1521, 1993
A;Title: Hibernation-associated gene regulation of plasma
A;Reference number: A48150; MUID:93180798; PMID:8441393
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A;Cross-references: GDB:119043; OMIM:120570
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Best Local S
Matches 48
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         iochem. J. 179, 307-371, Title: Complete amino
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Title:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Amino acid sequence of the N-terminal 108 amino nce number: A90301; MUID:79041552; PMID:708376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              J. 179, 367-371,
                                                                                                                                                                                                                                                                                                                                                                                                                        151 NNYEPRSGKFTCKVPGLYYFTYHASS--RGNLCVNLMRGRERAQKVVTFCDYAYNTFQVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         97
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                                                                                                                                                                                                                                                                                                                 TGGMVLKLEQGENVFLQATDKN--SLLGMEGANSIFSGFLLFPDM
                                                                                                                                                                                                                                                                                                                                                                    SQSVMLALRRGDAVWLLSHDHDGYGAYSNHGKYITFSGFLVYPDL 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PKGGPGAPGAPGPKGESGDYKATQKIAFSATRTINV-----PLRRDQTIRFDHVITNMN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PARGPPAPPEP------RSAFSAARTRSLVGSDAGPGPRHQPLAFDTEFVNIG
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Pred. No. 5
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A;Note: the source extracted from NCBI backbone (Note: sequence a; Note: sequence extracted from NCBI backbone (Note: sequence extracted from NCBI backbone 
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JC4708
                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Experimental source: adipose tissue
R; Nakano, Y; Tobe, T.; Choi-Miura, N.H.; Mazda, T.; Tc
J; Biochem. 120, 803-812, 1996
A; Title: Isolation and Characterization of GBP28, a nov
A; Reference number: JC4944; MUID:97103474; PMID:8947841
A; Accession: JC4944
A; Molecule type: protein
A; Residues: 19-38; 93-100; 101-112; 135-149; 173-178 < NAK-
A; Residues: 19-38; 93-100; 101-112; 135-149; 173-178
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F;167/Binding site: carbohydrate
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A;Residues: 29-62;84-130;172-183;187-192;201-215 <KON>
A;Residues: 29-62;84-130;172-183;187-192;201-215 <KON>
C;Superfamily: complement subcomponent Clq chain A; complement Clq carbox
C;Keywords: glycoprotein; hibernation; plasma
F;1-28/Domain: signal sequence #status predicted <SIG>
F;1-28/Domain: hibernation-related protein HP-25 #status experimental
F;29-215/Product: hibernation-related protein HP-25 #status experimental
F;29-215/Pomain: complement Clq carboxyl-terminal homology <ClQ>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Species: Homo sapiens (man)
C;Date: 10-May-1996 #sequence_revision 19-Jul-1996 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gelatin-binding 28K protein precursor - human N;Alternate names: adipose specific collagen-like
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A; Accession: B41752
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A;Note: the source is designated as Tamias asiaticus in Genbank entry TMSHP25,
A;Note: sequence extracted from NCBI backbone (NCBIN:125946, NCBIP:125947)
F;42-107/Region: collagen-like
F;114-241/Domain: complement Clq carboxyl-terminal homology <ClQ>
F;95/Modified site: 4-hydroxyproline (Pro) #status experimental
F;230/Binding site: carbohydrate (Asn) (covalent) #status predicte
                                                                                                                                                     C;Superfamily: unassigned collagens; complement Clq carboxyl-terminal C;Keywords: adipose tissue; glycoprotein; hydroxyproline F;1-18/Domain: signal sequence #status predicted <SIG> F;19-244/Product: gelatin-binding 28kDa protein #status experimental <
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A;Title: cDNA cloning and expression of a novel adipose specific
A;Reference number: JC4708; MUID:96224171; PMID:8619847
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                                                                                                                                                                                                                                                                                                                                                                                                           A; Residues: 19-38; 93-100; 10
C; Comment: This protein is
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HTSKTNQVNSGGVLLRLQVGEEVWLAVNDY--YDMVGIQGSDSVFSGFLLFPD

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A;Cross-references: GDB:128132; OMIM:120575
A;Map position: 1p36.3-1p34.1
A;Map position: 1p36.3-1p34.1
A;Introns: 60/3
C;Superfamily: complement subcomponent Clq chain A; complement Clq carboxyl-terminal C;Keywords: complement pathway; glycoprotein; homodimer; hydroxylysine; hydroxyprolin F;1-28/Domain: signal sequence #status predicted <SIGs F;29-245/Product: complement subcomponent Clq chain B #status predicted <MAT> F;31-114/Domain: collagenous, triple helix <COL> F;31-124/Domain: complement Clq carboxyl-terminal homology <ClQ> F;121-244/Domain: complement Clq carboxyl-terminal homology <ClQ> F;121-244/Domain: complement Clq carboxyl-terminal homology <ClQ> F;121-244/Domain: complement Clq carboxyl-terminal homology <ClQ> F;36,39,42,45,54,63,81,93,96,99,105/Modified site: 4-hydroxyproline (Pro) #status experimental F;36,39,42,45,54,63,81,93,96,99,105/Modified site: 4-hydroxyproline (Pro) #status experimental F;57,72,75/Modified site: 5-hydroxylysine (Lys) #status experimental F;57,75/Modified site: 5-hydroxylysine (Lys
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A;Residues: 29-56,'P',58-65,'K',67-71,'P',73-83,'K',85-86,'D',88-89,'N',91-122 <REI>C;Comment: The first component of complement is a calcium-dependent complex of the three ivation of C1r (enzyme), C1s (proenzyme), and the other eight components of complement.
C;Comment: The C1q subcomponent is composed of nine subunits, six of which are disulfide dimers of the C chain. Equimolar amounts of the A, B, and C chains are found after redu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R;Sellar,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement subcomponent Clq chain C precursor - human N,Alternate names: complement subcomponent Clq gamma chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ś
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Best Local S
Matches 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Reference number: A90304; MUID:80020137; Accession: A03207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                iochem. J. 179, 367-371, 197
Title: Complete amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Residues:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Molecule type:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Status: not compared with conceptual
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /Binding site: carbohydrate (Lys) (covalent) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
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J. 274, 481-490, 1991
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1-245 <SEL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ٦,
                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
GASRRREMQSQSVMLALRRGDAVWLLSHDHDGYGAYSNHGKYITFSGFLVYPD
                                                                                               RFNAVLTNPQGDYDTSTGKFTCKVPGLYYFVYHAS----HTANLCVLLYRSGVKVVTFCG
                                                                                                                                                                AFDTEFVNIGGDFDAAAGVFRCRLPGAYFFSFTLGKLPRKTLSVKLMKNRDEVQAMIYDD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NHYDGSTGKFHCNIPGLYYFAYHI-TVYMKDVKVSLFK-KDKAMLFTYDQYQENNVDQAS
                                                                                                                                                                                                                                    GPPGMPGVPGPMGIPGEPGEEGRYKOKFOSVFTVTR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GDFDAAAGVFRCRLPGAYFFSFTLGKLPRKTLSVKLMKNRDEVQAMIYDDGASRRREMQS 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ARGPPAPP-----EP----RSAFSAARTRSLVGSDAGPGPRHQPLAFDTEFVNIG 52
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31.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                 Score 170; DB 1;
Pred. No. 7.9e-09;
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Pred. No. 2.6e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                K. B. M.
                                                                                                                                                                                                                                                                                                                                                              Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                        Length
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A;Molecule type: protein
A;Rosidues: 104-112,'X', 114-117;453-466 <NIN2>
C;Superfamily: collagen alpha 1 (VIII) chain; complement Clq carboxyl
C;Superfamily: collagen alpha 1 (VIII) chain; complement Clq carboxyl
C;Keywords: colled coil; extracellular matrix; glycoprotein; homotri
F;1-18/Domain: signal sequence #status predicted <SIG>
F;547-673/Domain: complement Clq carboxyl-terminal homology <ClQ>
F;547-673/Domain: complement Clq carboxyl-terminal homology <ClQ>
F;453,456/Modified site: hydroxyproline (Pro) #status experimental
F;611/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                             complement protein Clq beta chain precursor - C;Species: Rattus norvegicus (Norway rat) C;Date: 16-Feb-1995 #sequence_revision 12-May.
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A;Residues: 'T', 9,'D',11-12,'EDQMKLYILFTM',30-31,'TCKSGRAFTTYMILQNVMADLVSSHT',48-89,'L'
629,'PQAVLSLISWRTIKCGSSCQIQNPMVSIPLNMFILLSQVSYLLKSNNIPLTMS' «NIN1»
A;Cross-references: EMBL:M13496; NID:g211699; PIDN:AAA48736.1; PID:g211700
                                                                       C;Accession: S49158
R;Schwaeble, W.; Petry,
                                                                                                                                                                                                                                                                                                                                                                                                                                        Ś
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A;Residues: 1-75 <LUV>
R;Ninomiya, Y; Gordon, M.; var
J. Biol. Chem. 261, 5041-5050,
A;Description: cDNA cloning and expression A;Reference number: S49158
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A;Title: The type X collagen gene. Intron sequences split A;Reference number: A31896; MUID:89054019; PMID:2461368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Residues: 1-674 <NIN>
R; LuValle, P.; Ninomiya,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R;Ninomiya, Y.; Castagnola, P.; Gerecke, D.; Gordon, M.K.; maguchi, N.; Olsen, B.R. in Extracellular Matrix Genes, Sandell L.J. and Boyd C.D., A;Title: The molecular biology of collagens with short trip
                                                submitted to the EMBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Accession: A31896
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Species: Gallus gallus (chicken);
Date: 07-0ct-1994 #sequence revision 10-Nov-1995;
Accession: S23297; A31896; $65594; $77711; I50218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Molecule type: mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                        39 HQPLAFDTEFVNIGGDFDAAAGVFRCRLPGAYFFSFTLGKLPRKTLSVKLMKNRDEVQAM 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9 GPPAPPEP----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                       IYDDGASRRREMQSQSVMLALRRGDAVWLLSHDHDGYGAYSNHGKYITFSGFL 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GPPGPPGPPGQSTIPEGYVKGESRELSGMSFMKAGANQALTGMPVSAFTVILSKAYPGAT
                                                                                                                                                                                                                                                                                            TYDEYQKGYLDQASGSAVIDLMENDQVWLQLPNSESNGLYSSEYVHSSFSGFL
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                                        /, F.; Loos, M.
Data Library, March 1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19;
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Pred. No. 5.8e-08;
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; homotrimer; hydroxyproline
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C;Species: Gallus gallus (chicken)
C;Date: 10-Sep-1999 #sequence_revision 10-S
C;Accession: S23298
R;Ninomiya, Y:; Castagnola, P:; Gerecke, D.
maguchi, N:; Olsen, B.R.
in Extracellular Matrix Genes, Sandell L.J.
A;Title: The molecular biology of collagens
A;Reference number: S22243
A;Accession: S2328
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A;Molecule type: mRNA
A:Residues: 1-253 <SCH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               collagen alpha 1(VIII) chain - chicken
C;Species: Gallus gallus (chicken)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
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                    collagen alpha 1(X) chain precursor - human

;Alternate names: procollagen alpha 1(X) chain
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence revision 03-Nov-1995 #text change 22-Jun-1999
C;Accession: S26396; S30086; S15836; S18249; A43901; I51870; S21856
C;Accession: S26396; S30086; S15836; S18249; A43901; I51870; S21856
R;Retchenberger, E; Beier, F; LuValle, P.; Olsen, B.R.; von der Mark, K.;
FEBS Lett: 311; 305-310, 1992
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Best Local S
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Best Local S
Matches 47
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47; Conser
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                                                                                                                                                                                                                                                                                                                                                        ALFKNNEPVM-YTYDEYKKGFLDQASGSAVLLLRPGDRVFLQNPSEQAAGLYAGQYVHSS
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27.6%;
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and full-length cDNA sequence
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of collagens
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Pred. No. 2.2e-08;
2; Mismatches 56
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Pred. No. 8.2e-08;
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h short triple-helical domains
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    of human
                                             der Mark, K.; Bertling,
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    collagen
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A;Note: the initial difference is probably due to trans R;Apte, S.; Mattei, M.G.; Olsen, B.R. FEBS Lett. 282, 393-396, 1991
A;Title: Cloning of human alpha-1(X) collagen DNA and 1 A;Reference number: S15826; MUID:91243838; PMID:2037056
A;Accession: S15826
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A;Molecule type: DNA
A;Residues: 1-26, 'T',28-680 <THO>
A;Residues: 1-26, 'T',28-680 <THO>
A;Residues: 1-26, 'T',28-680 <TDO
A;Roose-references: EMBL:X60382; NID:g30094; PIDN:CAA42933.1; PID:g30095
A;Note: the sequence from Fig. 3 is inconsistent with that from Fig. 2 ir
A;Note: the sequence from Fig. 3 is inconsistent with that from Fig. 2 ir
A;Reichenberger, E.; Aigner, T.; von der Mark, K.; Stoss, H.; Bertling, W
Dev. Biol. 148, 562-572, 1991
A;Title: In situ hybridization studies on the expression of type X collacy
A;Reference number: A43901; MUID:92077285; PMID:1743401
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A;Cross-references: EMBL:X58879; NID:g30013; PIDN:CAA41686.1; Pl R;Thomas, J.T.; Cresswell, C.J.; Rash, B.; Nicolai, H.; Jones, T Biochem. J. 280, 617-623, 1991
A;Title: The human collagen x gene. Complete primary translated A;Reference number: $18249; MUID:92109659; PMID:1764025
A;Accession: $18249
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A;Residues: 547-656 <RE2>
A;Residues: 547-656 <RE2>
A;Cross-references: GB:M74050; GB:D57494; NID:g339884; PIDN:AAA61221.1; PID:g553796
A;Note: sequence extracted from NCBI backbone (NCBIN:69012, NCBIP:69014)
A;Note: sequence extracted from NCBI backbone (NCBIN:69012, NCB
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                                                                                                                               F;1-18/Domain: signal sequence #status predicted <SIG> F;19-680/Product: collagen alpha 1(X) chain #status predicted F;19-56/Domain: amino-terminal nonhelical #status predicted F;57-519/Region: interrupted helical F;520-680/Domain amino-terminal predicted F;520-680/Domain amino-ter
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A; Residues: 'TIPFYGWVCWVCLL', 52-680
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                                                                                                                                                                                                                                                                                                                                                                                                           C; Superfamily: collagen alpha 1(VIII) chain; complement Clq C; Keywords: coiled coil; extracellular matrix; glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Note: mutant sequence from patient with metaphyseal chondrodysplasia A;Note: a second mutant sequence with 614-Pro is also described C;Comment: Prolines and lysines at the third position of the tripeptide ed and subsequently O-glycosylated.
F;520-680/Domain: amino-terminal F;553-679/Domain: complement Clq F;617/Binding site: carbohydrate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Note: a defect in this gene may cause Schmid C;Complex: type X collagen may be a homotrimer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Residues: 520-597,'D',599-680 <WAL>
A;Cross-references: GB:S68531; NID:g545180; PIDN:AAC60615.1; PID:g545181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: mRNA
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6q21-6q22
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EMBL:X65120; NID:g23129
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      nonhelical #status predicted <NCl>carboxyl-terminal homology <ClQ>(Asn) (covalent) #status predicted
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R;Apte, S.S
Matrix 13,
                                                                                                                                                                                  Bur. J. Biochem. 200, 21, 22, 31, A;Title: Cloning of the human and mouse typ. A;Reference number: 148299; MUID:92267014;
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                                                                                                                                                                                                                                    A;Molecule type: mRNĀ
A;Residues: 1-12,'F',14-26,'S',28-247,'L',249-285,'A',287-305,'F',307-416,'S',418-499,'
R;Apte, S.S.; Seldin, M.F.; Hayashi, M.; Olsen, B.R.
Eur. J. Biochem. 206, 217-224, 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: mRNA
A; Residues: 385-450, 'K', 452-627 A; Cross-references: EMBL: X63013;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Biochim. Biophys. Acta 1130, 78-80, 1992
A;Title: Specific hybridization probes for mouse alpha-2(IX) and alpha-1(X)
A;Reference number: S22215; MUID:92182017; PMID:1543751
A;Accession: S22215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Residues: 1-285; A; 287-680 <ELI>
A;Cross-references: EMBL:X67348; NID:g50480; PIDN:CAA47763.1; PID:g50481
A;Clima, K.; Metsaeranta, M.; Kallio, J.; Peraelae, M.; Eerola, I.; Garo
Biochim. Biophys. Acta 1130, 78-80, 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Title: The mouse collagen X gene: complete nucleotide A;Reference number: S28807; MUID:93143676; PMID:8424763 A;Accession: S28807
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S31216
                                                                           R; Summers, T.A.;
                                                                                                                                                                                                                                                                                                                                                                                  A; Title: Characterization of the mouse type X collagen A; Reference number: S30127; MUID:93261348; PMID:8492743
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R;Elima, K.; Eerola, I.; Rosati,
Biochem. J. 289, 247-253, 1993
                                                                                                                                                                                                                                                                                                                                                                    A; Accession: S30127
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                                                      Molecule type: DNA
;Residues: 52-247,'L',249-285,'A',287-305,'F',307-416,'S',418-499,'L',501-566,'C'
;Cross-references: EMBL:X65121; NID:g50482; PIDN:CAA48237.1; PID:g667031
:Summers, T.A.; Irwin, M.H.; Mayne, R.; Ballan, G.
Summers, T.A.; Irwin, M.H.; Mayne, R.; Balian, G.; Summers, T.A.; Irwin, M.H.; Mayne, R.; Balian, G.
Biol. Chem. 263, 581-587, 1988
;Title: Monoclonal antibodies to type X collagen. Biosynthetic reference number: S26397; MUID:88087150; PMID:2826450
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                                                                                                                                                                                                                                                                                                                                                                                                                             S.S., Olsen, B.R
13, 165-179, 1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GPPAPPEPRSAFSAARTRSLVGSDAGPGPRHQ-------
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                                                                                                                                                                                                         and mouse type X collagen
UID:92267014; PMID:1587271
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  <ELA>; NID:g49795; PIDN:CAA44741.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NID:g49793; PIDN:CAA79736.1; PID:g49794 R.; Metsaeranta, M.; Garofalo, S.; Pera
                                                                                                                                                               from
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Pred. No. 1e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PLAFDTEFVNIGGDFDAAAGVFRCRLPGAYFFSFTLGKL
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A;Residues: 1-744 <YAM>
A;Cross-references: GB:J05042; NID:g164895; PIDN:AAA31204.1; PID:g164896
C;Superfamily: collagen alpha 1(VIII) chain; complement Clq carboxyl-terminal F;1-20/Domain: signal sequence #status predicted <SIG>
F;1-20/Domain: collagen alpha 1(VIII) chain #status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Title: The cloning and sequencing of alphal(VIII) collagen omains similar to those of type X collagen.
A;Reference number: A34246; MUID:89380199; PMID:2476437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             collagen alpha 1(VIII) chain precursor - rabbit c;Species: Oryctolagus cuniculus (domestic rabbit) C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 C;Accession: A34246
R;Yamaguchi, N.; Benya, P.D.; van der Rest, M.; Nir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Accession: S2633,
A;Molecule type: protein
- macidues: 'SDGYFSQ',24
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A34246
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                                                                                                                                                                                                                                                                                                                                                                                                                                             F;21-117/Region: amino-terminal nonhelical
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Superfamily: collagen alpha 1(VIII) chain; complement C1q carboxyl-terminal homology C;Keywords: coiled coil; extracellular matrix; glycoprotein; homotrimer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Residues:
C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Introns: 51/3
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                                                                                                                                                                                                                                                                                                               Best
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                                                                                                                                                                                                                                                                                                                                                                                    ;617-743/Domain:
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                                                                  KLMKNRDEVQAMIYDDGASRRREMQSQSVMLALRRGDAVWLLSHDHDGYGAYSNHGKYIT
                                                                                                               FTAELTAPFPPVGAPIKFDRLLYNGRQNYNPQTGIFTCEVPGVYYFAYHV-HCKGGNVWV
                                                                                                                                                                                                    GPPGPPGPPAVMPPTPAPQGEYLPDMGLGIDGVKTPHAYAAKK-----GKNGGPAYEMPA
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                           ALFKNINEPVM-YTYDEYKKGFLDQASGSAVLLLRPGDRVFLQMPSEQAAGLYAGQYVHSS
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264, 16022-16029, 1
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                                                                                                                                                                                                                                                                                                                                                                               complement C1q carboxyl-terminal
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                                                                                                                                                         PRHOPLAFDTEFVNIGGDFDAAAGVFRCRLPGAYFFSFTLGKLPRKTLSV
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1989
                                                                                                                                                                                                                                                                                                               Score 163.5;
Pred. No. 1.:
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Pred. No. 1e-07;
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                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                               .3e-07;
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Length 744; Indels

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RESULT
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A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-224 <WADP
C;Superfamily: complement subcomponent Clq chain A; complement Clq carboxyl-terminal how
C;Keywords: glycoprotein; transmembrane protein
F;32-49/Domain: transmembrane #status predicted <TMM>
F;32-49/Domain: extracellular #status predicted <EXTP
F;94-223/Domain: complement Clq carboxyl-terminal homology <ClQ>
F;53,110/Binding site: carbohydrate (Asn) (covalent) #status predicted
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R;Wada, C.; Ohtani H.
Brain Res. Mol. Brain Res. 9, 71-77, 1991
A;Title: Molecular cloning of rat cerebellin-like protein A;Reference number: A60032; MUID:91203483; PMID:1850079
A;Accession: A60032
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C;Species: Rattus norvegicus (Norway
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A;Title: Isolation of CDNAs encoding the complete sequence
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C;Date: 21-Nov-1993 #sequence_revision 23-Feb-1996 #text_change 13-Aug-1999
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                                                                                                                                                                                                                                                                                                                                       A; Molecule type: mRNA
A; Residues: 1-674 < THO>
                                                                                                                                                                                                                                                                                                                                                                               A; Accession: S13301
                                                                                                                                                                                                                                                                                                                                                                                               A;Title: Isolation of cDNAs encoding the complete sequence A;Reference number: S13301; MUID:91113131; PMID:1703407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C; Accession: S13301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            collagen alpha
                                                                                                                                                                   Gene: COL10A1
;Superfamily: collagen alpha 1(VIII) chain; complement Clq carboxyl-terminal; Superfamily: colled coil; extracellular matrix; glycoprotein; homotrimer; Keywords: coiled coil; extracellular matrix; glycoprotein; homotrimer; 1-18/Domain: signal sequence #status predicted <SIG>;1-16/74/Product: collagen alpha 1(X) chain #status predicted <MAT>;547-673/Domain: complement Clq carboxyl-terminal homology <ClQ>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;Date: 03-Mar-1993 #sequence_revision
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                                                    9 GPPAPPEPRSAFSAARTRSLVGSDAGPGPRHQ----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AFSAARTRSLVGSDAGPGPRHQPLAFDTEFVNIGGDFDAAAGVFRCRLPGAYFFSFTLGK 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      YSNHGKYITFSGFLVYP 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VYNROTIQVSLMQNGYPVISAFAGD-QDVTREAASNGVLLLMEREDKVHLKLERGNLMGG
              GPPGPPGPR---GNAGEPGLPGPPGPPGPPGPPGPVALPEDFVKAGQRPFVSANQGVTGMPVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AFSA--TRSTNHEPSEMSNRTMTIYFDQVLVNIGNHFDLASSIFVAPRKGIYSFSFHVVK 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1(X) chain precursor - bovine
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Pred. No. 3.3e-08;
5; Mismatches 62
                                                                                            Pred. No. 1.30
6; Mismatches
                                                                                                                 Score 163;
Pred. No. 1
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.3e-07;
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C;Species: Mus musculus (house mouse)
C;Date: 13-Jan-1995 #sequence_revision
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A; Reference number: A; Accession: S29328
                                                        A; Title: Isolation,
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                                       ecerebellin.
                                                                               R; Petry, F.; Reid, K. I
Eur. J. Biochem. 209,
                                                                                                                   C; Accession: S29328
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C;Accession: S15435
R;Muragaki, Y.; Mattei, M.G.; Yamaguchi, N.; Olsen, B.R.; Ninomiya, Bur. J. Biochem. 197, 615-622, 1991
A;Title: The complete primary structure of the human alpha-1(VIII)
A;Reference number: S15435; MUID:91231001; PMID:2029894
                                                                                                                                                                                                                                                                                                                                                                                                           F;118-571/Region: interrupted helical
F;572-744/Region: carboxyl-terminal nonhelical
F;617-743/Domain: complement Cla Carbonni
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(;Superfamily: collagen alpha 1(VIII) chain; complement
F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-744/Product: collagen alpha 1(VIII) chain #status F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Accession: S15435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Cross-references: GDB:128104; OMIM:120251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Cross-references:
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A; Residues: 1-744 < MUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Gene: GDB:COL8A1
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                                                                            682 NEPVM-YTYDEYKKGFLDQASGSAVLLLRPGDRVFLQMPSEQAAGLYAGQYVHSSFSGYL
                                                                                                                                                                                                                                            563 GPPGPPGPPAVMPPTPPPQGEYLPDMGLGIDGVKPPHATGAKKGKNGGPAYEMPAFTAEL
741
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                                                                                                                       RDEVQAMIYDDGASRRREMQSQSVMLALRRGDAVWLLSHDHDGYGAYSNHGKYITFSGFL
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                                                                                                                                                                                                                                                                                                                                               Score 160.5;
Pred. No. 2.
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K.B.M.; Loos,

mouse

13-Jan-1995

#text\_change

20-Aug-1999

в.м.; Loos, М. 129-134, 1992

sequence analysis S29328; MUID:93011118;

and characterization

of.

CDNA

clones coding

for Ç,

PMID: 1396691

Search completed: January 12, 2004, 08:16:46 Job time : 11.8403 secs	QY 96 QAMIYDDGASRRREMQSQSVMLALRRGDAVWLLSHDHDGYGAYSNHGKYITFSGFLVYPD 155 :	QY 42LAFDTEFVNIGGDFDAAAGVFRCRLPGAYPFSFTLGKLPRKTLSVKLMKNRDEV 95	Qy 8 RGPPAPPEPRSAFSAARTRSLVGSDAGPGPRHQP	Query Match 17.4%; Score 155.5; DB 2; Length 246; Best Local Similarity 24.4%; Pred. No. 1.9e-07; Matches 44; Conservative 26; Mismatches 69; Indels 41; Gaps 4;	A;Status: preliminary A;Molecule type: mRNA A;Molecule type: mRNA A;Residues: 1-246 <pet> A;Cross-references: EMBL:X66295; NID:g50228; PIDN:CAA46993.1; PID:g50229 A;Cross-references: EMBL:X66295; NID:g50228; PIDN:CAA46993.1; PID:g50229 C;Superfamily: complement subcomponent C1q chain A; complement C1q carboxyl-terminal hom C;Superfamily: complement C1q carboxyl-terminal homology <c1q></c1q></pet>
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Result
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Perfect score:
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        on:
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                                                                     Score
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Gapop 10.0 , Gapext 0.5
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894
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Copyright (c) 1993 - 2004 Compugen Ltd
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CATA HUMAN
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CQT5 HUMAN
CQT7 HUMAN
CRRB MOUSE
CTRB MOUSE

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CQT15 HUMAN
CQT16 HUMAN
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APM1 MOUSE
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GLIC MOUSE
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6 homo sapien
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8 homo sapien
8 homo sapien
9 sallus gall
1 rattus norv
2 homo sapien
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7 bos taurus
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Q9BXJ0; Q9UFX4;
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
28-FEB-2003 (Rel. 41, Created)
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DOMAIN
SEQUENCE
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SIGNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
Sheppard P.O., Humes J.M.;
"Homo sapiens complement-clq tumor necrosis factor-related protein.";
Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AF329841; AAK17965.1; -. EMBL; AL110261; CAB53702.1; -. PIR; T14782; T14782.
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-!- SIMILARITY: Contains 1 C1Q domain.
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SMART; SM00110; C1Q; 1.
PROSITE; PS01113; C1Q; FALSE_NEG.
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Genew; HGNC:14344; C1QTNF5.
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Pfam; PF01391; Collagen; 1.
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InterPro; IPR000087; Collagen
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                                                                                                                                                              AGVFRCRLPGAYFFSFTLGKLPRKTLSVKLMKNRDEVQAMIYDDGASRRREMQSQSVMLA 118
                                                                                                                                                                                                                            EAGPAGPTGPAGECSVPPRSAFSAKRSESRV----PPPSDAPLPFDRVLVNEQGHYDAV 139
LEPEDQVWVQVGVGDYIGIYASIKTDSTFSGFLVYSD
                                                       LRRGDAVWLLSHDHDGYGAYSNHGKYITFSGFLVYPD 155
                                                                                                            TGKFTCQVPGVYYFA-VHATVYRASLQFDLVKNGESIASFFQFFGGWPKPASLSGGAMVR
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243
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35.7%;
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Pred. No. 1.7
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COLLAGEN-LIKE.
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COMPLEMENT-C1Q TUMOR NECROSIS FACTOR-
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  235
                                                                                                                                                                                                                                                                                                                                              Indels
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RA Strausberg R.D., Collins F.S., Wagner L., Schaefer C.F., Bhat N.K., RA Altechul S.F., Zeebberg B., Buetow K.H., Schaefer C.F., Bhat N.K., RA Altechul S.F., Zeebberg B., Buetow K.H., Schaefer C.F., Bhat N.K., RA Altechul S.F., Zeebberg B., Buetow K.H., Schaefer C.F., Bhat N.K., RA Altechuko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., RA Stapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., RA Browmstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., RA Browmstein M.J., Wadin T.B., Toshiyuki S., Carninci P., Prange C., RA Browmstein M.J., McKernan K.J., Malek J.A., Gunaratne P.H., RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., RA Richards S., Worley M.M., Sodergren E.J., Lu X., Gibbs R.A., RA Willalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., RA Willalon D.K., Muzny D.M., Green E.D., Dickeon M.C., RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., RA Blakesley R.W., Touchman J.W., Green E.D., Dickeon M.C., Ra Blakesley R.W., Touchman J.W., Green E.D., Dickeon M.C., Ra Blakesley R.W., Touchman J.W., Green E.D., Dickeon M.C., Shevin J.E., Jones S.J.M., Marra M.A.; Touchman and mouse cDNA sequences."; Thuman and mouse cDNA sequences."; Thuman and mouse cDNA sequences."; Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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Q9BXJ1; Q96NF2;
28-FEB-2003 (Rel
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15-SEP-2003 (Rel. 42, Last annotation update)
Complement-c1q tumor necrosis factor-related protein 1 precursor
(G protein coupled receptor interacting protein) (GIP).
C1QTNF1 OR CTRP1.
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Mammalia; Eutheria;
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                                                      the European Bioinformatics Institute. There are no rest
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or send an email to license@isb-sib.ch).
                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the E
                                                                                                                                                                                                                                                                                                                                                          "NEDO human cDNA sequencing project."; Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=22388257; PubMed=12477932;
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   EMBL; AJ272138; CAC20425.1;
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Primates;
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EMBL/GenBank/DDBJ
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                                                                                                                                  and
                                                                                                                                                                                                                       EMBL
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[sogai T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kanda K.,
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                                                                                                                                                                                                                       a collaboration
MBL outstation -
                                                                                                                               for
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RESULT 4
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X MEDLINE-22388257; PubMed=12477932;
A Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
A Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,
A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
A Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Heich F.,
A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heich F.,
A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
A Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
A Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
A Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
A Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
A Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
A Brownstein M.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
A Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Villalon M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Ma
Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                               Q9BXI9;
28-FEB-2003
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CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HUMAN
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DOMAIN
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SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AF232905; AAG44303.1; AL

EMBL; AF329840, AAK17964.1; ...

EMBL; AF329840, AAH21553.1; ...

EMBL; AK055541; BAB70947.1; ...

Genew; HGNC:14324; C1QTNF1.
                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                     28-FEB-2003 (Rel.
15-SEP-2003 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR001073; Clq.
InterPro; IPR000087; Collagen.
                                                                                                                                                                                                                                                               "Homo
                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                     Complement-clq tumor
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                                                                                                                                                                                                                                                                           iddington C.S.,
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                                                                                                                                                                                                      SSUE=Placenta;
                                                                                                                                                                                                                                                                                                                                                                           QTNF6 OR CTRP6
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                                                                                                                                                                                                                                                                                                                                                            sapiens (Human)
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PF01391; Collagen; 1.
; SM00110; C1Q; 1.
                                                                                                                                                                                                                                                             sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TEFVNLYDHFNMFTGKFYCYVPGLYFFSLNVHTWNQKETYLHIMKNEEEVVILFAQVG--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TEFVNIGGDFDAAAGVFRCRLPGAYFFSFTLGKLPRKTLSVKLMKNRDEVQAMIYDDGAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AGARGHTGPKGQKGSMGAPGERCKSHYAAFSVGRKK------PMHSNHYYQTVIFD
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                                                                                                                                                                                                                                                (DEC-2000)
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147
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                                                                                                                                                                                                                                               complement-clq tumor necrosis factor-related protein.";
C-2000) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
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31743
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281
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Primates;
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281
22
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35.5%;
                                                                                                                                                                                                                                                                                                                                                                                        necrosis
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Last annotation update)
necrosis factor-related
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                                                                                                                                                                                                                                                                           P.O.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18;
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COMPLEMENT-C10 TV
RELATED PROTEIN
COLLAGEN-LIKE.
C10.
L -> P (IN REF.
L -> Q (IN REF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ALT_INIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score
Pred.
                                                                                                                                                                                                                                                                                                                                 Craniata; Vertebrata;
Catarrhini; Hominidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -> P (IN REF. 1)
-> Q (IN REF. 1)
49E248CB88ACFB7C
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No. 7.
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                                                                                                                                                                                                                                                                                                                                                                                     protein
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                                                                                                                                                                                                                                                                                                                                              Euteleostomi;
                             6
                                                                                                                                                                                                                                                                                                                                                                                       precursor
     , Sanchez A.,
1 G.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                281;
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RESULT
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Best Loc
Matches
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C1RF_MOI
088992;
                                                                                                                                                                                                                                    16-OCT-2001
16-OCT-2001
16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CARBOHYD
CONFLICT
SEQUENCE
                    Berube
Baskin
                                                                                                                                                                                             Clq-related
ClQRF OR CRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
DOMAIN
                                                           SEQUENCE FROM N.A. MEDLINE=99097006; PubMed=9878755;
                                                                                                                                        Eukaryota;
Mammalia; !
                                                                                                                                                                           Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 human and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-
-i- SIMILARITY: Contains 1 collagenous
-i- SIMILARITY: Contains 1 ClQ domain.
                                                                                                                NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00386; Clq; 1.
Pfam; PF01391; Collagen; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; BC020551; AAH20551.1;
Genew; HGNC:14343; C1QTNF6.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Blakesley R.W., Touchman J.W., Green Rodriguez A.C., Grimwood J., Schmutz Butterfield Y.S.N., Krzywinski M.I.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS01113; C1Q; FALSE_NEG
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InterPro; IPR000087; Collagen.
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European Bioinformatics Institute. The
by non-profit institutions as long
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SWISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the EN
                                                                                                                                                                                                                                                                                                                   MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               190
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N.G., Swanson X.H., Bertram M.J., D.S., Smith J.R., Pereira-Smith O. ng and characterization of CRF, a n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PR00007; COMPLEMNTC1Q.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                               CRF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AYFFSFTLGKLPRKTLSVKLMKNRDEVQAMIYDDGASRRREMQSQSVMLALRRGDAVWLL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IYFFSLNVHSWNYKETYVHIMHNQKE--AVILYAQPSERSIMQSQSVMLDLAYGDRVWVR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PPAPPEPR-SAFSAARTRSLVGSDAGPGPRHQPLAFDTEFVNIGGDFDAAAGVFRCRLPG
                                                                                                                                    Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      SHDHDGYGA-YSN-HGKYITFSGFLV
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                                                                                                                                                                                                                                      (Rel.
                                                                                                                                                                                                                                                                         (Rel.
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139
91
21
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278
91
21
                                                                                                                                    Chordata;
Rodentia;
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Last
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                                                                                                                                                                                                                                    sequence u
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10;
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COMPLEMENT-C1Q TUMOR NECROSIS FACTOR-
RELATED PROTEIN 6.
COLLAGEN-LIKE.
C1Q.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 194;
Pred. No. 4
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G -> V (IN REF. 2)
                                                                                                                                    Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27A82CA863F23D47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
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                                                                                                                                                                                                                                                          update)
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  (See http://www.isb-sib.ch/announce/
  novel
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.6e-11;
                    Kittle J.D.,
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RESULT 6
CLRF H
ID "CLRF H
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DT 16-OCT
DT 15-SEP
DE C1Q-FE
GN C1QF-F
OS Homo s
OC Eukary
OC Mammall
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RN [1]
RP SEQUEN
RX MEDLIN
RA BERULE
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Best Local S
Matches 55
                                                                                                                                                                             C1RF HUMAN
075973;
16-OCT-2001
16-OCT-2001
15-SEP-2003
C1q-related
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       expressed in areas of the brain involved in motor function.";
Brain Res. Mol. Brain Res. 63:233-240(1999).
-1- TISSUE SPECIFICITY: EXPRESSED IN BRAINSTEM. MORE ABUNDANT IN ARE.
-0F THE NERVOUS SYSTEM INVOLVED IN MOTOR FUNCTION, SUCH AS THE
PURKINJE CELLS OF THE CEREBELLUM, THE ACCESSORY OLIVARY NUCLEUS,
THE PONS AND THE RED NUCLEUS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 use by non-profit institutions as long as modified and this statement is not removed. Usentities requires a license agreement (See httors eand an email to license@isb-sib.ch).
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PRINTS; PR000007; COMPLEMNTC1Q.
SMART; SM00110; C1Q; 1.
PROSITE; PS01113; C1Q; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GO; GO:0005737; C:cytoplasm; I
InterPro; IPR001073; Clq.
InterPro; IPR000087; Collagen.
 SEQUENCE FROM N.A.
MEDLINE=99097006; PubMed=9878755;
Berube N.G., Swanneon X.H., Bertral
Baskin D.S., Smith J.R., Pereira-
                                                                                                        Homo sapiens (Human)
Eukaryota; Metazoa;
Mammalia; Eutheria;
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                                                                                     NCBI_TaxID=9606;
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                                                                                                                                                                                            (Rel. 40, Created)
(Rel. 40, Last sequence update)
(Rel. 42, Last annotation updat
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                                                                                                                                                                                 factor
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   Swanson X.H., Bertram M.J., Smith J.R., Pereira-Smith O.
                                                                                                                                              (Human).
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Primates;
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29.7%;
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C10-RELATED FACTOR.
COLLAGEN-LIKE.
C10.
C10.
W; F776E2D206EBF763 CRC64;
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Pred. No. 5.8e
20; Mismatches
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                                                                                                        Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                       258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     noved. Usage by and for commercial (See http://www.isb-sib.ch/announce/
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                     Didenko
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RX MEDILINE=22388557; PubMed=12477932;

RA Klausher R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Klausher R.D., Collins F.S., Wagner L., Schaefer C.F., Bhat N.K.,

RA Allechul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Allechul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Rahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

RA Rodriguez A.C., Grimwood J., Schenutz J., Myers R.M.,

RA Rodriguez A.C., Grimwood J., Schenutz J., Myers R.M.,

RA Rodriguez A.C., Grimwood J., Schenutz J., Myers R.M.,

RA Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.",

Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

C. 1. TISSUE SPECIFICITY: EXPRESSED IN BARINSTEM.

C. 1. TISSUE SPECIFICITY: EXPRESSED IN BARINSTEM.
                                                                                                                                                                                                                                Query Match
Best Local S
Matches 54
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Collagen;
SIGNAL
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DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR001073; C1q.
InterPro; IPR0010087; C01lagen.
Pfam; PF00386; C1q; 1.
Pfam; PF01391; C01lagen; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AF095154; AAC64186.1; -.
EMBL; AF410771; AAK95548.1; -.
EMBL; BC006798; AAH00798.1; -.
GO; GO:0007626; P:locomotory behavior;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EWBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
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I; SM00110; C1Q; 1.
ITE; PS01113; C1Q; 1
155
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                                                     IGGDFDAAAGVFRCRLPGAYFFSFTLGKLPR----KTLSVKLMKNRDEVQAMIYDDGASR
                                                                                                                 GKPGPPGLPGAGGSGAISTATYTTVPRVAFYAGL-----KNPHEGYEVLKFDDVVTN
                                                                                                                                                                          GPPAPP--
LGNNYDAASGKFTCNIPGTYFFTYHV--LMRGGDGTSMWADLCKN
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123
258
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                                                                                                                                                                                                                                                                                                                                                                      POTENTIAL.
C1Q-RELATED FACTOR.
COLLAGEN-LIKE.
C1Q.
                                                                                                                                                                                                                                                              Score 189.5; DB 1
Pred. No. 1.1e-10;
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TISSUE=Adipocyte;
MEDLINE=96070757; PubMed=7592907;
Scherer P.E., Williams S., Fogliano M.,
Scherer P.E. wordein similar to Ciq, I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q60994; Q62400; Q9DC68; 01-NOV-1997 (Rel. 35, Created) 01-NOV-1997 (Rel. 35, Last sequence update) 01-SEP-2003 (Rel. 42, Last annotation update) adiponectin precursor (30 kDa adipocyte complement-related protein) (ACRP30) (Adipocyte specific protein AdipoQ).
MEDLINE=21372498; PubMed=11479627;
Yamauchi T., Kamon J., Waki H., Terauchi Y., Kubota N., Hara K.,
Mori Y., Ide T., Murakami K., Teuboyama-Kasaoka N., Ezaki O.,
Akanuma Y., Gavrilova O., Vinson C., Reitman M.L., Kagechika H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. STRAIN=C57BL/6J; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Biochem.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    of the mouse gene Acrp30.";
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Das K., Lin Y., Widen
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Mammalia; Eutheria;
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Q is a novel adipose-specific g
l. Chem. 271:10697-10703(1996).
                                                                                                           ional annotation of 409:685-690(2001).
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to H., Adachi J., Fukuda S
" Kondo S., Yamanaka I
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Lming L.,
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Pfam; PF00386; Clq; 1.
Pfam; PF01391; Collagen; 1.
PRINTS; PR00007; COMPLEMNTC1Q.
ProDom; PD000007; Clg helix; 1.
SMART; SM00110; ClQ; 1.
PROSITE; PS01113; ClQ; 1.
Hormone; Collagen; Signal; Repe;
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EMBL; U49915; AAB06706.1; -.
EMBL; AF304466; AAK13417.1; -.
EMBL; AK003138; BAB22597.1; -.
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Berg A.H., Combs T.P., Du X., Brownlee
"The adipocyte-secreted protein Acrp30
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INDUCTION: DURING HORMON
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GO:0005576; C:extracellular; IDA.
GO:0005515; F:protein binding activity; I
GO:0006635; P:fatty acid beta-oxidation;
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SUBCELLULAR LOCATION: Secreted.
TISSUE SPECIFICITY: Synthesized
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RUNCTION: IMPORTANT NEGATIVE REGULATOR IN HEMATOPOIESIS AND IMMUNE SYSTEMS; MAY BE INVOLVED IN ENDING INFLAMMATORY RESPONSES THROUGH ITS INHIBITORY FUNCTIONS. INHIBITS ENDOTHELIAL NF-KAPPAB SIGNALING THROUGH A CAMP-DEPENDENT PATHWAY. INHIBITS TWF-ALPHA-INDUCED EXPRESSION OF ENDOTHELIAL ADHESION MOLECULES. INVOLVED IN THE CONTROL OF FAT METABOLISM AND INSULIN SENSITIVITY.
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RA Klausner R.D., Collins F.S., Wagner L. Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Brownstein M.J., Usdin T.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Robask S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Sarchen K.J., Lu X., Gibbs R.A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grimwood J., Schmutz J.M., Warran M.A.;
"Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences."

"Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences."

"Generation and initial analysis of more than 15,000 full-length
"C. -- SIMILARITY: Contains 1 collagenous domain.

"C. -- SIMILARITY: Contains 1 collagenous domain.
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Best Local S
Matches 53
EMBL;
                                                                                         use by non-profit institutions as long modified and this statement is not removed: entitles requires a license agreement (See lor send an email to license@isb-sib.ch).
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                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Elthe European Bioinformatics Institute. There are no restues by non-profit institutions as long as its content
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=22388257; PubMed=12477932;
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Piddington C.S., Bishop
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Mammalia; Eutheria;
NCBI_TaxID=9606;
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ted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
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                                 AF329836;
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AAH11699.
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Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Catarrhini; Hominidae;
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                                                                                                                              (See http://www.isb-sib.ch/announce/
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SIGNAL
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                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                             Koide T., Aso A., Yorihuzi T., Nagata K.; "Conformational requirements of collagenous by the chaperone protein HSP47."; J. Biol. Chem. 275:27957-27963 (2000).
                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. MEDLINE=20428709;
                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                          Q9ESN4;
16-OCT-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
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SMART; SM00110; C1Q; 1.
PROSITE; PS01113; C1Q; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00386; Clq; 1.
Pfam; PF01391; Collagen; 2.
                                                          MGD; MGI:2387350; Clql.
GO; GO:0005515; F:protein binding
                                                                                                                                                                                                                                                                                                                                                                 Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                       Gliacolin precursor
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InterPro; IPR000087; Collagen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Genew; HGNC:14325; C1QTNF2.
 Pfam; PF00386; Clq; 1.
Pfam; PF01391; Collagen; 1.
PRINTS; PR00007; COMPLEMNTC1Q
                                                                                   EMBL; AB044560; BAB15806.1;
                                                                                                           or send an email to license@isb-sib.ch).
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                                   InterPro; IPR001073; Clq.
                                                                                                                                                                                                       SIMILARITY: Contains 1 collagenous domain. SIMILARITY: Contains 1 C1Q domain.
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143
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(Rel. 40,
(Rel. 41,
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Rodentia;
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Pred. No. 1.9e-10;
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COMPLEMENT-C1Q TUMOR NECROSIS FACTOR-
RELATED PROTEIN 2.

COLLAGEN-LIKE.
                                                                                                                                                                                                                                                                                                                                        Craniata; Vertebrata; |
Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                      protein)
                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                 collagenous peptides
                                                             activity;
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; Murinae; Mus
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AC CONTRACTOR OF THE CONTRACT 
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XX MEDLINE=2238257; PubMed=12477932;

XX Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

XX Allausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

XX Allschul S.F., Zeeberg B., Buerow K.H., Schaefer C.F., Bhat N.K.,

XX Allschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

XX Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

XX Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

XX Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

XX Hopkins R.F., Jordan K., Farmer A.A., Rubin G.M., Hong L.,

XX Hopkins R.F., Jordan K., Farmer A.A., Rubin G.M., Hong L.,

XX Hopkins R.F., Jordan K., Farmer A.A., Rubin G.M., Hong L.,

XX Hopkins R.F., Jordan T.B., Toshiyuki S., Carninci P., Prange C.,

XX Hownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

XX Hownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

XX Hownstein M.J., Willah, Peters G.J., Abramon R.D., Mullahy S.J.,

XX Hopkins R.F., Jordey R.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

XX Hillalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

XX Hillalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

XX Hallalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

XX Hallalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

XX Hallalon D.K., Muzny D.M., Shevchenko Y., Bouffard G.G.,

XX Hallalon D.K., Muzny D.M., Shevchenko Y., Bouffard G.G.,

XX Hallalon D.K., Muzny D.M., Schentz J., Myers R.M.,

XX Hallalon D.K., Muzny D.M., Schentz J., Myers R.M.,

XX Hallalon D.K., Muzny D.M., Schentz J., Myers R.M.,

XX Hallalon D.K., Muzny D.M., Schentz J., Myers R.M.,

XX Hallalon D.K., Muzny D.M., Schentz J., Myers R.M.,

XX Hallalon D.K., Muzny D.M., Mazra M.A.,

YX Hallalon D.K., Muzny D.M., Muzny M.A.,

YX Hallalon D.K., Muzny D.M.,

YX Hallalon D.K., Muzny D.M.,

YX Halla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local S
Matches 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P02746; Q96H17;
21-JUL-1986 (Re]
01-JUL-1993 (Re]
15-SEP-2003 (Re]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; F
Collagen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Complement Clq subcomponent,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Biochem.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement system.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Molecular cloning and characterization of the complementary DNA gene coding for the B-chain of subcomponent Clq of the human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=86076906; PubMed=3000358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                147
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E; PS01113; C1Q;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ഗ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GLKROHEGYEVLKFDDVVTNLGNHYDPTTGKFTCSIPGIYFFTYHV--LMRGGDGTSMWA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FSGFIIYAD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ------LAFDTEFVNIGGDFDAAAGVFRCRLPGAYFFSFTLGKLPR----KTLSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AGPRGPPGEPGPPGPVGPPGEKGEPGRQGLPGPPGAPGLNAAGAISAATYSTVPKIAFYA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       120
255 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (Rel. 26, Last sequence update)
(Rel. 42, Last annotation updat
Clq subcomponent, B chain precur
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    231:729-735(1985).
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61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20
255
111
255
26687
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20.7%;
28.0%;
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Pred. No. 2.6e
21; Mismatches
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GLIACOLIN.
COLLAGEN-LIKE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C1Q.
; 529FBAF4B2191BC1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        n update)
precursor.
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                EMBL; BC008983; AAH08983.
EMBL; M36278; AAC41692.1;
Genew; HGNC:1242; ClQB.
                                                                                                    entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                   EMBL; X03084; CAA26880.1;
                                                                                                                                                                                                                                                                                                                                                      ÷
                                                                                                                                                                                                                                                                                                                                                                                                                Immunobiology 199:286-294 (1998).

-i- FUNCTION: C1Q ASSOCIATES WITH THE PROENZYMES C1R AND C1S TO YIELD C1, THE FIRST COMPONENT OF THE SERUM COMPLEMENT SYSTEM. THE COLLAGEN-LIKE REGIONS OF C1Q INTERACT WITH THE CA(2+)-DEPENDENT C1R(2)C1S(2) PROENZYME COMPLEX, AND EFFICIENT ACTIVATION OF C1 TAKES PLACE ON INTERACTION OF THE GLOBULAR HEADS OF C1Q WITH THE FC REGIONS OF IGG OR IGM ANTIBODY PRESENT IN IMMUNE COMPLEXES.
-i- SUBUNIT: C1 IS A CALCIUM-DEPENDENT TRIMOLECULAR COMPLEX OF C1Q, R AND S IN THE MOLAR RATION OF 1:2:2. C1Q SUBCOMPONENT IS COMPOSED OF NINE SUBUNITS, SIX OF WHICH ARE DISULFIDE-LINKED DIMERS OF THE AND B CHAINS, AND THREE OF WHICH ARE DISULFIDE-LINKED DIMERS OF THE AND B CHAINS, AND THREE OF WHICH ARE DISULFIDE-LINKED DIMERS OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Reid K.B.M., Bentley D.R., Wood K.J.; "Cloning and characterization of the complementary DNA for the chain of normal human serum Clq.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIINE=82283890; PubMed=6981411; Reid K.B.M., Gagnon J., Frampton J.; Completion of the amino acid sequences subcomponent C1q of the first component Biochem. J. 203:559-569(1982).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               B chain of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Complete amino acid sequences of t
present in subcomponent Clq of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Petry F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=98450587;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Philos. Trans. R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=85038855;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Amino acid sequence of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 26-193.
MEDLINE=79041552; F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Biochem.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 26-133.
MEDLINE=80020137; PubMed=486087;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REVIEW OF CIQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 134-251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Reid K.B.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Proc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Molecular basis of hereditary Clq deficiency.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 224-251 FROM N.A.
                                                                                                                                                                                                                                          erythematosus-like symptoms. It is characterized activation of the complement classical pathway. SIMILARITY: Contains 1 collagenous domain. SIMILARITY: Contains 1 C1Q domain.
                                                                                                                                                                                                                                                                                                                              PTM: O-linked glycans consist of Glc-Gal disaccharides bound to the oxygen atom of post-translationally added hydroxyl groups. DISEASE: Defects in C1QB are a cause of C1Q deficiency [MIM:120570]. It is a rare genetic disorder which is associated
                                                                                                                                                                                                                                                                                                              with recurrent infections and a high prevalence of lupus
                                                                                                                                                                                                                                                                                                                                                                                                       THE C CHAIN
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Natl. Acad. Sci. U.S.A. 99:
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                                                   AAH08983.1;
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R. Soc. Lond., B, B
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                                                                                                                     is not removed. Usage by and for commercial agreement (See http://www.isb-sib.ch/announce/
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Best Local S
Matches 48
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GO; GO:0003811; F:comp
InterPro; IPR001073; C
InterPro; IPR000087; C
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Pfam; PF01391; Collagen;
                     01-NOV-1995
01-NOV-1995
28-FEB-2003
                                          HP25_TAMSI
Q06576;
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VARIANT
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01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Hibernation-associated plasma protein HF-25 precursor
specific blood complex, 25 kDa subunit).
Tamias sibiricus (Siberian chipmunk) (Asian chipmunk)
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SM00110; C1Q; 1.
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                                                                                                                   NNYEPRSGKFTCKVPGLYYFTYHASS--RGNLCVNLMRGRERAQKVVTFCDYAYNTFQVT
                                                                                                                                                PKGGPGAPGAPGPKGESGDYKATOKIAPSATRTINV-----PLRRDQTIRFDHVITNMN
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G -> D (in C1Q deficiency).

/FTId=VAR 008541.

Q -> E (IN REF. 3).

N -> D (IN REF. 3).

G -> P (IN REF. 3 AND 4).
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                                                                                                                                                              ----RSAFSAARTRSLVGSDAGPGPRHQPLAFDTEFVNIG
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Pred. No.
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N -> D (IN REF. 3).
G -> P (IN REF. 3 A)
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(WITH C-26 )
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                precursor (Hibernator-
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=93180798;
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Mammalia;
Tamias.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              J. Biol. Chem. 267:47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Identification of novel blood hibernation.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  or send an email to license@isb-sib.ch).
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between the Swiss Institute of Bio:
                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00386; Clq; 1.
Pfam; PF01391; Collagen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PIR; B48150; B48150.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR001073;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     s SWISS-PROT entry is copyright. It is produced through a collab ween the Swiss Institute of Bioinformatics and the EMBL outst European Bioinformatics Institute. There are no restrictions by non-profit institutions as long as its content is in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUBCELLULAR LOCATION: Extracellular TISSUE SPECIFICITY: PLASMA; SYNTHESIZED IN DEVELOPMENTAL STAGE: THE PROTEIN COMPLEX DIPLASMA AT ONSET OF HIBERNATION AND REAPPEAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIMILARITY: Contains 1 collagenous domain. SIMILARITY: Contains 1 C1Q domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3iol. Chem. 267:473-478(1992).
FUNCTION: PLASMA PROTEINS HP-20.
140 kDa COMPLEX VIA DISULFIDE BO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HIBERNATION SPECIFIC
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TE; PS01113; C1Q; 1
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Collagen; Glycoprotein;
                                                                                                                                                                                                            Similarity
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--REKEAQANDSYKHAMGSVIMALGKGDKVWLESKLK---GTESEKGITHİVFFGYLLY
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                                                                                            FDTEFVNIGGDFDAAAGVFRCRLPGAYFFSFTLGKLPRKTLSVKLMKNRDEVQAMIYDDG
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Eutheria; Rodentia; Sciurognathi; Sciuridae; Sciurinae;
                                                                                                                                                                                             Conservative
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                              -SVMLALRRGDAVWLLSHDHDGYGAYSNHG-KYITFSGFLVY
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THE PLASMA
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RESULT 12

RESULT 12

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CHARACTERIZATION.
MEDLINE=20417747; PubMed=10961870;
WCPOta T., Oritani K., Takahashi I., T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=99333693; PubMed=10403784; Schaeffler A., Orso E., Palitzsch K.D., Buechler C., Fuerst A., Schoelmerich J., Schmitz G.; "The human apM-1, an adipocyte-specific gene linked TWF's and to genes expressed in activated T cells, i chromosome 1q21.3-q23, a susceptibility locus identi combined hyperlipidemia (FCH)."; Biochem. Biophys. Res. Commun. 260:416-425(1999).
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                                     Yamauchi T., Kamon J., Waki H., Terauchi Y., Kubota N., Hara Mori Y., Ide T., Murakami K., Tsuboyama-Kasaka N., Ezaki O., Akanuma Y., Gavrilova O., Vinson C., Reitman M.L., Kagechika Shudo K., Yoda M., Nakano Y., Tobe K., Nagai R., Kimura S., T Proguel P., Kadowaki T.; "The fat-derived hormone adiponectin reverses insulin resista associated with both lipoatrophy and obesity.";
                                                                                                                                                                                                                                                                                   Ouchi N., Kihara S., Arita Y., Okamoto Y., Maeda K., Kuri
Hotta K., Nishida M., Takahashi M., Muraguchi M., Ohmoto
Nakamura T., Yamashita S., Funahashi T., Matsuzawa Y.;
"Adiponectin, an adipocyte-derived plasma protein, inhibi
endothelial NF-kappaB signaling through a cAMP-dependent
Circulation 102:1296-1301(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       negatively regulates the growth functions of macrophages."; Blood 96:1723-1732(2000).
                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=20440368; PubMed=10982546; Ouchi N., Kihara s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gene 229:67-73(1999)
[3]
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Saito K., Tobe T., Minoshima S., Asakawa S., S
Nakano Y., Shimizu N., Tomita M.;
"Organization of the gene for gelatin-binding
                                                                                                                                                                                                               MEDLINE=21372498; PubMed=11479627;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Adiponectin, a new member of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matsuzawa Y.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE=Adipose tissue;
MEDLINE=96224171; PubMed=8619847;
Maeda K., Okubo K., Shimomura I.,
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APM1 OR ACRP30 C
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01-NOV-1997 (Rel. 35, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Adiponectin precursor (30 kDa adipocyte compl
(ACR) (Adipose most abundant gene transcri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1997
15-SEP-2003
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                         7:941-946(2001).
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Catarrhini; Hominidae,
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Tenner A.J., T
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omiyama Y.,
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nmoto Y.,
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Pfam; PF01391; Collagen; 1.
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SMART; SM00110; ClQ; 1.
PROSITE; PS01113; ClQ; 1.
Hormone; Collagen; Signal; Repeat; Hydroxylation;
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EMBL; AB012165; BAA86716.1; JOINED.
EMBL; AB012164; BAA86716.1; JOINED.
EMBL; AJ131460; CAB52413.1; -
EMBL; AJ131461; CAB52413.1; JOINED.
EMBL; AJ131461; CAB52413.1; JOINED.
EMBL; JC4708; JC4708.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            use by non-profit institutions as long as modified and this statement is not removed. U entities requires a license agreement (See htt or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Otabe S., Okada T., Sto K., Kadowaki H., Hagura R., Akanuma Y., Yazaki Y., Nagai R., Taniyama M., Matsubara K., Yoda M., Nakano Y., Kimura S., Tomita M., Kimura S., Ito C., Froguel P., Kadowaki T.; "Genetic variation in the gene encoding adiponectin is associated with an increased risk of type 2 diabetes in the Japanese population.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MIM;
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Otabe S., Okada
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Horie M., Shi
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MEDLINE=20378830; PubMed=10918532;
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[8]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     [MIM:605441], resulting in very low concentration of plasma adiponectin. Decreased adiponectin plasma levels are associated with obstity insulin resistance, and diabetes type 2. PHARMACEUTICAL: Adiponectin might be used in the treatment of diabetes type 2 and insulin resistance. SIMILARITY: Contains 1 collagenous domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EXPRESSION OF ENDOTHELIAL ADHESION MOLECULES. INVOLVED IN THE CONTROL OF FAT METABOLISM AND INSULIN SENSITIVITY.
SUBUNIT: HOMOOLIGOMER (POTENTIAL).
SUBCELLULAR LOCATION: Secreted.
TISSUE SPECIFICITY: Synthesized exclusively by adipocytes and secreted into plasma.
DISEASE: Defects in APM1 are the cause of adiponectin deficier
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FUNCTION: IMPORTANT NEGATIVE REGULATOR IN HEMATOPOIESIS AND IMMUNE SYSTEMS; MAY BE INVOLVED IN ENDING INFLAMMATORY RESPONSES THROUGH ITS INHIBITORY FUNCTIONS. INHIBITIS ENDOTHELIAL NF-KAPPAB SIGNALING THROUGH A CAMP DEPENDENT PATHWAY. INHIBITS THF-ALPHA, INDUCED THROUGH A CAMP DEPENDENT PATHWAY. INHIBITS THF-ALPHA, INDUCED THROUGH A CAMP DEPENDENT PATHWAY. INHIBITS THE ALPHA INDUCED TO THE PROPERTY OF THE PROPE
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                                                                                                                                                                                                                            Disease mutation;
    244
107
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COLLAGEN-LIKE.
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Matches 51
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P88085; O91080;
01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
1nner ear-specific collagen precursor (Saccular collagen).
Inner ear-specific collagen precursor (Saccular collagen).
Lepomis macrochirus (Bluegill).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostei; Neoteleostei;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Actinopterygii; Neopterygii; Percomorpha; Perciformes; Percoidi
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              between
the Euro
                                                                                                                                                                                                          Davis J.G., Oberholtzer J.C., Burns F.R., "Molecular cloning and characterization or tructural protein."; Science 267:1031-1034(1995).
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MEDLINE=95167486; PubMed=7863331;
Davis J.G., Oberholtzer J.C., Bur
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                                                                                                                                                                      Submitted (MAR-1995) to
                                                                                                                                                                                  Gibson
                                                                                                                                                                                              CONCEPTUAL TRANSLATION
                                                                                                                                                                                                                                                                                                              NCBI_TaxID=13106;
                                                                                                                                                                                                                                                                                                                           Acanthomorpha; Acanthopterygii; Percomorpha; Centrarchidae; Lepomis.
                                                                         MILTED (MAR-1995) to the SWISS-PROT data bank.
FUNCTION: FORMS A MICKOSTRUCTURAL MATRIX WITHIN THE
MEMBRANE (PROBABLY).
TISSUE SPECIFICITY: SPECIALIZED SECRETORY SUPPORTING
OUTER PERIMETER OF THE SACCULAR EPITHELIUM.
SIMILARITY: Contains 1 C10 domain.
CAUTION: THIS IS A CONCEPTUAL TRANSLATION; A FRAMESH
INTRODUCED FOR POSITIONS 391-419 SO AS TO MAXIMIZE T
s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation. European Bioinformatics Institute. There are no restrictions on it by non-profit institutions as long as its content is in no was
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                                                                 OTHER SHORT-CHAIN COLLAGENS
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HYDROXYLATION
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Pred. No. 2.4e-09;
4; Mismatches 65
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Best Local S
Matches 59
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CIQC HUMAN
STANDARD;
PRT; 245
P02747; Q96DL2; Q96H05;
21-JUL-1986 (Rel. 01, Created)
28-FEB-2003 (Rel. 41, Last sequence upda
15-SEP-2003 (Rel. 42, Last annotation up
Complement C1q subcomponent, C chain pre
C1QG OR C1QC.
                                     SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

TISSUE-Monocytes;

MEDLINE-91174759; PubMed=1706597;

MEDLINE-91174759; PubMed=1706597;

Sellar G.C., Blake D.J., Reid K.B.M.;

Characterization and organization of the genes encoding the A-,

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Pfam; PF01391; Collagen;
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InterPro; IPR000087;
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Extracellular matrix; Repeat;
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Hata H., N
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Mammalia; Eutheria;
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Nakagawa S.,
Nakagawa K.,
Mar., Irie R.,
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Primates;
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Otsuki
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N-LINKED (GLCNAC. .) ()
N-LINKED (GLCNAC. .) ()
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Catarrhini; Hominidae;
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 Mizuguchi H., Inagaki
Morinaga M., Kawamura
Sato H., Nishikawa T.,
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     Sugiyama
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                                           Suzuki Y.,
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RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Stapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Rounstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Willalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Willalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
"Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
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                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaborate between the Swiss Institute of Bioinformatics and the EMBL outstations on the European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for commen
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MEDLINE=80020137;
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"NEDO human
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                                                                                                non-profit institutions as lond and this statement is not remove requires a license agreement (SG an email to license@isb-sib.ch).
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an cDNA sequencing project.";
(OCT-2001) to the EMBL/GenBank/DDBJ databases
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Repeat; Signal; Disease mutation.
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(Rel. 08, Created)
(Rel. 20, Last sequence update)

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15-JUL-1999 (Rel. 38, Last annotation update) Collagen alpha 1(X) chain precursor. COL10A1.
CHAIN
DOMAIN
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Yamaguchi N., Benya P.D., van der Rest M., Ninomiya Y.;
"The cloning and sequencing of alpha 1(VIII) collagen cDNAs
"The cloning and sequencing of alpha 1(VIII) collagen cDNAs
demonstrate that type VIII collagen is a short chain collagen and
contains triple-helical and carboxyl-terminal non-triple-helical
domains similar to those of type X collagen.";
J. Biol. Chem. 264:16022-16039 (1999).
-!- FUNCTION: TYPE X COLLAGEN IS A PRODUCT OF HYPERTHROPHIC
CHONDROTOCYTES AND HAS BEEN LOCALIZED TO PRESUMPTIVE
MINERALIZATION ZONES OF HYALINE CARTILAGE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Luvalle P., Ninomiya Y., Rosenblum N.D., Olsen B.R.;
"The type X collagen gene. Intron sequences split the 5'-untranslated region and separate the coding regions for the non-collagenous aminoterminal and triple-helical domains.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=86168227; PubMed Ninomiya Y., Gordon M., Olsen B.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gallue.
                                                                                                                                                                                                                                                                                                                                               Pfam; PF00386; Clq; 1.
Pfam; PF01391; Collagen; 8.
PRINTS; PR00007; COMPLEMNTCLQ.
PRODOM; PD000007; Clq helix; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; M13496; AAA48736.1; ALT_SEQ
EMBL; J04194; AAA48634.1; -.
PIR; S23297; S23297.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -I- PTM: Prolines at the third position of the tripeptide repeating unit (G-X-Y) are hydroxylated in some or all of the chains.
-i- SIMILARITY: STRONG, TO ALPHA 1 AND 2 TYPE VIII COLLAGENS.
-I- SIMILARITY: Contains 1 ClQ domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- SUBUNIT: Homotrimer.
-!- PTM: Prolines at the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=89054019;
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                                                                                                                                                                                                                      SIGNAL
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                                                                                                                                                                                                                                                                                                     PROSITE;
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InterPro; IPR000087; Collagen.
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                         COLLAGEN ALPHA 1(X) CHAIN.
NONHELICAL REGION (NC2).
TRIPLE-HELICAL REGION (NC1).
NONHELICAL REGION (NC1).
CIQ.
HYDROXYLATION.
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     EAB48B1EF174B145 CRC64;
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                                                                      HQPLAFDTEFVNIGGDFDAAAGVFRCRLPGAYFFSFTLGKLPRKTLSVKLMKNRDEVQAM
                                                                                                    GPPGPPGPPGQSTIPEGYVKGESRELSGMSFMKAGANQALTGMPVSAFTVILSKAYPGAT
TYDEYOKGYLDOASGSAVIDLMENDOVWLOLPNSESNGLYSSEYVHSSFSGFL
                        IYDDGASRRREMQSQSVMLALRRGDAVWLLSHDHDGYGAYSNHGKYITFSGFL
                                                                                                                            GPPAPPEP-----SDAGPGPR
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Search completed: January 12, 2004, 08:12:59 Job time: 7.10778 secs

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Copyright (c) 1993 - 2004 Compugen Ltd.
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## ALIGNMENTS

RESULT Q9D0W2	B &	망 왕	g 99	Ma Ma	RP RC RA RL SQ	E E E C C C C C E	RESULT Q8IV25 ID Q AC Q
LT 2	121 RGDAVWLLSHDHDGYGAYSNHGKYITFSGFLVYPDLAPAAPPGLGASELL 170 	61 VFRCRLÞGAYFFSFTLGKLÞRKTLSVKLMKNRDEVQAMIYDDGASRRREMQSQSVMLALR 120 - 	1 ADADAPARGPPAPPEPRSAFSAARTRSLVGSDAGPGPRHQPLAFDTEEVNIGGDFDAAAG 60 	Query Match 100.0%; Score 894; DB 4; Length 329; Best Local Similarity 100.0%; Pred. No. 2.9e-82; Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	SEQUENCE FROM N.A.  SEQUENCE FROM N.A.  TISSUE=Brain;  Strausberg R.;  Stbmitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.  EMBL; BC035628; AAH35628.1;  SEQUENCE 329 AA; 35256 MW; 16064DA8182A6732 CRC64;	(TrEMBLrel. 23, (TrEMBLrel. 23, Clq and tumor nec s (Human) Metazoa; Chordata utheria; Primates 9606;	ILT 1 725 QBIV25 PRELIMINARY; PRT; 329 AA. QBIV25; 01-MAR-2003 (Trembirel 23. Created)

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RC STRAIN=C57BL/63; PIDSUB=Embryo;
RX MEDLINE=210B5660; PIDSUB=Embryo;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konnoo H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yasanaka I.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yasanaka R.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuchl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Kuchl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Blake J., Boffelli D., Bojunga N., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazarelli J., Mombaerts P.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Hayashizaki Y.,
T., Toshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
T. Torkana J., Toshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
T. Torkana J., Toshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
T. Torkana J., Toshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
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Pfam; PF00350; CUP.

PRINTS; PR00007; CUP.

PMART; SM00110; C1Q; 1.

PS01113; C1Q; 1.
                                                   01-JUN-2002 (TrEMBLrel. 21
01-JUN-2002 (TrEMBLrel. 21
01-MAR-2003 (TrEMBLrel. 23
Similar to Clq and tumor n
0710001E10RIK.
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Mammalia; Eutheria;
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EMBL; AK004340; BAB23268.1; -.

MGD; MGI:1914695; 0710001E10Rik.

InterPro; IPR001073; C1q.
Mus musculus (Mouse).
Eukaryota; Metazoa; C
Mammalia; Eutheria; R
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Rodentia;
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 Chordata;
Rodentia;
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92.9%;
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PROBLEM SERVICE REPORTS OF SERVI
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Best Local S
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SMART; SM00110; C1Q; 2.
PROSITE; PS01113; C1Q; 2.
SEQUENCE 326 AA; 35057
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EMBL; BOT315; AAH27315.1; -.
EMBD; MGI:1914655; 071.0001E10Rik
InterPro; IPR001073; C1q.
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0710001E10RIK.
Mus musculus (Mouse).
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STRAIN=C57BL/6J; TISSUE=Brain;
MEDLINE=21085660; PubMed=11217851;
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Mammalia; Eutheria;
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01-JUN-2001
                                                                                                    Nature 409:685-690(2001).
EMBL; AK002948; BAB22473.1;
MGD; MGI:1914695; 0710001E10
                         Pfam; PF00386; Clq;
PRINTS; PR00007; CO
                                                                           InterPro;
                                                                                                                                                                                         Functional annotation
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                                                                              IPR001073;
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0710001E10Rik.
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92.9%;
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Submitted (MAY-2001) to the
EMBL; AK026222; BAB15398 1;
EMBL; BC007520; AAH07520.1;
InterPro; IPR001073; C1q.
                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00386; Clq; 1.
PRINTS; PR00007; COMPLEMN'
SMART; SM00110; ClQ; 1.
PROSITE; PS01113; ClQ; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Watanabe K., Kumagai A., Itakura S., Yamazaki M., Tashi Suzuki Y., Obayashi M., Nishi T., Shibahara T., Tanaka Nakamura Y., Isogai T., Sugano S.;
"NEDO human cDNA sequencing project.";
Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                            Hypothetical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAR-2001 (TrEMBLrel. 16, 01-MAR-2001 (TrEMBLrel. 16, 01-OCT-2002 (TrEMBLrel. 22,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q9H667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE=Uterus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=Small intestine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hypothetical protein FLJ22569.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       v
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      156;
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NHAILQLFQGDQIWLRLH----RGAIYGSSWKYSTFSGYLLYQD
                                                                                                                                  DFDAAAGVFRCRLPGAYFFSFTLGKLP-RKTLSVKLMKNRDEVQAMIYDDGASRRREMQS
                                                                                                                                                                                DVPVTNPAATILPVHVYPLPQQMRVAFSAART----SNLAPGTLDQPIVPDLLLNNLGE
                                                                                                                                                                                                                                  DAPARGP--
                                             QSVMLALRRGDAVWLLSHDHDGYGA-YSNHGKYITFSGFLVYPD
                                                                                        TFDLQLGRFNCPVNGTYVF1FHMLKLAVNVPLYVNLMKNEEVLVSAYANDGAP-DHETAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RGDAVWLLSHDHDGYGAYSNHGKYITFSGFLVYPDLAPAAPPGLGASEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VFRCRLPGAYFFSFTLGKLPRKTLSVKLMKNRDEVQAMIYDDGASRRREMQSQSVMLALR 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RGDAVWLLSHDHDGYGAYSNHGKYITFSGFLVYPDLAAAGPPALKPPEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VFRCRLPGAYFFSFTLGKLPRKTLSVKLMKNRDEVQAMIYDDGASRRREMQSQSVRLPLR
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                                                                                                                                                                                                                                                                                                                                                                  al protein.
158 AA; 1
                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPLEMNTC1Q.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C1Q; 1.
; 22215 MW;
                                                                                                                                                                                                                                                                                                                                                                     17625 MW;
                                                                                                                                                                                                                                                                                                25.7%;
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                                                                                                                                                                                                                             ----PAPPEPRSAFSAARTRSLVGSDAGPGPRHQPLAFDTEFVNIGG
                                                                                                                                                                                                                                                                             16;
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EMBL/GenBank/DDBJ
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Last
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Pred. No. 3.7e
1; Mismatches
                                                                                                                                                                                                                                                                     Score 230; DB 4;
Pred. No. 2.1e-15;
6; Mismatches 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Craniata; Vertebrata; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                     47DB10EDD6DC9760 CRC64;
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                                                                                                                                                                                                                                                                          63;
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; Homo.
                                             155
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RESULT

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DVPVTSPAAAILPVHIYPLPQQMRVAFSAART----

SNLAPGTLDQPIVFDLLLNNLGE

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Matches
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Best L
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Submitted (JAN-2002) to the E:
Submitted (JAN-2002) to the E:
EMBL; AY074490; AAL71549.1; -
InterPro; IPR001073; C1q.
Pfam; PF00386; C1q; 1.
SMART; SM00110; C1Q; 1.
PROSITE; PS01113; C1Q; 1.
                                                                                                                                                                                                                                                                                    Q8K1IO;
01-OCT-2002
01-OCT-2002
                                                                                                                                  Straubberg R.;
Submitted (APR-2002) to the
EMBL; BC027523; AAH27523.1;
InterPro; IPR001073; C1q.
Pfam; PF00386; C1q; 1.
                                                                                          PRINTS; PRO0007; COMPLEMN
SMART; SM00110; C1Q; 1.
PROSITE; PS01113; C1Q; 1.
Hypothetical protein.
                                                                                                                                                                                                                                                     Similar to hypothetical protein FLJ22569 Mus musculus (Mouse).
                                                                                                                                                                                                                                 Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                     Q8K110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (Human
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                  SEQUENCE
                                                                                                                                                                                        TISSUE=Uterus;
                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                           01-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EEG1
                                                                                                                                                                                                                      NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
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01-MAR-2003
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01-JUN-2002
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                                                   Local
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                                        62; Conserv
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                    DAPARGP---
                                                                                                                                                                                                                                                                                                                                                                        NHAILQLFQGDQIWLRLH
                                                                                                                                                                                                                                                                                                                                                                                                                                    DFDAAAGVFRCRLPGAYFFSFTLGKLP-RKTLSVKLMKNRDEVQAMIYDDGASRRREMQS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DAPARGP-----PAPPEPRSAFSAARTRSLVGSDAGPGPRHQPLAFDTEFVNIGG
                                                                                                                                                                                                                                                                                                                                                                                           QSVMLALRRGDAVWLLSHDHDGYGA-YSNHGKYITFSGFLVYPD
                                                                                                                                                                                                                                                                                                                                                                                                                TFDLQLGRFNCPVNGTYVFIFHMLKLAVNVPLYVNLMKNEEVLVSAYANDGAP-DHETAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                         DVPVTNPAATILPVHVYPLPQQMRVAFSAART----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1077 AA;
                                        25.3%;
ilarity 37.8%;
Conservative 1
                                                                                                                                                                                                                                                                       (TrembLrel. 22, Created)
(TrembLrel. 22, Last sequence update)
(TrembLrel. 23, Last annotation update)
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                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
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                                                                                  A
                                                                                                                         COMPLEMNTC1Q
                                                                                                                                                                                                                                 Chordata;
Rodentia;
                                                                                 17533 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25.7%;
38.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            120974 MW;
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21,
23,
                PAPPEPRSAFSAARTRSLVGSDAGPGPRHQPLAFDTEFVNIGG
                                        17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16;
                                      Score 226; DB
Pred. No. 5.3e-
17; Mismatches
                                                                                                                                                                   EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 230; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Created)
                                                                                                                                                                                                                              Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Craniata; Vertebrata; Euteleostomi;
                                                                                  86E9321C99225FCB
                                                                                                                                                                                                                                                                                                                                                                        RGAIYGSSWKYSTFSGYLLYQD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2B88BF3C47D032D6 CRC64;
                                                 226;
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                                                                                                                                                                                                                                                                                                                    158
                                  DB 11.
5.3e-15;
63;
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RESULT
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Best Local S
Matches 56
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Submitted (FEB-2002) to the EMBL/G
EMBL; BCO23468; AAH23468.1; -.
MGD; MGI:1919254; 1600017K21Rik.
InterPro; IPR001073; C1q.
InterPro; IPR001087; Collagen.
Pfam; PF00386; C1q; 1.
                        SEQUENCE FROM N.A.
Sheppard P., Deisher T
Whitmore T., O'Hara P.
"Mus musculus putative
                                                                                                                                                                                                                                                                                        Q9QXP7;
01-MAY-2000 (TrEMBLrel. 13, Createu,
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                           Q9QXP7
Q9QXP7;
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Mammalia; Eutheria; Rodentia;
NCBI_TaxID=10090;
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation updat similar to RIKEN cDNA 1600017K21 gene (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SMART; SM00110; CIQ;
NON TER 1
SEQUENCE 182 AA; ;
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                                                                                                                                                                       NCBI_TaxID=10090;
                                                                                                                                                                                                         Mammalia; Eutheria;
                                                                                                                                                                                                                                 Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                Mus musculus (Mouse)
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ilus putative secreted protein.";
(OCT-1999) to the EMBL/GenBank/DDBJ databases.
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Rodentia;
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                                                                                     Grant F.,
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Pred. No. 2.
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Sciurognathi; Muridae;
                                                                                                                                                                                                      Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus.
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                                                                                           Haldeman
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; Murinae; Mus
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                                                                                           McKnight
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RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., RA Arakawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I., RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R., RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., RA Kuchl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J., RA Kuchl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J., RA Schrimi L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T., RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., RA Gustincich S., Hill D., Hofmann M., Garriboldi J., Mombaerts P., RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., A Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilning L., Wa Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S., A Hayashizaki Y.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR001073; C1q.
InterPro; IPR000087; Collagen.
Pfam; PF00386; C1q; 1.
Pfam; PF01391; Collagen; 1.
PRINTS; PR00007; COMPLEMNTC1Q.
SMART; SM00110; C1Q; 1.
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SEQUENCE FROM N.A.
STRAIN=CS7BL/6J; TISSUE=Placenta;
                                                                                                                                                                                                                                                              QBN6P2;
01-OCT-2002 (TrEMBLrel. 22, Cr
01-OCT-2002 (TrEMBLrel. 22, La
01-MAR-2003 (TrEMBLrel. 23, La
C1q and tumor necrosis factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nature 409:685-690(2001).
EMBL; AF192499; AAF06664.1; -.
EMBL; AK005484; BABZ4070.1; -.
MGD; MGI:1919254; 1600017K2iRik.
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              Strausberg R.;
Submitted (MAY-2002) to the EM
EMBL; BC029485; AAH29485.1; -.
InterPro; IPR001073; Clq.
InterPro; IPR000087; Collagen.
                                                                                                                                                                           NCBI_TaxID=9606;
                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                             Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Functional annotation of a full-length mouse cDNA collection.";
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                                                                                                                       TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  136 GAYSNHGKYITFSGFLVYPDLAP
PF00386;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
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                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
C1q;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           32009 MW;
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39.2%; Pred. No. 4e-
tive 20; Mismatches
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lated protein 5.
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR001073; C1q.
InterPro; IPR000087; Collagen.
Pfam; PF00386; C1q; 1.
Pfam; PF01391; Collagen; 1.
SMART; SM00110; C1Q; 1.
Hypothetical protein.
SEQUENCE 243 AA; 25420 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hypothet:
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-UN-2002 (TrEMBLrel. 21, Created)
01-UN-2002 (TrEMBLrel. 21, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Similar to DKFZP586B0621 protein (Hypothetical 25.4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q8R002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Strausberg
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Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRINTS; PR00007; COME SMART; SM00110; C1Q;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (MAR-2002) to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q8R002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MGD; MGI:2385958; Clqtnf5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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                     12
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                                                                                                                                   111
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BC023068; AAH23068.1;
BC025174; AAH25174.1;
                                                                                                                                                                                                                              51
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              56;
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                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                         IGGDFDAAAGVFRCRLPGAYFFSFTLGKLPRKTLSVKLMKNRDEVQAMIYDDGASRRREM 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DAPARGPPAPP-----EPRSAFSAARTRSLVGSDAGPGPRHQPLAFDTEFVNIGGDFDAA 58
                                                                                                                                 QSQSVMLALRRGDAVWLLSHDHDGYGAYSNHGKYITFSGFLVYPD
                                                                                                                                                                                                                                                                         RGEPGPRGEAGPMGAIGPAGECSVPPRSAFSAKRSESRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LEPEDQVWVQVGVGDYIGIYASIKTDSTFSGFLVYSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TGKFTCQVPGVYYFA-VHATVYRASLQFDLVKNGESIASFFQFFGGWPKPASLSGGAMVR 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AGVFRCRLPGAYFFSFTLGKLPRKTLSVKLMKNRDEVQAMIYDDGASRRREMQSQSVMLA 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EAGPAGPTGPAGECSVPPRSAFSAKRSESRV----PPPSDAPLPFDRVLVNEQGHYDAV 139
                                                                                        LSGGAMVRLEPEDQVWVQVGVGDYIGIYASIKTDSTFSGFLVYSD
                                                                                                                                                                              EQGHFDPTTGKFTCQVPGVYYFA-VHATVYRASLQFDLVKNGQSIASFFQYFGGWPKPAS 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LRRGDAVWLLSHDHDGYGAYSNHGKYITFSGFLVYPD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPLEMNTCIQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chordata;
Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25326 MW;
                                                                                                                                                                                                                                                                                                                  22.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23.3%;
35.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                Score 197.5;
Pred. No. 7.1e
.6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 208.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Craniata; Vertebrata; E
Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           498129CD051DB97B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6D9306A0EB21B44A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                          .le-12;
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                                                                                                                                                                                                                                                                                                                                                                                                           DB 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 4;
                                                                                                                                                                                                                                                                                                                                                                71;
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                                                                                                                                                                                                                                                                         ----PPPADTPLPFDRVLLN
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                                                                                                                                                                                                                                                                                                                                                                                                             Length
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; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              kDa protein)
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                                                                                                                                   155
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                                                                                                                                                                                                                                                                                                                                                                Gaps
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RESULT 13
Q8BRW2
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Best I
Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q8BRW2;
                                                              the RIKEN Genome Exploration Research "Analysis of the mouse transcriptome 10,710 full-length cDNAs."; 600 full-length cDNAs."; Nature 420:563-573(2002).

EMBL; AK041214; BAC30866.1; - SEQUENCE 247 AA; 26751 MW; 0D3FA64
                                                                                                                                                                                                                                                                                                                                                                                                Q8BRW2;
01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                   Mus musculus (Mouse)
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q8K479
Q8K479;
                                                                                                                                                                                                  STRAIN=C57BL/6J; TISSUE=Aorta and vein, MEDLINE=22354683; PubMed=12466851; The FANTOM Consortium,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRINTS; PR00007; COMPLEMNTC1Q SMART; SM00110; C1Q; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR001073; C1q.
InterPro; IPR000087; Collagen.
Pfam; PF00386; C1q; 1.
Pfam; PF01391; Collagen; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MGD; MGI:2385958; Clqtnf5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hum. Mol. Genet. 11:1879-1886 (2002).
EMBL; AF469650; AAM89217.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Mfrp, a gene encoding a frizzled related protein, mouse retinal degeneration 6.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=C57BL/60;
MEDLINE=22135657; PubMed=12140190;
MEDLINE=2135657; PubMed=12140190;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus
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01-OCT-2002
                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                          NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RGPPAP-----PEPRSAFSAARTRSLVGSDAGPGPRHQPLAFDTEFVN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QSQSVMLALRRGDAVWLLSHDHDGYGAYSNHGKYITFSGFLVYPD 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EQGHYDPTTGKFTCQVPGVYYFA-VHATVYRASLQFDLVKNGQSIASFFQYFGGWPKPAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IGGDEDAAAGVERCRLPGAYEESETLGKLPRKTLSVKLMKVRDEVQAMIYDDGASRRREM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RGEPGPRGEAGPMGAIGPAGECSVPPRSAFSAKRSESRV-----PPPADTPLPFDRVLLN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              243 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (TrEMBLrel. 22, Created)
(TrEMBLrel. 22, Last sequence update)
'(TrEMBLrel. 23, Last anoutation update)
clq tumor necrosis factor-related protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chordata;
Rodentia;
                                                                                                                                                                                                                                                                                                                                   Chordata; Craniata; Vertebrata; Euteleostomi; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25436 MW;
  21.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17;
Score
Pred.
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Pred. No. 1.4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Craniata; Vertebrata; |
Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                     0D3FA64C789CAEF3
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  No. 5
                                                                                                                                                        h Group
based o
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  ); DB 11;
5.3e-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ..4e-11;
71;
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                                                                     CRC64;
                       Length 247;
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                                                                                                                                                                                                                                                                                                                                        Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          mutated in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                235
                                                                                                                                                           annotation
                                                                                                                                                                               Team;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  243;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23;
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w 53 ;

ADAPARGPPAPP----EPRSAFSAARTRSLYGSDAGPGPRHQPLAFDTEFVNIGGDFDAA

Matches

Conservative

24;

Mismatches

73;

Indels

8

Gaps

58

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RESULT 14
Q9D8U4
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                                                                                               Query Match
Best Local S
Matches 52
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01-JUN-2001
01-MAR-2003
                                                                                                                                                                                                                             SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                               EMBL; AK007683; BAB25187.1; -.
EMBL; BC030324; AAH30324.1; -.
EMBL; BC130324; 1810033K05Rik,
INCELPTO; IPR001073; C1q.
INCELPTO; IPR001073; Collagen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Strausberg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=C57BL/6J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (MAY-2002) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hayashizaki Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=21085660; PubMed=11217851;
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                                                                                                                                                                                                                          Pfam; PF00386; Clq; 1.
Pfam; PF01391; Collagen; 2.
PRINTS; PR00007; COMPLEMNTC1Q.
PROSTITE; PS01113; ClQ; 1.
SEQUENCE 294 AA; 30865 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Functional
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus (Mouse).
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                                                                                                                                 Similarity
                                 RGPPAPPEP-
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                                                                                                   Conservative
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6J; TISSUE=Pancreas;
                                                                                                                                 21.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                of a
RSAFSAARTRSLVGSDAGPGPRHQ-PLAFDTEFVNIGGDFDAA
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Last annotation updat
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                                                                                                                                 Score 187.5;
Pred. No. 9.
                                                                                                                                                                                                                             6D3905AE7C19E6FA CRC64;
                                                                                                   Mismatches
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RESULT 15
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Q95MQ4;
01-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Collagen.
SEQUENCE
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Pfam; PF01391; Collagen; 1.
PRINTS; PR00007; COMPLEMNTCIQ.
ProDom; PD000007; Collagen; 1.
SMART; SM00110; ClQ; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sato C., Yasukawa Z., Honda N., Matsuda T., Kitajima K.; "Identification and Adipocyte Differentiation-dependent Expression Unique Disialic Acid Residue in an Adipose Tissue-specific Glycoprotein, Adipo Q."; J. Biol. Chem. 276:28849-28856(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bos taurus (Bovine).
Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Pecora; Bovoidea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AF269230; AAK58902.1;
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MEDLINE=21369933; PubMed=11382781;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-DEC-2001 (TrEMBLrel. 19, Last sequence update) 01-MAR-2003 (TrEMBLrel. 23, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Adipose tissue-specific protein adipo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR001073; Clq.
InterPro; IPR000087; Collagen
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                                                                                                                                                           LRRGDAVWLLSHDHDGY-GAYSNHGKYITFSGFLVYPDL
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Pred. No. 1.3e-10;
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Copyright

GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.

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Result
No.
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Maximum DB
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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                                                                                                                                                                                                                      Pred. No. is the number of results predicted by chance to have score greater than or equal to the score of the result being pu and is derived by analysis of the total score distribution.
                                                                                                                                                  Score
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Match
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Gapop 10.0 , Gapext 0.5
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83.1
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77.9
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ABG79643
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AAB61479
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AAB61423
ABG70385
ABG70383
AAB61473
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            Monkey MANGO 245 p
Human MANGO 245 cy
Human MANGO 245 ma
Human MANGO 245 ma
Human MANGO 245 pr
Adipocyte compleme
Adipocyte compleme
                                                                                                                                              Description
                                                                                                                    Human ZACRP4.
Monkey MANGO
                                                                                                                                                                                                                                   printed,
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## ALIGNMENTS

RESULT 1 AAB61606

AAB61606 standard; Protein;

329 AA.

Human ZACRP4

05-APR-2001 AAB61606;

(first entry)

Human; zacrp4; complement factor Clq domain; chromosome llq11; energy balance; cellular metabolic reaction; autocrine factor; development; cell proliferation; differentiation; cell surviva Domain 11-JAN-2001 WO200102565-A2 Domain Peptide Key Homo sapiens /label= Signal\_peptide 17..159 Location/Qualifiers /label= Clq\_domain\_#2 /label=\_Clq\_domain\_#1

01-JUL-1999;

99US-0346502

28-JUN-2000; 2000WO-US17692

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RESULT 2
ABG79643
ID ABG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         domains,
cellular
                                                                                                                                                                                                   Human; SECP; secreted protein; cell proliferative disorder; actinic keratosis; arteriosclerosis; bursitis; hepatitis; cancer; autoimmune disorder; inflammatory disorder; AIDS; asthma; allergy; acquired immunodeficiency syndrome; anaemia; atopic dermatitis; cardiovascular disorder; congestive heart failure; vascular tumour; ischaemic heart disease; myocardial infarction; epilepsy; stroke; hypertensive heart disease; neurological disorder; cerebral neoplasm; Alzheimer's disease; developmental disorder; renal tubular acidosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel secreted protein ZACRP4 polypeptides having tandem C1q globular domains, useful for studying cell-cell communication and regulation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
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 02-FEB-2001;
08-FEB-2001;
                                              28-JAN-2002; 2002WO-US02616
                                                                                                                                           Homo
                                                                                                                                                                        Becker muscular dystrophy.
                                                                                                                                                                                       Alzheimer's disease; develops
Cushing's syndrome; Duchenne
                                                                                                                                                                                                                                                                                                                                             Human novel secreted protein SECP19, Incyte ID No.
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2001US-266195P
2001US-267924P
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Pred. No. 3.9e-89;
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on, ZACRP4
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n

Monkey MANGO 245 protein

04-APR-2001

(first entry)

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concer), autoimmune/inflammatory (e.g. AIDS (acquired immunodeficiency syndrome), attached; a respective heart disease, or vascular tumours), curvous syndrome, anaematory (e.g. Alburocascid), corresponding to the recombinant polynucleotide, an control of the diagnosis. Treatment and prevention of cell proliferative (e.g. actinic keratosis, arteriosclerosis, burstis; hepatitis or concer), autoimmune/inflammatory (e.g. AIDS (acquired immunodeficiency syndrome), astima, anaemia, allergies or atopic dermatitis), corresponding infarction, hypertensive heart disease, or vascular tumours), congestive heart
RESULT 3
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ID AAB6
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AC AAB6
AC AAB6
DT 04-A
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09-FEB-2001; 2001US-268112P.
26-FEB-2001; 2001US-271639P.
07-SEP-2001; 2001US-317818P.
21-DEC-2001; 2001US-343553P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New human secreted proteins and nucleic acids useful in diagnosing, treating and preventing cell proliferative, autoimmune/inflammatory, cardiovascular, neurological, and developmental disorders -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to twenty four human secreted proteins (SECP1-24), proteins 90% identical to them and active fragments Also included are nucleic acids encoding the SECP proteins, a re
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB;
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Y, Yang J,
RA, Richardson T
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                                                                                                                                                 standard; protein;
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elu K, L
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Lal PG, Honch
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'lliott VS;
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                                                                            TANGO; MANGO; colon; autoimmune; allergy;
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                                                                                                                                                                                                 AAB61479 standard;
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Pred. No. 1.3e-86;
1; Mismatches 3
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The nucleic acids, proteins and protein modulators are useful for treating colonic disorders, inflammatory diseases, tumors, renal disorders, liver disorders, lung disorders, autoimmune diseases, renal disorders, cardiovascular diseases, brain disorders, liver disorders, autoimmune diseases, cardiovascular diseases, brain disorders, liver disorders, liver diseases, brain disorders, liver disorders, liver diseases, brain disorders, liver disorders, liver diseases, brain disorders, liver diseases, li
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disorders
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                                    (MILL-) MILLENNIUM PHARM INC
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention relates to cDNAs encoding TANGO 244, TANGO 246, TANGO 275, TANGO 300 and MANGO 245 proteins. The nucleic acids, proteins and protein modulators are useful for treating colonic disorders, inflammatory diseases, tumors, renal disorders, liver disorders, lung disorders, autoimmune diseases, allergic diseases, cardiovascular diseases, brain disorders, degenerative diseases placental, pancreatic, skeletal and muscle
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     disorders (e.g. jaundice)
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pancreatic;
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Isolated cDNAs encoding TANGO 244, TANGO 246, TANGO 275, TANGO 300 and MANGO 245 proteins, useful in the treatment of inflammatory diseases (e.g. idiopathic ulcerative colitis), tumors, renal disorders and lived disorders (e.g. jaundice) -
                                                                                                                                                                                                                                                                                                                                                                                                   04-JAN-2001
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allergy; cardiovascular; brain; degenerative; placental;
skeletal; muscle.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   83.1%;
ilarity 100.0%;
Conservative
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Pred. No. 1.2e-72;
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RESULT 7
ABG70385
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Best Local S
Matches 141
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20-DEC-2000;
02-MAY-2001;
29-MAY-2001;
24-JUL-2001;
10-AUG-2001;
10-AUG-2001;
29-AUG-2001;
                                                                                                                                                                                                                                                                           pigmentation disorder; endocrine disorder; respiratory disease; health gastro-intestinal disease; reproductive; neurological disease; pone marrow transplantation; endocrine disease; allergy; inflammation; nephrological disorder; urinary system disorder; age-related disorder; neuropsychiatric disorder; EGF-related protein; SCUBE1; TEN-M4; adipocyte complement-related C1q tumour necrosis factor; out at first; beta adrenergic receptor kinase; EphA6(ehk-2; glucose transporter; type la membrane sushi-containing domain; butyrophilin;
                                                                                                                                                                                                                                                                                                                                                                                                   Human; NOVX; NOVX-associated disorder; cardiomyopathy; atherosclerosis; cell signal processing; metabolic pathway modulation; metabolic disorder obesity; diabetes; infectious disease; neurodegenerative disorder; acne Alzheimer's disease; parkinson's disease; immune disorder; cancer; haematopoietic disorder; cirrhosis; pancreatitis; learning defect; memory defect; infertility; congenital heart defect; hair growth;
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                                                                                                                                         19-DEC-2001;
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                                                                                                                                                                                                                                 Homo sapiens
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                                                                                                         19-DEC-2000;
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              2000US-265704P.

2000US-257314P.

2001US-288153P.

2001US-294075P.

2001US-307506P.

2001US-311590P.

2001US-311613P.
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                                                                                                                                                                                                                                                                   containing.
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                                                                                                                                                                                                                                                                                                                                                                                        disease; health;
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14-SEP-2001; 2001US-322358P

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RESULT 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cc useful for treating or preventing a NOVX-associated disorder such as a cc cardiomyopathy or atherosclerosis, where the disorder is related to cell signal processing and metabolic pathway modulation in a subject, considerably human. The invention is also useful for treating metabolic disorders (e.g. obesity), diabetes, infectious disease, neurodegenerative disorders (e.g. Alzheimer's disease, Parkinson's disease), immune cd disorders, haematopoietic disorders and various cancers. The molecules of the invention are also useful for treating or preventing cirrhosis, cancreatitis, learning and memory defects, infertility, congenital heart defects, acne, hair growth, pigmentation disorders reproductive, health, respiratory disease, gastro-intestinal diseases, reproductive, health, callergy and infilammation, nephrological diseases, urinary system callergy and infilammation, nephrological disorders, neuropsychiatric disorders and age-related disorders.

The present amino acid sequence represents a NOVX protein of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local
obesity; diabetes; infectious disease; neurodegenerative disorder; Alzheimer's disease; Parkinson's disease; neurodegenerative disorder; Alzheimer's disease; Parkinson's disease; immune disorder; cancer; haematopoietic disorder; cirrhosis; pancreatitis; learning defect; memory defect; infertility; congenital heart defect; hair growth; pigmentation disorder; endocrine disorder; respiratory disease; hea gastro-intestinal disease; reproductive: neurological disease; hea
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Stone DJ,
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                                                                                              cell signal
                                                                                                              Human; NOVX; NOVX-associated disorder;
                                                                                                                                            Adipocyte
                                                                                                                                                                                05-NOV-2002
                                                                                                                                                                                                                ABG70383
                                                                                                                                                                                                                                           ABG70383 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
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                                                                                                                                                                                                                                                                                                                              LVYPDLAPAAPPGLGASELL 299
                                                                                                                                                                                                                                                                                                                                                                                           NRDEVQAMIYDDGASRRREMQSQSVMLALRRGDAVWLLSHDHDGYGAYSNHGKYITFSGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADAGPGPRHQPLAFDTEFVNIGGDFDAAADVFRCRLPGAYFFSFTLGKLPRKTLSVKLMK
                                                                                                                                       complement-related Clq Tumour Necrosis Factor-like protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              299
                                                                                             processing; metabolic pathway modulation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       invention relates to new NOVX polypeptides. The invention
                                                                                                                                                                                (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ΑA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Patturajan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ι SJ,
                                                                                                                                                                              entry.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           81.7%;
98.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 n M, Vernet
Shimkets RA
Boldog FL,
                                                                                                                                                                                                                                              221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Vernet CAM, Mal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 730; DB 23;
Pred. No. 2.9e-71;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Smithson G,
                                                                                                          cardiomyopathy; atherosclerosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Malyankar UM,
rgess CE, Zerh
hson G, Li L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 299;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
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                                                                                              metabolic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ji W;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kekuda
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0
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Liu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
             health;
                                                                                             disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        õ
                                                                                                                                            #1
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맑 8

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EFVNIGGDFDAAAGVFRCRLPGAYFFSFTLGKLPRKTLSVKLMKNRDEVQAMIYDDGASR VYVNIGGDFDAAAGVFRCRLPGAYFFSFTLGKLPRKTLSVKLMKNRDEVQAMIYDDGASR

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                                                                                                                          cc cardiomyopathy or atherosclerosis, where the disorder such as cardiomyopathy or atherosclerosis, where the disorder is related to cell cignal processing and metabolic pathway modulation in a subject, coreferably human. The invention is also useful for treating metabolic disorders (e.g. obesity), diabetes, infectious disease, neurodegenerative disorders (e.g. Alzheimer's disease, Parkinson's disease), immune considers, haematopoietic disorders and various cancers. The molecules of the invention are also useful for treating or preventing cirrhosis, cancreatitis, learning and memory defects, infertility, congenital heart defects, anne, hair growth, pigmentation disorders, endocrine disorders, respiratory disease, gastro-intestinal diseases, reproductive, health, consultation, disorders, uninary system conversed disorders, neuropsychiatric disorders and age-related disorders.

Cf invention amino acid sequence represents a NOVX protein of the
                                                              Matches
                                                                           Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gangolli Stone DJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel isolated NOVX polypeptide useful for treating cardiomyopathy, atherosclerosis, metabolic disorders, diabetes, obesity, infectious disease, anorexia, neurodegenerative disorders, Alzheimer's disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               bone marrow transplantation; endocrine disease; allergy; inflammation; nephrological disorder; urinary system disorder; age-related disorder; neuropsychiatric disorder; EGF-related protein; SCUBE1; TEN-M4; adipocyte complement-related tumour protein; actor; out at first; beta adrenergic recenter times.
                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2002-590744/63.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Stone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19~DEC-2000;
20-DEC-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14-SEP-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10-AUG-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24-JUL-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29-MAY-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     02-MAY-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19-DEC-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200257453-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10-AUG-2001;
                                                                                                                                                                                                                                                                                                                                                                                                     present invention relates to new NOVX polypeptides. The invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        lá membrane-sushi domain containing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      adrenergic receptor kinase; EphA6/ehk-2; glucose transporter; la membrane sushi-containing domain; butyrophilin;
 44
                                9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURAGEN
 GPPTPPGLPGRGRAGLSGKNGFPGDGSSAMRSAFSAARTTPLEGTS---
                                GPPAPP---
                                                                                                                                                                                                                                                                                                                                                                                                                                      Page
                                                                                                                       221 AA;
                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2001US-288153P.
2001US-294075P.
2001US-307506P.
2001US-311590P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Casman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2001US-311613P.
2001US-315617P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2000US-265704P.
2000US-257314P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                     28; 318pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Patturajan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SJ,
                                                                          77.9%;
76.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           n M, Vernet CAM, Malyankar UM,
Shimkets RA, Burgess CE, Zerh
Boldog FL, Smithson G, Li L,
                                                                          Score 696; DB 2
Pred. No. 1e-67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Vernet CAM,
                                                           Mismatches
                             -EPRSAFSAARTRSLVGSDAGPGPRHQPLAFDT
                                                                                        23;
                                                           13;
                                                                                        Length
                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Zerhusen BD,
i L, Ji W;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kekuda R;
---EMAVTFDK
                                                          28;
                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Liu X;
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97
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RESULT 9
AAB61473
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                                                                                                                          Query Match
Best Local Sim
Matches 131;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TANGO; MANGO; colon; :
autoimmune; allergy; (
pancreatic; skeletal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Monkey MANGO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      04-APR-2001
                                                                                                                                                                                                 The present invention relates to cDNAs encoding TANGO 244, TANGO 246, TANGO 275, TANGO 300 and MANGO 245 proteins. The nucleic acids, proteins and protein modulators are useful for treating colonic disorders, inflammatory diseases, tumors, renal disorders, liver disorders, lung disorders, autoimmune diseases, allergic diseases, cardiovascular diseases, brain disorders, degenerative diseases placental, pancreatic, skeletal and muscle
                                                                                                                                                                                                                                                                                                                    Isolated cDNAs encoding TANGO 244, TANGO 246, TANGO 275, TANGO 300 and MANGO 245 proteins, useful in the treatment of inflammatory diseases (e.g. idiopathic ulcerative colitis), tumors, renal disorders and liver
                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-050127/06
                                                                                                                                                                                                                                                                                                                                                                                                                                29-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     29-JUN-2000; 2000WO-US18184.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200100672-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Catarrhini sp..
                                                                                                                                                                                                                                                                                                                                                                                                           (MILL-) MILLENNIUM PHARM INC
                                                                                                                                                                                                                                                                                        Disclosure;
                                                                                                                                                                      Sequence
                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    218
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 121
                     139
                                          61
                                                             79
                                                                                                       19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SELL
                                                                                                                                                                                                                                                                                                                                                                                       DA,
                                                        LPRKTLSVKLMKNRDEVQAMIYDDGASRRREMQSQSVMLALRRGDAVWLLSHDHDGYGAY 138
                                                                                             AFSAARTRSLVGSDAGPGPRHQPLAFDTEFVNIGGDFDAAAGVFRCRLPGAYFFSFTLGK
                                         LPRKTLSVKLMKNRDEVQAMIYDDGASRRREMQSQSVMLALRRGDAVWLLSHDHDGYGAY
                                                                                  SNHGKYITFSGFLV 134
                      SNHCKYITFSGFLV 152
                                                                                                                                                                                                                                                                                                            (e.g. jaundice)
                                                                                                                                                                      134 AA;
                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  245 Clq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     221
                                                                                                                                                                                                                                                                                                                                                                                       Barnes
                                                                                                                                                                                                                                                                                                                                                                                                                                 99US-0342687
                                                                                                                                                                                                                                                                                       28; 262pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein; 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        entry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cardiovascular; brain; degenerative; placental;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            inflammation; tumor; renal; liver; lung;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   domain
                                                                                                                                      76.4%;
97.8%;
                                                                                                                                                                                                                                                                                                                                                                                        Ĭ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        muscle.
                                                                                                                                                                                                                                                                                                                                                                                        Fraser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   #2
                                                                                                                                       Score 683; DB 22;
Pred. No. 1.4e-66;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Å
                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                        3
                                                                                                                                                                                                                                                                                                                                                                                         Sharp
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                                                                                                                                                  22;
                                                                                                                                                 Length 134;
                                                                                                                                Indels
                                                                                                                                0,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      166
                                                                                      60
                                              120
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The present invention relates to new NOVX polypeptides. The invention is useful for treating or preventing a NOVX-associated disorder such as cardiomyopathy or atherosclerosis, where the disorder is related to cell signal processing and metabolic pathway modulation in a subject preferably human. The invention is also useful for treating metabolic disorders (e.g. obesity), diabetes, infectious disease, neurodegenerative disorders (e.g. Alzheimer's disease, Parkinson's disease) immune disorders, haematopoletic disorders and various cancers. The molecules of the invention are also useful for treating metabolic disorders (e.g. Alzheimer's disease, Parkinson's disease). The molecules of

the invention are also useful for treating or preventing cirrhosis, pancreatitis, learning and memory defects, infertility, congenital defects, acne, hair growth, pigmentation disorders, endocrine disorders.

Novel isolated NOVX polypeptide useful for treating cardiomyopathy, atherosclerosis, metabolic disorders, diabetes, obesity, infectious disease, anorexia, neurodegenerative disorders, Alzheimer's disease cancer

õ

Claim 1; Page 30; 318pp;

English

Gangolli

EΑ,

Anderson Casman

SJ,

Zerhusen B i L, Ji W;

BD,

Liu X;

Spytek Stone DJ,

ζ,

2002-590744/63.

ABS52096

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RESULT 10
ABG70384
20-DEC-2000; 2000US-257314P.
02-MAY-2001; 2001US-288153P.
29-MAY-2001; 2001US-29075P.
24-JUL-2001; 2001US-307506P.
10-AUG-2001; 2001US-31153P.
29-AUG-2001; 2001US-315617P.
14-SEP-2001; 2001US-322358P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 haematopoietic disorder; cirrhosis; pancreatitis; learning defect; memory defect; infertility; congenital heart defect; hair growth; pigmentation disorder; endocrine disorder; respiratory disease; health; gastro-intestinal disease; reproductive; neurological disease; bone marrow transplantation; endocrine disease; allergy; inflammation; nephrological disorder; urinary system disorder; age-related disorder; neuropsychiatric disorder; EGF-related procein; SCUBEL; TEN-M4; adipocyte complement-related C1q tumour necrosis factor; out at first; beta adrenergic receptor kinase; Ephh6/ehk-2; glucose transporter; type la membrane sushi-containing domain; butyrophilin; type la membrane-sushi domain containing.
                                                                                                                                                                                                                                                                                                                                                                                                                  19-DEC-2000;
20-DEC-2000;
02-MAY-2001;
29-MAY-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABG70384 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            obesity; diabetes; infectious disease; neurodegenerative disorder; Alzheimer's disease; Parkinson's disease; immune disorder; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cell signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; NOVX;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Adipocyte complement-related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    05-NOV-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19-DEC-2001; 2001WO-US50331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200257453-A2
                                                                                                                                                                                                                                                                                                                              (CURA-)
                                                                                                                                                                                                                                                                                                                                CURAGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     , NOVX-associated disorder; cardiomyopathy; atherosclerosis; processing; metabolic pathway modulation; metabolic disorde
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                           2000US-265704P
                                                                                                                                                                                                                                                                                                        Patturajan M,
                                                                                                                                                                                                                                                                                                                                 CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    entry)
                                                                                                                                                                                                                                                                             n M, Vernet CAM, Malyankar UM,
Shimkets RA, Burgess CE, Zerh
Boldog FL, Smithson G, Li L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        284
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tumour Necrosis Factor-like protein #2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            disorder;
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RESULT 11
ABB11578
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                               inhibin; chemotaris; chemokinesis; thrombolysis; oncogenesis; proliferation; metastasis; cancer; tumour; haematopoietic disorder myeloid cell disorder; proliferation; metastasis; cancer; tumour; haematopoietic disorder; proliferation; proliferative retrinopathy; chronic inflammatory condition; proliferative retrinopathy; atherosclerosis; coronary heart disease; arterial ischaemia; bone disorder; osteoporosis; vascular growth disorder; tissue regeneration; wound healing; infection; immune disorder; cell culture; drug screening; gene therapy; antiaflammatory; antiasthmatic; antiarthritic; haemostatic; antiarteriosclerotic; cyrostatic; osteopathic; vascotropic; cardiant; virucide; antibact
                                                                                                                                                                                                                                                                                                                                                                                                                                Human; cytokine; cell proliferation; cell differentiation; growth factor; haematopoiesis regulation; tissue growth; immunomodulator; activin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABB11578 standard; peptide; 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       neurological diseases, bone marrow transplantation, endocrine diseallersy and inflammation, nephrological disorders, urinary system disorders, neuropsychiatric disorders and age-related disorders. The present amino acid sequence represents a NOVX protein of the
                                                                                                                          05-FEB-2001;
                                                                                                                                                                                                                        Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human secreted protein homologue,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         respiratory disease, gastro-intestinal diseases, neurological diseases, bone marrow transplantation
                                                                           03-FEB-2000;
27-APR-2000;
                                                                                                                                                          09-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                           (HYSE-) HYSEQ INC
                                                                                                                                                                                          WO200157188-A2
               ΥŦ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 142
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             136 LHGAPQYALGAPGATFSGYLVYADAEFVNIGGDFDAAAGVFRCRLPGAYFFSFTLGKLPR 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               82
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GKYITFSGFLVYPDLAPAAPPGLGASELL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ARGP---PAPPEPRSAFSAARTRSL------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GKYITFSGFLVYPDLAPAAPPGLGASELL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KTLSVKLMKNRDEVQAMIYDDGASRRREMQSQSVMLALRRGDAVWLLSHDHDGYGAYSNH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KTLSVKLMKNRDEVQAMIYDDGASRRREMQSQSVMLALRRGDAVWLLSHDHDGYGAYSNH 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YFFSFTAGKAPHKSLSVMLVRNRDEVQALAFDEQRRPGARRAASQSAMLQLDYGDTVWLR 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ALGPTPGPGSSELRSAFSAÄRTTPLEGTSEMAVTFDKVYVNIGGDFDVATGQFRCRVPGA 75
           Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             284 AA;
                                                                                                                                                                                                                                                        vulnerary;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                           2000US-0496914.
2000US-0560875.
                                                                                                                        2001WO-US03800.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -AGPGPRH------QPLAF-----
             Drmanac RT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            74.6%;
55.4%;
                                                                                                                                                                                                                                                        antiulcer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 666.5; 1
Pred. No. 2.3e
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ۲.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Å
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -DTEFVNIGGDFDAAAGVFRCRLPGAYFFSFTLGKLPR 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQ ID NO:1948
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3e-64;
                                                                                                                                                                                                                                                                                                                                                                                                     haematopoietic disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----VGSD-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        reproductive,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels 105;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         endocrine diseases,
                                                                                                                                                                                                                                                                     antibacterial;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             44
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Human proteins and DNA encoding sequences useful for preventing, treating or ameliorating a medical condition in a mammalian sub-
e.g. arthritis and cancer -
e.g. arthritis
                                                                                                                   N-PSDB;
                             in a mammalian subject
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Claim 20;

Page 214-215; 1963pp; English

CC giving an insight into their probable biological activities, and hence CC potential therapeutic applications. The polypeptides of the invention may CC have various activities, including cytokine, cell proliferation or cell CC differentiation activities; stem cell growth factor activity; have various activity; activity; tissue growth activity; chemotractic or chemokinetic activity; tissue growth activity; chemotractic or chemokinetic activities; haemostatic, thrombotic or thrombolytic activities; receptor or ligand activities; or may be CC involved in oncogenesis, cancer cell proliferation or metastasis. CC Depending on their biological activities, polypeptides and nucleotides of CC chemotractic or their biological activities, polypeptides and nucleotides of CC conditions, e.g., by protein or gene therapy. Such conditions include CC cancers, haematopoietic disorders (e.g., myeloid or lymphoid cell conditions, c.g., chronic inflammatory conditions (e.g., asthma or arthritis), CC proliferative retinopathy, atherosclevosis, coronary heart disease, CC arterial ischaemia, bone disorders (e.g., oronary heart disease, CC arterial ischaemia, bone disorders (e.g., oronary heart disease, CC arterial ischaemia, bone disorders (e.g., oronary heart disease, CC arterial ischaemia, bone disorders (e.g., oronary heart disease, CC arterial ischaemia, bone disorders (e.g., oronary heart disease, CC arterial ischaemia, bone disorders (e.g., oronary heart disease, CC arterial ischaemia, bone disorders (e.g., oronary heart disease, CC arterial ischaemia, bone disorders (e.g., oronary heart disease, CC arterial ischaemia, bone disorders (e.g., oronary heart disease, CC arterial ischaemia, bone disorders (e.g., oronary heart disease, CC arterial ischaemia, bone disorders (e.g., oronary heart disease, CC arterial ischaemia, bone disorders (e.g., oronary heart disease, CC arterial ischaemia, bone disorders, coronary heart disorders (e.g., oronary heart disorders (e.g., oronary heart disorders), coronary heart disorders (e.g., oronary Sequences ABB10981-ABB12330 represent 1350 novel human polypeptides, and sequences ABA08225-ABA09574 represent nucleic acids encoding them. The invention also relates to vectors and recombinant host cells comprising a nucleotide of the invention, methods of producing the novel polypeptides, antibodies against the polypeptides, methods of detecting the nucleotides or polypeptides in a sample, and methods of identifying compounds which bind to polypeptides of the invention. Although novel, many of the polypeptides of the invention have homology to known proteins, thereby interesting the polypeptides of the invention have homology to known proteins, thereby polypeptide techniques. 127 of the A invention present sequence represents a novel human

Sequence

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RESULT 12
AAB61470
ID AAB61
XX
AC AAB61
XX
DT 04-AF
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                                                                                                                                                                      Query Match
Best Local S
Matches 126
                                 AAB61470
                                                                                                                       104
                                                                                      164
                                                                                                       61
                                                                                                                                                        44
                                                                                                                                                                        126;
                                                                                                                                        Similarity
                                standard; protein; 117
                                                                                      LGASELL 170
                                                                                                      LGASELL
                                                                                                                                        FDTEFVNIGGDFDAAAGVFRCRLPGAYFFSFTLGKLPRKTLSVKLMKNRDEVQAMIYDDG
                                                                                                                                                       FDTEFVNIGGDFDAAAGVFRCRLPGAYFFSFTLGKLPRKTLSVKLMKNRDEVQAMIYDDG
                                                                                                                                                                        Conservative
                                                                                                                                                                               74.3%;
                                                                                                                                                                      1;
                                                                                                                                                                              Score 664;
Pred. No. 1.
                                                                                                                                                                        Mismatches
                                                                                                                                                                              DB 22;
                                                                                                                                                                                     22;
                                                                                                                                                                                     Length 127;
                                                                                                                                                                       Indels
                                                                                                                                                                      0
                                                                                                                                                                      Gaps
                                                                                                                       163
                                                                                                                                                       103
                                                                                                       120
                                                                                                                                       60
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04-APR-2001 AAB61470;

(first entry)

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RESULT 13
AAB61468
ID AAB61
XX AAB61
AC AAB61
XX                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ś
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 117; Conserv
                                                                                                                                             TANGO; MANGO; colon; inflammation; tumor; resultoimmune; allergy; cardiovascular; brain; pancreatic; skeletal; muscle.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention relates to cDNAs encoding TANGO 244, TANGO 246, TANGO 275, TANGO 300 and MANGO 245 proteins.

The nucleic acids, proteins and protein modulators are useful for treating colonic disorders, inflammatory diseases, tumors, renal disorders, liver disorders, lung disorders, autoimmune diseases, allergic diseases, cardiovascular diseases, brain disorders, degenerative diseases placental, pancreatic, skeletal and muscle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MANGO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     disorders (e.g. jaundice) -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    pancreatic; skeletal; muscle.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           autoimmune;
                                                                                               Catarrhini sp..
                                                                                                                                                                                                                                                       Mature monkey
                                                                                                                                                                                                                                                                                                        04-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                     AAB61468 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Fig 26; 262pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-050127/06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Holtzman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      04-JAN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200100672-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TANGO; MANGO;
                                                      WO200100672-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (MILL-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ted cDNAs encoding TANGO 244, TANGO 246, TANGO 275, TANGO 300 and 245 proteins, useful in the treatment of inflammatory diseases idiopathic ulcerative colitis), tumors, renal disorders and liver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MANGO 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MILLENNIUM PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LPRKTLSVKLMKURDEVQAMIYDDGASRRREMQSQSVMLALRRGDAVWLLSHDHDGY 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AFSAARTRSLVGSDAGPGPRHQPLAFDTEFVNIGGDFDAAAGVFRCRLPGAYFFSFTLGK 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AFSAARTRSLVGSDAGPGPRHQPLAFDTEFVNIGGDFDAAAGVFRCRLPGAYFFSFTLGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2000WO-US18184
                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  colon;
                                                                                                                                                                                                                                                       MANGO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Barnes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8
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                                                                                                                                                                                                                                                                                                                                                                                                     protein; 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    domain
                                                                                                                                                                                                                                                     245 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          68.1%;
100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           inflammation; tumor; renal; liver; lung; cardiovascular; brain; degenerative; pla
                                                                                                                                                                                                    inflammation; tumor; renal; liver; lung;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ĭ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fraser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 609; DB; Pred. No. 1.500; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sharp JD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1.5e-58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22;
                                                                                                                                                                            degenerative;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   <u>,</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length
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                                                                                                                                                                            placental;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           placental;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                        ABG70386
                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local S
Matches 101
                                                                                      haematopoietic disorder; cirrhosis; pancreatitis; learning defect; memory defect; infertility; congenital heart defect; hair growth; pigmentation disorder; endocrine disorder; respiratory disease; health gastro-intestinal disease; reproductive; neurological disease; bone marrow transplantation; endocrine disease; allergy; inflammation; nephrological disorder; urinary system disorder; age-related disorder; neuropsychiatric disorder; EGF-related protein; SCUBE1; TEN-M4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention relates to cDNAs encoding TANGO 244, TANGO 246, TANGO 275, TANGO 300 and MANGO 245 proteins.

The nucleic acids, proteins and protein modulators are useful for treating colonic disorders, inflammatory diseases, tumors, renal disorders, liver disorders, lung disorders, autoimmune diseases, allergic diseases, cardiovascular diseases, brain disorders, degenerative diseases placental, pancreatic, skeletal and muscle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI;
                            adipocyte complement-related C1q tumour necrosis factor; out at first; beta adrenergic receptor kinase; EphA6/ehk-2; glucose transporter; type 1a membrane sushi-containing domain; butyrophilin; type 1a membrane-sushi domain containing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Isolated cDNAs encoding TANGO 244, TANGO 246, TANGO 275, TANGO 300 au MANGO 245 proteins, useful in the treatment of inflammatory diseases (e.g. idiopathic ulcerative colitis), tumors, renal disorders and live
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29-JUN-2000;
                                                                                                                                                                                                          Alzheimer's disease; Parkinson's disease; immune disorder; cancer
                                                                                                                                                                                                                            obesity;
                                                                                                                                                                                                                                                            Human; NOVX; NOVX-associated disorder; cardiomyopathy; atherosclerosis;
                                                                                                                                                                                                                                                                                        Adipocyte complement-related Clq Tumour Necrosis Factor-like protein
                                                                                                                                                                                                                                                                                                                          05-NOV-2002
                                                                                                                                                                                                                                                                                                                                                          ABG70386;
                                                                                                                                                                                                                                                                                                                                                                                        ABG70386
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                                                                                                                                                                                                                                          signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  101;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      86
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DA,
                                                                                                                                                                                                                           nal processing; metabolic pathway modulation; metabolic dia
diabetes; infectious disease; neurodegenerative disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WLLSHDHDGYGAYSNHGKYITFSGFLVYPDLAPAAPPGLGASELL
                                                                                                                                                                                                                                                                                                                                                                                         standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WLLSHDHDGYGAYSNHGKYITFSGFLVYPDLAGGAPPGLGAPELL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VPGAYFFSFTVGKAPHKSL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PAPG-PGSSELRSAFSAARTTPLEGAS-----EMAVTFDKVYVNIGGDFDAATGQFRCR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PARGPPAPPEPRSAFSAARTRSLVGSDAGPGPRHQPLAFDTEFVNIGGDFDAAAGVFRCR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (e.g. jaundice)
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                                                                                                                                                                                                                                                                                                                        (first
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                                                                                                                                                                                                                                                                                                                                                                                        Protein;
                                                                                                                                                                                                                                                                                                                        entry)
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M.
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Pred. No. 1.3e-44;
6; Mismatches 22
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                                                                                                                                                             air growth;
disease; health;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            and liver
                                                                                                                                                                                                                                           disorder;
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Homo sapiens

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                                                                                                                                                                                                                                                                      cc useful for treating or preventing a NOVX-associated disorder such as a cardiomyopathy or atherosclerosis, where the disorder is related to cell signal processing and metabolic pathway modulation in a subject, comprehensing the invention is also useful for treating metabolic disorders (e.g. obssity), diabetes, infectious disease, neurodegenerative disorders (e.g. Alzheimer's disease, Parkinson's disease), immune cc disorders, haematopoietic disorders and various cancers. The molecules of the invention are also useful for treating or preventing cirrhosis, cancreatitis, learning and memory defects, infertility, congenital heart defects, acne, hair growth, pigmentation disorders, endocrine disorders, respiratory disease, gastro-intestinal diseases, reproductive, health, consurological diseases, bone marrow transplantation, endocrine diseases, callergy and inflammation, nephrological disorders, uninary system constitution acid sequence represents a NOVX protein of the
                                                                                                                                                                            Matches
                                                                                                                                                                                        Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19-DEC-2000;
20-DEC-2000;
02-MAY-2001;
29-MAY-2001;
24-JUL-2001;
                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; Page 32; 318pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel isolated NOVX polypeptide useful for treating cardiomyopathy, atherosclerosis, metabolic disorders, diabetes, obesity, infectious disease, anorexia, neurodegenerative disorders, Alzheimer's disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2002-590744/63.
N-PSDB; ABS52098.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19-DEC-2001;
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14-SEP-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    present invention relates to new NOVX polypeptides. The invention is
                           124
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Similarity 56.3%;
94; Conservative
               AVWLLSHDHDGYGAYSNHGKYITFSGFLVYPDLAPAAPPGLGASELL
                                                                                                                                 ARGP---PAPPEPRSAFSAARTRSLVGSDAGPGPRHQPLAFDTEFVNIGGDFDAAAGVFR
                                                                                  CRLPGAYFFSFTLGKLPRKTLSVKLMKNRDEVQAMIYDDGASRRREMQSQSVMLALRRGD 122
                                                                                                               ALGPTPGPGSSELRSAFSAARTTPLEGTS-----EMAVTFDKVYVNIGGDFDVATGQFR
AVWLLSHDHDGYGAYSNHGKYITFSGFLVYPDLAPAAPPGLGASELL
                                                                                                                                                                                                                                   133 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Casman SJ,
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2001US-315617P.
2001US-322358P.
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2001US-294075P.
2001US-307506P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 M. Vernet CAM, PRALYWHILL Schimkets RA, Burgess CE, Zerhusen BD, Boldog FL, Smithson G, Li L, Ji W;
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                                                                                                                                                                      Score 432; DB 23;
Pred. No. 3.8e-39;
3; Mismatches 18
                                                                                                                                                                                                     23;
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                                                                                                                                                                         Indels
                                                       ---REMOSOSVMLALRRGD
                         170
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133
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RESULT 15 AAB61488 ID AAB61

AAB61488

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protein;

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Search completed: January Job time: 26.6188 secs
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Best Local :
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The nucleic acids, proteins and protein modulators are useful treating colonic disorders, inflammatory diseases, tumors, renal disorders, liver disorders, lung disorders, autoimmune callergic diseases, cardiovascular diseases, brain disorders, allergic diseases, cardiovascular diseases, brain disorders,
                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Isolated cDNAs encoding TANGO 244, TANGO 246, TANGO 275, TANGO 300 and MANGO 245 proteins, useful in the treatment of inflammatory diseases (e.g. idiopathic ulcerative colitis), tumors, renal disorders and liver disorders (e.g. jaundice) -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TANGO; MANGO; colon; inflammation; tumor; renal; liver; lung; autoimmune; allergy; cardiovascular; brain; degenerative; placental; pancreatic; skeletal; muscle.
                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; Fig 29; 262pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Holtzman
                                                                                                                                                                                                                                                                                                                 degenerative diseases placental, pancreatic, skeletal and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-050127/06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29-JUN-2000; 2000WO-US18184
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87; Conserv
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                                                                                GDAVWLLSHDHDGYGAYSNHGKYITFSGFLVYPDL-----APAAP 161
                                                                                                                                   RLPGAYFFSFTLGKLPRKTLSVKLMKNRDEVQAMIYDDGASRR---REMQSQSVMLALRR 121
                                                                                                                                                                                 ARGP--PAPPEPRSAFSAARTRSLVGSDAGPGPRHQPLAFDTEFVNIGGDFDAAAGVFRC
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                                                     GDTVWLRLH--
                                                                                                          RVPGAYFFSFTAGKAPHKNLSVMLVRNRDEVQALAFD--KQRRPGARRAASQSAMLQLDY
                                                                                                                                                                ALGPAGPGSSELRSAFSAARTTPLEGTS-----EMAVTFDKVYVNIGGDFDAATGRFRC
                                                                                                                                                                                                                                                                          199 AA;
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Pred. No. 8.7e-31;
0; Mismatches 47
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                                                                                                                                                                                                                    47;
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                                                                                                                                                                                                                                               199;
                                                                                                                                                                                                                                                                                                                 muscle
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Result
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Total number of hits satisfying chosen parameters:
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                                                                                                                                                                                                                                                                                                           Score
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807.5
237.5
                                                                                                                                                                                                                                                                                                                                                                                                 is the number of results predicted by chance to have a ster than or equal to the score of the result being printed, rived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                         Match Length
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         100.0
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Cgn2_6/ptodata/1/pubpaa/US06 PUBCOMB.pep:*
Cgn2_6/ptodata/1/pubpaa/US07_NEW PUB.pep:*
Cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        n2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep:*
n2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep:*
n2_6/ptodata/1/pubpaa/US09Sew_PUB-pep:*
n2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
n2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
n2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*
n2_6/ptodata/1/pubpaa/US10Sew_PUB.pep:*
n2_6/ptodata/1/pubpaa/US10Sew_PUB.pep:*
         6/ptodata/1/pubpaa/US08 NEW PUB.pep:*
6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
6/ptodata/1/pubpaa/US09A_PUBCOMB.pep:*
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   US-10-236-055A-14
US-10-085-167-2
US-10-2085-16-055A-16
US-09-893-737-52
US-10-091-458-43
US-10-91-458-43
US-09-738-973-185
US-09-854-133-185
US-09-854-133-185
US-10-309-422-10
US-10-309-422-14
US-10-309-422-14
US-10-309-422-18
US-10-309-422-18
US-10-309-422-18
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US-10-309-422-3
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Sequence 14, Appl
Sequence 2, Appli
Sequence 16, Appl
Sequence 52, Appl
Sequence 43, Appl
Sequence 24, Appl
Sequence 185, App
Sequence 185, App
Sequence 10, Appl
Sequence 10, Appl
Sequence 22, Appl
Sequence 22, Appl
Sequence 24, Appl
Sequence 26, Appl
Sequence 26, Appl
Sequence 27, Appl
Sequence 28, Appl
Sequence 28, Appl
Sequence 28, Appl
Sequence 30, Appl
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US-10-236-055A-14

# ALIGNMENTS

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TITLE OF INVENTION: MAMMALIAN GENES; RELATED REAGENTS; FILE REFERENCE: DX01343K; CURRENT APPLICATION UNMER: US/10/236,055A; CURRENT FILING DATE: 2003-02-28; PRIOR APPLICATION NUMBER: US 60/317,988; PRIOR FILING DATE: 2001-09-06; NUMBER OF SEQ ID NOS: 36; SOFTWARE: Patentin version 3.1; SEQ ID NO 14; LENGTH: 329; TYPE: PRIOR COLORS (1997)
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                                                                                                                                                                                                                                  Query Match 100.0%; Score 894; DB 12; Best Local Similarity 100.0%; Pred. No. 7.1e-84;
                                                                                                                                                                                                                Matches 170;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 14, Application US/10236055A
Publication No. US20030134328A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Mattson, Jeanine
APPLICANT: Moshrefi, Mehrdad
APPLICANT: Parham, Christi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Basham, Beth E.
APPLICANT: Forsythe, Ian
APPLICANT: Gorman, Daniel M.
                                                                                                                                                                                                                                                                                                                            ORGANISM: Homo sapiens
121 RGDAVWLLSHDHDGYGAYSNHGKYITFSGFLVYPDLAPAAPPGLGASELL 170
                                                                                                                            160 ADADAPARGPPAPPEPRSAFSAARTRSLVGSDAGPGPRHOPLAFDTEFVNIGGDFDAAAG
                                                                                   61 VFRCRLPGAYFFSFTLGKLPRKTLSVKLMKNRDEVQAMIYDDGASRRREMQSQSVMLALR 120
                                                                                                                                                                     1 ADADAPARGPPAPPEPRSAFSAARTRSLVGSDAGPGPRHQPLAFDTEFVNIGGDFDAAAG
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US-10-085-167-2

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APPLICANT: Gorman, Daniel M.
APPLICANT: Mattson, Jeanine
APPLICANT: Mattson, Jeanine
APPLICANT: Moshrefi, Mehrdad
APPLICANT: Moshrefi, Mehrdad
APPLICANT: Parham, Christi
TITLE OF INVENTION: MAMMALIAN GENES; RELATED REAGENTS
FILE REFERENCE: DX01343K
CURRENT APPLICATION NUMBER: US/10/236,055A
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/317,988
PRIOR FILING DATE: 2001-09-06
NUMBER OF SEQ ID NOS: 36
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US-10-236-055A-16
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TYPE: PRT
ORGANISM: Homo sapiens
US-10-085-167-2
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SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 2
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Best Local :
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Best Local Similarity
                                                                                                                                                 SOFTWARE: PatentIn version 3.1
SEQ ID NO 16
LENGTH: 326
TYPE: PRT
ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 16, Application US/10236055A Publication No. US20030134328A1
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APPLICANT: Lok, Si
TITLE OP INVENTION: SECRETED PROTEIN ZACRP4
FILE REFERENCE: 99-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/10/085,167
CURRENT FILING DATE: 2002-02-27
PRIOR APPLICATION NUMBER: 60/141,928
PRIOR FILING DATE: 1999-07-01
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ADADAPARGPPAPPEPRSAFSAARTRSLVGSDAGPGPRHQPLAFDTEFVNIGGDFDAAAG
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                                                           Conservative
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92.9%;
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                                                          Score 807.5; DB 12;
Pred. No. 5.8e-75;
1; Mismatches 10;
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Pred. No. 7.1e-84;
); Mismatches 0;
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SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 52

LENGTH: 252

TYPE: PRT

ORGANISM: Homo sapiens

US-09-893-737-52
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US-09-893-737-52
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                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 43, Application US/10091458 Publication No. US20030068627A1
                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
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CURRENT APPLICATION NUMBER: US/09/893,737
CURRENT FILING DATE: 2001-06-28
CURRENT FILING DATE: 1IS 60/215,446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: US 60/215,446
PRIOR FILING DATE: 2000-06-30
NUMBER OF SEQ ID NOS: 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Sheppard, Paul O.
APPLICANT: Presnell, Scott R.
TITLE OF INVENTION: MAMMALIAN SECRETED PROTEINS
                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/10/091,458
CURRENT FILING DATE: 2002-03-07
PRIOR APPLICATION NUMBER: 09/764,900
PRIOR FILING DATE: 2001-01-17
                                                                                                                                        PRIOR
                                                                                                                                                                                                                                                                                                                        APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins,
FILE REFERENCE: PTZ06C1
                                                                            PRIOR PRIOR PRIOR
                                                                                                                                                                            PRIOR APPLICATION NUMBER: 60/179,065
PRIOR FILING DATE: 2000-01-31
PRIOR APPLICATION NUMBER: 60/180,628
                   PRIOR
                                                         PRIOR
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              APPLICATION NUMBER: 60/217,487
FILING DATE: 2000-07-11
APPLICATION NUMBER: 60/225,758
FILING DATE: 2000-08-14
APPLICATION NUMBER: 60/220,963
                                                                                                                    APPLICATION NUMBER: 60/214,886 FILING DATE: 2000-06-28
                                                                                                                                                               FILING DATE: 2000-02-04
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APPLICATION NUMBER: 60/226,868 FILING DATE: 2000-08-22 APPLICATION NUMBER: 60/216,647 FILING DATE: 2000-07-07

APPLICATION NUMBER: 60/218,290 FILING DATE: 2000-07-14 APPLICATION NUMBER: 60/225,757 FILING DATE: 2000-08-14

APPLICATION NUMBER: 60/217,496
FILING DATE: 2000-07-11
APPLICATION NUMBER: 60/225,447
FILING DATE: 2000-08-14

FILING DATE: 2000-08-14 APPLICATION NUMBER: 60/ FILING DATE: 2000-07-07

60/216,880

APPLICATION NUMBER: 60/225,270

APPLICATION NUMBER: 60/225,267

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ЯŽ	2000	NUMBER	2000-	ATIMBER	NUMBER	2000-		- OOOD	NUMBER:	2000-	-0002	NUMBER:	2000-	VIJMBER - NEW PROPERTY	NUMBER:	2000-	NUMBER	NUMBER:	2000-	NUMBER:	NUMBER	2000-06	NUMBER:	NUMBER:	2000-09	NUMBER:	NUMBER:	2000-08	2000-08	NUMBER:	NUMBER:	2000-08	2000-11	2000-11 NUMBER:	NUMBER:	NUMBER:	2000-	-0000 Z	NUMBER:	2000-	2000-	NUMBER:	-0000 S	2000-	NUMBER	NUMBER:	2000	2000-	NUMBER	NUMBER:
60/232,400	17	60/249,297	17	60/249.214			17	-17 60/249		-17	-17 60/349 34	თ	-17	60/249		-17	60/249	0	-17	σ.	. 0	-30	60	. თ	-27	60/235,836	σ	ισ	-14	σ 1	െ	-22 )	-17	-17 60/249	09	1 6	-08	-20 60/246	60	-13	-13	60		-02	60/237,040	60	60/236,802 )-02	-29	60/236,370	60

APPLICATION NUMBER: 60/236,369
FILING DATE: 2000-09-29
APPLICATION NUMBER: 60/224,519
FILING DATE: 2000-08-14
APPLICATION NUMBER: 60/220,964

APPLICATION NUMBER: 60/224,518 FILING DATE: 2000-08-14

APPLICATION NUMBER: 60/234,223 FILING DATE: 2000-09-21 APPLICATION NUMBER: 60/228,924 FILING DATE: 2000-08-30

FILING DATE: 2000-08-14
APPLICATION NUMBER: 60/251,869
FILING DATE: 2000-12-08
APPLICATION NUMBER: 60/235,834
FILING DATE: 2000-09-27
APPLICATION NUMBER: 60/234,274
FILING DATE: 2000-09-21

FILING DATE: 2000-07-26
APPLICATION NUMBER: 60/241,809

LING DATE: 2000-10-20

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OR APPLICATION NUMBER: 60/229,513
OR FILLING DATE: 2000-09-05
OR FILLING DATE: 2000-09-08
OR FILLING DATE: 2000-09-08
OR APPLICATION NUMBER: 60/229,509
OR FILING DATE: 2000-09-05
OR FILING DATE: 2000-09-05
OR APPLICATION NUMBER: 60/236,367
OR APPLICATION NUMBER: 60/237,039
OR APPLICATION NUMBER: 60/237,039

APPLICATION NUMBER: 60/225,268
OR FILING DATE: 2000-08-14
OR APPLICATION NUMBER: 60/236,368
OR FILING DATE: 2000-09-29
OR APPLICATION NUMBER: 60/251,856
OR FILING DATE: 2000-12-08
OR APPLICATION NUMBER: 60/251,868
OR FILING DATE: 2000-12-08
OR APPLICATION NUMBER: 60/25,344
OR FILING DATE: 2000-09-01
OR APPLICATION NUMBER: 60/234,997
OR APPLICATION NUMBER: 60/234,997
OR FILING DATE: 2000-09-25
OR APPLICATION NUMBER: 60/23,343
OR FILING DATE: 2000-09-01
OR APPLICATION NUMBER: 60/29,343
OR APPLICATION NUMBER: 60/29,345
OR APPLICATION NUMBER: 60/229,345
OR APPLICATION NUMBER: 60/229,387
OR APPLICATION NUMBER: 60/229,387
OR APPLICATION NUMBER: 60/229,287

APPLICATION NUMBER: 60/241,785 FILING DATE: 2000-10-20 APPLICATION NUMBER: 60/244,617 FILING DATE: 2000-11-01

APPLICATION NUMBER: 60/249,299
FILING DATE: 2000-11-17
APPLICATION NUMBER: 60/236,327
FILING DATE: 2000-09-29

APPLICATION NUMBER: 60/232,080

APPLICATION NUMBER: 60/ FILING DATE: 2000-09-08

APPLICATION NUMBER: 60/231,242 FILING DATE: 2000-09-08

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US-10-236-055A-2
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                                                   SEQ ID NO 2
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                                                                                    FILE REFERENCE: DX01343K
CURRENT APPLICATION NUMBER: US/10/236,055A
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/317,988
PRIOR FILING DATE: 2001-09-06
NUMBER OF SEQ ID NOS: 36
                                                                                                                                                                                               APPLICANT: Basham, Beth E.
APPLICANT: Forsythe, Ian
APPLICANT: Gorman, Daniel M.
APPLICANT: Mattson, Jeanine
APPLICANT: Mattson, Jeanine
APPLICANT: Moshrefi, Mehrdad
APPLICANT: Parham, Christi
TITLE OF INVENTION: MAMMALIAN GENES; RELATED REAGENTS
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                                                                      SOFTWARE: PatentIn version 3.1
                   TYPE: PRT
ORGANISM: Homo sapiens
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APPLICATION NUMBER: 60/231,414
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APPLICATION NUMBER: 60/241,221
FILING DATE: 2000-10-20
APPLICATION NUMBER: 60/246,475
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APPLICATION NUMBER: 60/231,243
FILING DATE: 2000-09-08
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APPLICATION NUMBER: 60/241,786
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63; Conser
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38.4%;
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16; Mismatches
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US-09-854-133-185

Sequence 185, Application US/09854133 Publication No. US20020183499A1 GENERAL INFORMATION:

APPLICANT:

Lodes, Michael J.

Mohamath,

Raodoh

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RESULT 7
US-09-738-973-185
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RESULT 8
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CURRENT FILING DATE: 2000-12-14
NUMBER OF SEQ ID NOS: 587
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 185
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Patent No.
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APPLICANT:
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TYPE: PRT
ORGANISM: Homo &
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                                                                   113 QSVMLALRRGDAVWLLSHDHDGYGA-YSNHGKYITFSGFLVYPD 155
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Kalos, Michael D.
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Elliot, Mark
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Secrist, Heather
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Pred. No. 5.8e-15;
L6; Mismatches 63;
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Pred. No. 2.8e-15;
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; ORGANISM: Homo sapien
US-10-144-649A-185
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CURRENT APPLICATION NUMBER: US/10/144,649A
CURRENT FILING DATE: 2002-08-21
NUMBER OF SEQ ID NOS: 749
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 185
LENGTH: 746
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CURRENT APPLICATION NUMBER: US/09/854,133
CURRENT FILING DATE: 2001-05-11
NUMBER OF SEQ ID NOS: 735
SOFTWARE: FRASESEQ for Windows Version 3.0
SEQ ID NO 185
LENGTH: 746
THERET SERVICE OF SEQ ID NO 185
LENGTH: 746
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Best Local
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-09-854-133-185
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APPLICANT: Wang, Tongtong
APPLICANT: Fan, Liqun
APPLICANT: Algate, Paul A.
APPLICANT: MCNeill, Patricia D.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: THE THERAPY AND DIAGNOSIS OF
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NHAILQLFQGDQIWLRLH----RGAIYGSSWKYSTFSGYLLYQD 746
                                     QSVMLALRRGDAVWLLSHDHDGYGA-YSNHGKYITFSGFLVYPD 155
                                                                                TFDLQLGRFNCPVNGTYVFIFHMLKLAVNVPLYVNLMKNEEVLVSAYANDGAP-DHETAS
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                                                                                                                                                                                     LENGTH: 909
TYPE: PRT
ORGANISM: homo sapiens
US-10-309-422-22
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 10
LENGTH: 908
TYPE: PRT
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                                                                                                                                                                                                                                                                                        SEQ ID NO 22
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Best Local (
                                                                                          Matches
                                                                                                                                        Query Match
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CURRENT FILING DATE: 2002-12-03
PRIOR APPLICATION NUMBER: US/09/798,771
PRIOR FILING DATE: 2001-03-02
PRIOR APPLICATION NUMBER: US 60/186,557
PRIOR FILING DATE: 2000-03-02
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APPLICANT: Wilganowski, Nathaniel L.
APPLICANT: Turner, C. Alexander Jr.
TITLE OF INVENTION: No. US20030119587A1el Human Proteins and
FILE REFERENCE: LEX-0142-USA
                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: US 60/186,557
PRIOR FILING DATE: 2000-03-02
NUMBER OF SEQ ID NOS: 43
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TITLE OF INVENTION: NO. US20030139587A1el Human Proteins and Polynucleotides Encoding
FILE REFERENCE: LEX-0142-USA
CURRENT APPLICATION NUMBER: US/10/309,422
CURRENT FILING DATE: 2002-12-03
CURRENT FILING DATE: 2002-12-03
CURRENT FILING DATE: 2002-12-03
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                                                                                                                                                                                                                                                                                                            SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                 Local Similarity
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                           4 DAPARGP-----PAPPEPRSAFSAARTRSLVGSDAGPGPRHOPLAFDTEFVNIGG 53
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                                                                                          63;
DVPVTNPAATILPVHVYPLPQQMRVAFSAART----
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                                                                                        Conservative
                                                                                        25.7%; Score 230; DB 12; 38.4%; Pred. No. 7.5e-15; tive 16; Mismatches 63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nathaniel L.
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; Pred. No. 7.4e-15;
16; Mismatches 63;
SNLAPGTLDOPIVEDLLLNNLGE 810
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APPLICANT: Walke, D. Wade
APPLICANT: Wilganowski, Nathaniel L.
APPLICANT: Wilganowski, Nathaniel L.
APPLICANT: TYNERY C. Alexander Jr.
TITLE OF INVENTION: NO. US20030139587A1el Human Proteins and Pol:
FILE REFERENCE: LEX-0142-USA
CURRENT APPLICATION NUMBER: US/10/309,422
CURRENT FILING DATE: 2002-12-03
PRIOR APPLICATION NUMBER: US/09/798,771
PRIOR FILING DATE: 2001-03-02
PRIOR FILING DATE: 2001-03-02
PRIOR FILING DATE: 2000-03-02
PRIOR FILING DATE: 2001-03-07
PRIOR FILING DATE: 2001-03-07
PRIOR FILING DATE: 2001-03-07
PRIOR FILING DATE: 2001-03-07
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US-10-309-422-26
Sequence 26, Application US/10309422
Publication No. US20030139587A1
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; LENGTH: 958
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-309-422-26
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; TYPE: PRT
; ORGANISM: homo sapiens
US-10-309-422-14
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                                                                                      SOFTWARE: FastSEQ for Windows Version SEQ ID NO 26
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Best Local :
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CURRENT FILING DATE: 2002-12-03
PRIOR APPLICATION NUMBER: US/09/798,771
PRIOR FILING DATE: 2001-03-02
PRIOR APPLICATION NUMBER: US 60/186,557
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APPLICANT: Turner, C. Alexander Jr.
TITLE OF INVENTION: No. US20030139587A1el Human Proteins and Polynucleotides Encoding
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Pred. No. 8e-15;
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Best Local S
Matches 63
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Publication No.
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Best Local
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APPLICANT: Wilganowski, Nathaniel L.
APPLICANT: Turner, C. Alexander Jr.
TITLE OF INVENTION: NO. US20030139587A1el Human
FILE REFERENCE: LEX-0142-USA
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APPLICANT: Turner, C. Alexander Jr.
TITLE OF INVENTION: No. US20030139587A1el Human Proteins and Polynucleotides Encodin
FILE REFERENCE: LEX-0142-USA
CURRENT APPLICATION NUMBER: US/10/309,422
CURRENT FILING DATE: 2002-12-03
PRIOR APPLICATION NUMBER: US/09/798,771
PRIOR FILING DATE: 2001-03-02
PRIOR FILING DATE: 2001-03-02
                      CURRENT APPLICATION NUMBER: US/10/309,422
CURRENT FILING DATE: 2002-12-03
PRIOR APPLICATION NUMBER: US/09/798,771
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PRIOR FILING DATE: 2000-03-02
NUMBER OF SEQ ID NOS: 43
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TYPE: PRT
ORGANISM: homo sapiens
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PRIOR FILING DATE:
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No. US20030139587A1
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; Pred. No. 8e-15;
16; Mismatches 63;
                                                                                                            Proteins
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                                                                                                          Polynucleotides Encodir
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Result
No.
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Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed,
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894
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           Issued_Patents_AA:*
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/cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/2/iaa/backfiles1.pep:*
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           GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd
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                                                     US-09-370-838-185
US-09-118-408-44
US-09-506-855-44
US-09-619-740-44
US-09-506-852-44
US-09-336-536-4
US-09-336-536-3
US-09-686-838B-2
US-09-188-840-2
US-09-118-76B-2
US-09-118-930-295
US-09-118-936-36-10
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        -188-930-294
-312-283C-294
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Sequence 185, App
Sequence 44, Appl
Sequence 44, Appl
Sequence 44, Appl
Sequence 44, Appl
Sequence 4, Appl
Sequence 2, Appli
Sequence 10, Appli
Sequence 10, Appl
Sequence 24, Appli
Sequence 27, Appli
Sequence 294, Appli
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# ALIGNMENTS

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PAGENT NO. 6444425

GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Lodes, Michael J.
APPLICANT: Mohamath, Roadoh
COMPOUNDS FOR THERAPY AND DIAGNOSIS OF
TITLE OF INVENTION: LUNG CANCER AND METHODS FOR THEIR USE
TILE REFERENCE: 210121.475C1
CURRENT APPLICATION NUMBER: US/09/370,838
CURRENT FILING DATE: 1999-08-09
EARLIER APPLICATION NUMBER: US 09/285,323
EARLIER APPLICATION NUMBER: US 09/285,323
EARLIER FILING DATE: 1999-04-02
NUMBER OF SEQ ID NOS: 289
SOFTWARE: PastSEQ for Windows Version 3.0
LENGTH: 746
                                                                                                                                                                                           US-09-118-408-44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; ORGANISM: Homo sapien US-09-370-838-185
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                                                                                                          Sequence 44, Application US/09118408A Patent No. 6265544
GENERAL INFORMATION:
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 185, Application
APPLICANT: Sheppard, Paul O.
TITLE OF INVENTION: ADIPOCYTE-SPECIFIC PROTEIN HOMOLOGS
FILE REFERENCE: 97-30
CURRENT APPLICATION NUMBER: US/09/118,408A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     593 DVPVTNPAATILEVHVYPLPQQMRVAFSAART----SNLAPGTLDQPIVFDLLLNNLGE
                                                                                                                                                                                                                                                                                                      707 NHAILQLFQGDQIWLRLH----RGAIYGSSWKYSTFSGYLLYQD 746
                                                                                                                                                                                                                                                                                                                                                           113 QSVMLALRRGDAVWLLSHDHDGYGA-YSNHGKYITFSGFLVYPD
                                                                                                                                                                                                                                                                                                                                                                                                                648 TFDLQLGRFNCPVNGTYVFIFHMLKLAVNVPLYVNLMKNEEVLVSAYANDGAP-DHETAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                          54 DFDAAAGVFRCRLPGAYFFSFTLGKLP-RKTLSVKLMKNRDEVQAMIYDDGASRRREMQS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   63;
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38.4%;
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Pred. No. 2.6e-17;
6; Mismatches 63
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CURRENT FILING DATE: 1998-07-17

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EARLIER APPLICATION NUMBER: 60/053,154
EARLIER FILING DATE: 1997-07-18
NUMBER OF SEQ ID NOS: 47
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 44
LENGTH: 281
TYPE: PRT
ORGANISM: Mus musculus
US-09-118-408-44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Sheppard, Paul O.
APPLICANT: Lasser, Gerald W.
APPLICANT: Lasser, Gerald W.
APPLICANT: Bishop, Paul D.
TITLE OF INVENTION: INHIBITORS FOR USE IN HEMOSTASIS AND TITLE OF INVENTION: INMUSE FUNCTION
FILE REFERENCE: 99-12
CURRENT APPLICATION NUMBER: US/09/506,855
CURRENT APPLICATION NUMBER: US/09/506,855
CURRENT FILING DATE: 2000-02-17
NUMBER OF SEQ ID NOS: 50
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 44
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GENERAL INFORMATION:
APPLICANT: Sheppard, Paul O.
TITLE OF INVENTION: ANTIBODIES THAT BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 44, Application US/09506855 Patent No. 6448221
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                                                        Sequence 44, Application US/09911176B Patent No. 6518403
                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                               146 AAFSVGRKKALHSND-----YFQPVVFDTEFVNLYKHFNMFTGKFYCYVPGIYFFSLNVH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    78 KLPRKTLSVKLMKNRDEVQAMIYDDGASRRREMQSQSVMLALRRGDAVW--LLSHDHDGY 135
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                                                                                                                                                                                                                       GAYSNHGKYITFSGFLVYPDLAP 158
                                                                                                                                                                                                                                                                                                       KLPRKTLSVKLMKNRDEVQAMIYDDGASRRREMQSQSVMLALRRGDAVW--LLSHDHDGY 135
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                                                                                                                                                                                   IFSDEFDTYITFSGYLVKPASEP 281
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Pred. No. 8.1e-17
0; Mismatches 5
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US-09-619-740-44
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; TYPE: PRT
; ORGANISM: Mus musculus
US-09-911-176B-44
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                                                                                                                                                                                                                                                                                                 ; TYPE: PRT ; ORGANISM: Mus musculus US-09-619-740-44
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CURRENT APPLICATION NUMBER: US/09/619,740
CURRENT APPLICATION DATE: 2000-07-19
PRIOR APPLICATION NUMBER: 09/253,604
PRIOR FILING DATE: 1999-02-19
PRIOR APPLICATION NUMBER: 09/444,794
PRIOR APPLICATION NUMBER: 09/506,855
PRIOR APPLICATION NUMBER: 09/506,855
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SOFTWARE: FastSEQ fo
SEQ ID NO 44
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APPLICANT: Sheppar
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Best Local Similarity
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Best Local
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CURRENT APPLICATION NUMBER: US/09/911,176B
CURRENT FILING DATE: 2001-07-23
PRIOR APPLICATION NUMBER: 09/118,408
PRIOR FILING DATE: 1998-07-17
PRIOR APPLICATION NUMBER: 60/053,154
PRIOR APPLICATION NUMBER: 60/053,154
PRIOR FILING DATE: 1997-07-18
NUMBER OF SEQ ID NOS: 52
NUMBER OF SEQ ID NOS: 52
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APPLICANT: Lasser, Gerald W.
APPLICANT: Bishop, Paul D.
TITLE OF INVENTION: INHIBITORS FOR USE IN HEMOSTASIS AND IMMUNE FUNCTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                             ENGTH: 281
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136 GAYSNHGKYITFSGFLVYPDLAP
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                                                                                                                                                                  18 SAFSAARTRSLVGSDAGPGPRHQPLAFDTEFVNIGGDFDAAAGVFRCRLPGAYFFSFTLG
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                                                                                              KLPRKTLSVKLMKNRDEVQAMIYDDGASRRREMQSQSVMLALRRGDAVM---LLSHDHDGY 135
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                                                           TWNQKETYLHIMKNEEEV-VILYAQ-VSDRSIMQSQSLMMELREEDEVWVRLFKGERENA
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Pred. No. 8.1e-17;
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Pred. No. 8.1e-17;
Pred. No. 8.8:10:17;
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IFSDEFDTYITFSGYLVKPASEP 281

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US-09-506-852-44
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APPLICANT: Leiby, K.
APPLICANT: McKay, C.
APPLICANT: McKay, C.
APPLICANT: McKay, C.
APPLICANT: Bossone, S.
TITLE OF INVENTION: SECRETED PROTEINS AND USES THEREOF
FILE REFERENCE: 7853-144
CURRENT APPLICATION NUMBER: US/09/336,536
CURRENT FILING DATE: 1999-06-18
NUMBER OF SEQ ID NOS: 75
                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 4
LENGTH: 228
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SEQ ID NO 44
LENGTH: 281
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                                                                                                                                                                                                                                   Query Match
Best Local Similarity
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Patent No. 6566499
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TITLE OF INVENTION: ADIPOCYTE-SPECIFIC PROTEIN HOMOLOGS
FILE REFERENCE: 97-30
CURRENT APPLICATION NUMBER: US/09/506,852
CURRENT FILING DATE: 2000-02-17
EARLIER APPLICATION NUMBER: 60/053,154
EARLIER FILING DATE: 1997-07-18
NUMBER OF SEQ ID NOS: 44
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119 LRRGDAVWLLSHDHDGYGAYSNHGKYITFSGFLVYPD
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                                                                              59 AGVFRCRLPGAYFFSFTLGKLPRKTLSVKLMKNRDEVQAMIYDDGASRRREMQSQSVMLA 118
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                                                                                                                        EAGPAGPTGPAGECSVPPRSAFSAKRSESRV----PPPSDAPLPFDRVLVNEQGHYDAV 124
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                                          TGKFTCQVPGVYYFA-VHATVYRASLQFDLVKNGESIASFFQFFGGWPKPASLSGGAMVR 183
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ilarity 35.7%;
Conservative 18
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Pred. No. 1.4e-15;
.8; Mismatches 72;
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155
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; ORGANISM: Homo sapiens
US-09-140-804-2
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US-09-140-804-2
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APPLICANT: Humes, Jacquellne M.
TITLE OF INVENTION: ADIPOCYTE-SPECIFIC PROTEIN HO!
FILE REPERENCE: 97-49
CURRENT APPLICATION NUMBER: US/09/140,804
CURRENT FILING DATE: 1998-08-26
EARLIER APPLICATION NUMBER: 60/056,983
EARLIER FILING DATE: 1997-08-26
NUMBER OF SEQ ID NOS: 47
                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                     SEQ ID NO 3
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SEQ ID NO 2
LENGTH: 243
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APPLICANT: McKay, C.
APPLICANT: McKay, C.
APPLICANT: Bossone, S.
TITLE OF INVENTION: SECRETED PROTEINS AND USES THEREOF
FILE REFERENCE: 7853-144
FULLE REPERENCE: 7853-144
CURRENT APPLICATION NUMBER: US/09/336,536
CURRENT FILING DATE: 1999-06-18
NUMBER OF SEQ ID NOS: 75
SOPTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                               ENGTH:
                                                                                                                                                                                        Local Similarity
      140
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                                       59 AGVFRCRIPGAYFFSFTLGKLPRKTLSVKLMKNRDEVQAMIYDDGASRRREMQSQSVMLA 118
                                                                                85 EAGPAGPTGPAGECSVPPRSAFSAKRSESRV-----PPPSDAPLPFDRVLVNEQGHYDAV 139
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                                                                                                                         4 DAPARGPPAPP----EPRSAFSAARTRSLVGSDAGPGPRHQPLAFDTEFVNIGGDFDAA 58
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TGKFTCQVPGVYYFA-VHATVYRASLQFDLVKNGESIASFFQFFGGWPKPASLSGGAMVR 198
                                                                                                                                                                  Conservative
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35.7%; Pred. No. 1.5e-15;
18: Mismatches 72;
                                                                                                                                                                                 23.3%; Score 208.5; DB 4; 35.7%; Pred. No. 1.5e-15;
                                                                                                                                                                  18; Mismatches
                                                                                                                                                                72;
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LRRGDAVWLLSHDHDGYGAYSNHGKYITFSGFLVYPD 155

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Sequence 2, Application US/09118408A

Patent No. 6265544

GENERAL INFORMATION:
APPLICANT: Sheppard, Paul O.
TITLE OF INVENTION: ADIPOCYTE-SPECIFIC PROTEIN HOMOLOGS
FILE REFERENCE: 97-30
CURRENT APPLICATION NUMBER: US/09/118,408A
CURRENT FILING DATE: 1998-07-17
EARLIER APPLICATION NUMBER: 60/053,154
EARLIER APPLICATION NUMBER: 60/053,154
EARLIER FILING DATE: 1997-07-18
NUMBER OF SEQ ID NOS: 47
SOFTWARE: PASTSEQ for Windows Version 3.0
SEQ ID NO 2
LENGTH: 281
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APPLICANT: Humes, Jacqueline M.
APPLICANT: Humes, Jacqueline M.
APPLICANT: Humes, Jacqueline M.
FILE REFERENCE: 97-49D1
CURRENT APPLICATION NUMBER: US/09/686,838B
CURRENT APPLICATION NUMBER: US 09/140,804
PRIOR APPLICATION NUMBER: US 09/140,804
PRIOR APPLICATION NUMBER: US 60/056,983
PRIOR FILING DATE: 1999-08-26
PRIOR FILING DATE: 1997-08-26
NUMBER OF SEQ ID NOS: 50
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US-09-686-838B-2
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Best Local Simi
Matches 56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
SEQ ID NO 2
SENGTH: 243
TYPE: PRT
ORGANISM: Homo sapiens
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Patent No. 6482612
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                                                                                 Matches
                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                             TYPE: PRT
ORGANISM: Homo sapien
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AGARGHTGPKGQKGSMGAPGERCKSHYAAFSVGRKK-----
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                                     APARGPPAP-----PEPR-----SAFSAARTRSLVGSDAGPGPRH-----QPLAFD
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                                                                                                 22.7%;
35.5%;
                                                                               18;
                                                                             Score 202.5; DB 3;
Pred. No. 8.7e-15;
8; Mismatches 58;
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                                                                                                                  Length 281;
-PMHSNHYYQTVIFD 168
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                                                                             Gaps
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TITLE OF INVENTION: ANTERODIES THAT BIND AN
TITLE OF INVENTION: ANTERODIES THAT BIND AN
TITLE OF INVENTION: ANTERODIES THAT BIND AN
TITLE REFERENCE: 97-30D1
CURRENT APPLICATION NUMBER: US/09/911,176B
CURRENT FILING DATE: 2001-07-23
PRIOR APPLICATION NUMBER: 09/118,408
PRIOR FILING DATE: 1998-07-17
PRIOR FILING DATE: 1998-07-17
PRIOR FILING DATE: 1998-07-18
PRIOR FILING DATE: 1997-07-18
NUMBER: 09/103,154
PRIOR FILING DATE: 1997-07-18
NUMBER: FOLTE OF THE WINDOWS NAMED OF THE OWNER OWNER OF THE OWNER OWNER OF THE OWNER 
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US-09-506-855-2
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TYPE: PRT
ORGANISM: Homo sapien
US-09-506-855-2
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                                                                                                                          US-09-911-176B-2
                                                                                                                                                        SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 2
LENGTH: 281
TYPE: PRI
ORGANISM: Homo sapien
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Patent No. 6448221
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CURRENT FILING DATE: 2000-02-17
NUMBER OF SEQ ID NOS: 50
SOFTWARE: FastSEQ for Windows Version 3.0
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APPLICANT: Lasser, Gerald W.
APPLICANT: Bishop, Paul D.
TITLE OF INVENTION: INHIBITORS FOR USE IN HEMOSTASIS
TITLE OF INVENTION: IMMUNE FUNCTION
FILE REFERENCE: 99-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Match 22.7%;
Local Similarity 35.5%;
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22.7%;
35.5%;
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; Pred. No. 8.7e-15; 
18; Mismatches 58;
    Score 202.5; DB 4
Pred. No. 8.7e-15;
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                                              Length 281;
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Query Match Best Local Similarity

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SOFTWARE: FASTSEQ FOR W
SEQ ID NO 2
LENGTH: 281
TYPE: PRT
ORCANISM: Homo sapien
US-09-619-740-2
                                                                                                                                                                                                                                            NESULT 15
US-09-506-852-2
; Sequence 2, Application US/09506852
; Patent No. 6566499
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US-09-619-740-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 60; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILE REFERENCE: 99-12C3
CURRENT APPLICATION NUMBER: US/09/619,740
CURRENT FILING DATE: 2000-07-19
PRIOR APPLICATION NUMBER: 09/253,604
PRIOR FILING DATE: 1999-02-19
PRIOR PRIOR DATE: 1999-02-19
PRIOR PRIOR DATE: 09/444,794
PRIOR PRIOR DATE: 1999-11-22
PRIOR APPLICATION NUMBER: 09/444,794
PRIOR PRIOR PRIOR DATE: 1999-11-22
                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2, Application US/09619740 Patent No. 6544946
APPLICANT: Sheppard, Paul O.
TITLE OF INVENTION: ADIPOCYTE-SPECIFIC PROTEIN HOMOLOGS
FILE REFERENCE: 97-30
CURRENT APPLICATION NUMBER: US/09/506,852
CURRENT FILING DATE: 2000-02-17
EARLIER APPLICATION NUMBER: 60/053,154
EARLIER APPLICATION NUMBER: 60/053,154
EARLIER FILING DATE: 1997-07-18
NUMBER OF SEQ ID NOS: 44
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
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PRIOR APPLICATION NUMBER: 09/506,855
PRIOR FILING DATE: 2000-02-17
NUMBER OF SEQ ID NOS: 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        119 AGARGHTGPKGQKGSMGAPGERCKSHYAAPSVGRKK------PMHSNHYYQTVIFD 168
                                                                                                                                                                                                                                                                                                                                                                       227 DRSIMOSOSIMLELREODOVWVRLYKGERENAIFSEELDTYITFSGYLV 275
                                                                                                                                                                                                                                                                                                                                                                                                             106 RRREMOSOSVMLALRRGDAVWLLSHDHDGYGAYSNH--GKYITFSGFLV 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                       169 TEFVNLYDHFNMFTGKFYCYVPGLYFFSLNVHTWNQKETYLHIMKNEEEVVILFAQVG--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              46 TEFVNIGGDFDAAAGVFRCRLPGAYFFSFTLGKLPRKTLSVKLMKNRDEVQAMIYDDGAS 105
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Lasser, Gerald W.
Bishop, Paul D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22.7%; Score 202.5; DB 4 35.5%; Pred. No. 8.7e-15;
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Best Local S
                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Homo sapien
                                                                                                                                                                                                                                                                                                                                 LENGTH: 281
                                                                                                                                   119 AGARGHTGPKGQKGSMGAPGERCKSHYAAFSVGRKK-----PMHSNHYYQTVIFD 168
                                  106 RRREMOSOSVMLALRRGDAVWLLSHDHDGYGAYSNH--GKYITFSGFLV 152
                                                                    169 TEFVNLYDHFNMFTGKFYCYVPGLYFFSLNVHTWNQKETYLHIMKNEEEVVILFAQVG--
                                                                                                    46 TEFVNIGGDFDAAAGVFRCRLPGAYFFSFTLGKLPRKTLSVKLMKNRDEVQAMIYDDGAS 105
                                                                                                                                                                                                           60;
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                                                                                                                                                                                                                             Similarity
DRSIMOSOSIMIELREODOVWVRLYKGERENAIFSEELDTYITFSGYLV 275
                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                         22.7%;
35.5%;
                                                                                                                                                                                                         18; Mismatches
                                                                                                                                                                                                                           Score 202.5; DB 4; Pred. No. 8.7e-15;
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                                                                                                                                                                                                                                         Length 281;
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Search completed: January 12, 2004, 08:20:05
Job time : 9.65269 secs

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OM protein protein search, using sw model

Run on: January 12, 2004, 08:12:09; Search time 1.79441 Seconds (without alignments)
1661.397 Million cell updates,

cell updates/sec

Title: Perfect score: US-10-085-167-3 57

Sequence:

Scoring table: BLOSUM62

Searched:

Gapop 10.0 , Gapext 0.5

283308 segs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB Maximum DB seq length: 0 seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

PIR 76:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

	28				24		22	21	20	19	18	17	16	15	14	13	12	11	10	9	80	7	σ	5	4	ω	2	۲	No.	,
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<b>4</b> 5	44	43	42	41	40	9	86	37	36	ω 5	34 4	ω ω	32	31	30
20	20	20	20	21	21	21	21	21	21	21	21	21	21	21	21
35.1	35.1	35.1	35.1	36.8	36.8	36.8	36.8	36.8	36.8	36.8	36.8	36.8	36.8	36.8	36.8
129	127	119	40	1417	1417	1316	1138	976	885	826	779	724	724	713	704
N	N	N	N	N	N	N	N	N	N	N	N	N	N	N	N
B90175	H64012	A53257	G81731	D85521	H90670	B86240	G71554	G82209	AC2444	E81706	T44659	D96949	A42953	AE0531	T13665
NADH dehydrogenase	sufI protein homol	H+-transporting AT	hypothetical prote	probable adhesin e	probable invasin [	protein F20B24.12	probable transmemb	GGDEF family prote	hypothetical prote	conserved hypothet	nitrous oxide redu	secreted protein c	nitrous oxide redu	lysine decarboxyla	NADH2 dehydrogenas

# ALIGNMENTS

Query Match  Best Local Similarity 36.4%; Pred. No. 2e+02;  Matches 4; Conservative 0; Mismatches 7; Indels 0; Gaps 0;  Qy 19 FXXXXXGXYXF 29	RESULT 1  83651 hypothetical protein BH0013 [imported] - Bacillus halodurans (strain C-125) C;Species: Bacillus halodurans C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001 C;Accession: B3651 R;Takami, H; Nakasone, K; Takaki, Y; Maeno, G; Sasaki, R; Masui, N; Fuji, F; Hiran Nucleic Acids Res. 28, 4317-4331, 2000 A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and capacitation number: A83650; MUID:20512582; PMID:11058132 A;Accession: B3651 A;Accession: B3651 A;Status: preliminary A;Molecule type: DNA A;Residues: 1-250 <sto> A;Cross-references: GB:AP001507; GB:BA000004; NID:g10172612; PIDN:BAB03732.1; GSPDB:GN001 A;Experimental source: strain C-125 C;Genetics: A;Gene: BH0013</sto>

tyra protein VC2145 [imported] - Vibrio cholerae (strain N16961 serogroup O1)
(;Species: Vibrio cholerae
(;Date: 18-Aug-2000 #sequence\_revision 20-Aug-2000 #text\_change 02-Feb-2001
(;Accession: D82112
(;Acc

A;Molecule type: DNA, A;Residues: 1-302 kHB19 A;Cross-references: GB:AE004287; GB:AE003852; NID:g9656689; PIDN:AAF95290.1; GSPDB:GN001; A;Experimental source: serogroup O1; strain N16961; biotype El Tor C;Genetics:

A;Gene: VC2145 A;Map position: 1 C;Superfamily: Es Escherichia coli hypothetical protein b2431

Query Match 38.6%; Score 22; В 2 Length 302;

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hypothetical protein C15C8.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
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H90490
C;Accession:
R;Sims, M.
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A,Description: Sulfolobus sc
A,Reference number: A99139
A,Accession: H90490
A,Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Accession: H90490
R;She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, R;She, Q.; Singh, R.K.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P. Jong, T.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P. arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      membrane transporter SSO3079 [imported] - Sulfolobus solfataricus C;Species: Sulfolobus solfataricus C;Species: Sulfolobus solfataricus C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 24-May-2001 C;Accession: H90490
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Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Pe
arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost,
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                                                                                                                       RESULT 5
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A; Residues: 1-421 < KUR>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          submitted to GenBank, April 2001
A;Description: Sulfolobus solfataricus complete genome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         membrane transporter SSO1505 [imported] - Sulfolobus solfataricus
                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: DNA
A; Residues: 1-423 < KUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Status: preliminary
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Matches
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                                                                                                                                                                                                                                                                                 Query Match
Best Local
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Pred. No. 3.4e
0; Mismatches
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Pred. No. 3.4e+02;
0; Mismatches 7
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); Mismatches 7;
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3.4e+02;
                                                                                                                                                                                                                                                            7; Indels
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H.P.;
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RESULT 7
AD0123
                                                                                                                                                              R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B. deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, Nature 413, 523-527, 2001
                                                                                                                                                                                                                                                         C;Species: Yersinia pestis
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001
C;Accession: AD0123
                                                                                                                                                                                                                                                                                                         probable autotransporter protein yapH [imported] - C;Species: Yersinia bestis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Genome: plasmid
A; Mobile element: plasmid
C; Superfamily: slime mold
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R;Rieben Jr., W.K.; Gonzales, C.M.; Gonzales, S.T.; Pilkington, K.J.; Kiyosawa, Genetics 148, 1117-1125, 1998
A;Title: Dictyostelium discoideum nuclear plasmid Ddp5 is a chimera related to 1
A;Reference number: Z14684; MUID:98198836; PMID:9539429
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T02635
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A; Introns: 156/2; 205/3;
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A;Molecule type: DNA
A;Residues: 1-3705 <KUR>
A;Cross-references: GB:AL590842; PIDN:CAC89847.1; PID:g15979073; GSPDB:GN00175
                                                                                          A;Title: Genome sequence of Yersinia pestis, the causative agent of plague. A;Reference number: AB0001; MUID:21470413; PMID:11586360 A;Accession: AD0123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: EMBL:AF000580; NID:g3068582; PIDN:AAC14391.1; PID:g3068584
A;Experimental source: strain WS2162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                D2 protein homolog - slime mold (Dictyostelium discoideum) plasmid Ddp5
C;Species: Dictyostelium discoideum
C;Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 24-Nov-
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A; Residues: 1-441 <WIL>
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                                                                         Status: preliminary;
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Best Local
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Best Local Similarity
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Pred. No.
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Pred. No. 7.2e+02
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. 3.6e+02;
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                                                                                                                                                                                                                                                                                                                                    Yersinia pestis (strain CO92)
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A;Gene: fxbC

G;Superfamily: acetate-CoA ligase homology; acyl carrier protein homology
C;Reywords: carrier protein; phosphopantetheine; phosphoprotein
F;68-566/Domain: acetate-CoA ligase homology <ACL>
F;582-649/Domain: acyl carrier protein homology <ACL1>
F;1620-2062/Domain: acyl carrier protein homology <ACL1>
F;2078-2144/Domain: acyl carrier protein homology <ACL2>
F;3139-3591/Domain: acyl carrier protein homology <ACL2>
                                                                                                                                                                                                                                          A;Residues: 1-156 <ARN>
A;Cross-references: GB:AE001648; GB:AE001363; NID:g4376946; PIDN:AAD18799.1; PID:g437699
A;Experimental source: strain CWL029
                                                                                                                                                                                                                                                                                                                   A;Title: Comparative genomes of Clamydia pneumoniae and C. A;Reference number: A72000; MUID:99206806; PMID:10192388 A;Accession: E72052 A;Status: preliminary A;Molecule type: DNA A;Molecule type: DNA
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A;Molecule type: DNA
A;Molecule type: DNA
A;Roslecule type: DNA
A;Roslecule: 1-4976 <YUS>
A;Cross-references: EMBL:AF027770; NID:g3560502; PID:g3560507; PIDN:AAC82550.1
C;Genetics:
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R:YU, S: Fiss E: Jacobs Jr., W.R.
J: Bacteriol. 180, 4676-4685, 1998
A:Title: Analysis of the exochelin locus in mycobacterium smegmatis: biosynt A:Reference number: Z17898; MUID:98389687; PMID:9721311
A:Accession: T14165
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            rRNA methylase - Chlamydophila pneumoniae (strain CWL029)
C;Species: Chlamydophila pneumoniae, Chlamydia pneumoniae
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 03-Nov-2000
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C;Species: Mycobacterium smegmatis
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                                                                                                                                                              ;Gene: spoU_2;Superfamily: Chlamydophila pneumoniae rRNA methylase
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;614,3643,4669/Binding site: phosphopantetheine (Ser) (covalent) #status
                                                                      Query Match
Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                        Genetics:
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Best Local
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19 FXXXXXGXYXF 29
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Similarity 36.4%;
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                                                                        Conservative
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pred. No. 4.5e+03;
                                                                                           Score 21; DB 2;
Pred. No. 2.2e+02;
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                                                                                                                  DB 2; Length 156;
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hypothetical protein jhp0656 - Helicobacter pylori (strain J99)
c;Species: Helicobacter pylori
A;Variety: strain J99
C;Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 17-Mar-2000
C;Accession: B71906
C;Accession: B71906
R;Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.;
I'ves, C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; V.
Nature 397, 176-180, 1999
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A;Residues: 1-156 <3TO>
A;Cross-references: GB:BA000008; NID:g8979032; PIDN:BAA98867.1; GSPDB:GN00142
A;Experimental source: strain J138
C;Genetics:
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A;Title: Comparison of whole genome sequences of chlamydia A;Reference number: A86491; MUID:20330349; PMID:10871362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       rRNA methylase [imported] - Chlamydophila pneumoniae (strain J138) c;Species: Chlamydophila pneumoniae, Chlamydia pneumoniae (C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 23-Mar-2001 C;Accession: A86573
                   A; Title: Genomic sequence comparison of two unrelated isolates of the human gastric patho
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Molecule type: DNA
A;Residues: 1-210 <TOM>
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A; Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser,
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Pred. No. 2.2e+02;
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A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-210 <ARN>
                                                                                                                                                                                                                                                     R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, J. Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000

A;Title: Complete genome sequence of Pseudomonas aeruginosa PAO1, an A;Reference number: A82950; MUID:20437337; PMID:10984043
                                                                                                                                                                                                                                                                                                                                                                                          hypothetical protein PA4685 [imported] - Pseudomonas aeruginosa (strain PAO1) C;Species: Pseudomonas aeruginosa C;Species: Pseudomonas aeruginosa C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000 C;Accession: B83060
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A;Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hyp A;Reference number: A81250; MUID:20150912; PMID:10688204
A;Accession: H81344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hypothetical protein Cj0733 (imported) - Campylobacter jejuni (strain NCTC 11168)
C;Species: Campylobacter jejuni
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 03-Jun-2002
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A;Experimental source: strain J99
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                                                                                     A;Gene:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 14
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A;Residues: 1-212 <PAR>
                                                                                                                                                                         A;Molecule type: DNA
A;Residues: 1-231 <STO>
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A;Experimental source: serotype O2, strain NCTC 11168
                                                                                                                                                                                                                   A;Status: preliminary
                                                                                                                                                                                                                                      Accession: B83060
                                                                                                                              ;Cross-references: GB:AE004882; GB:AE004091; NID:g9950939; PIDN:AAG08072.1; GSPDB:GN001;Experimental source: strain PAO1
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ilarity 36.4%;
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A.; Larbig,
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K.; Lim,
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R;Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, ; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M. Science 269, 496-512, 1995.

Science 269, 496-512, 1996.

A;Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, A;Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd. A;Reference number: A64000; MUID:95350630; PMID:7542800
                                                                                                                                                            A;Cross-references: GB:U32835; GB:L42023; NID:g1574459; PIDN:AAC23269.1; PID:g1574467;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hypothetical protein HI1626 - Haemophilus influenzae (strain Rd KW20)
C;Species: Haemophilus influenzae
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  FALAGMGSYYF
                                         FXXXXXGXYXF 29
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Pred. No.
                                                                                   Mismatches
                                                                                                     3.4e+02;
                                                                                                                           DB 2;
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Search completed: January 12, 2004, 08:16:52 Job time: 4.79441 secs

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Title:
Perfect score:
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No.
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Gapop 10:0 , Gapext 0.5
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P24 HUMAN
P24 MOUSE
P24 RAT
P24 RAT
SIGC HAEIN
GLGC AGRTT
GLGC RHITR
HAEIN
YCH3 SCHPO
YO13 BPL2
ATP6 NAEFO
Y731 HAEIN
YGB2 ALCEU
YJ51 FUSNN
PAAD FYRAB
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ARY2 RAT
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Y995 THETN
Y177 METMA
YG14 METAC
P24 CRIGR
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        0993b3 homo sapien
064131 m runt-rela
08rb30 thermonner
08q0f9 methanosarc
08q0f9 methanosarc
08tqd0 methanosarc
09tqd0 methanosarc
09tj67 thermoplasm
015363 homo sapien
09rq3 mus musculu
063524 rattus norv
044278 haemophilus
08u815 agrobacteri
039669 agrobacteri
039669 agrobacteri
039669 arhizobium t
098p574 xanthomonas
08p574 xanthomonas
08p574 xanthomonas
079693 schizosacch
040153 lithospermu
000790 pseudomonas
09hgq3 schizosacch
040548 bacteriopha
02067 naegleria f
044044 haemophilus
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Runt-related transcription factor 3 (Core-binding factor, alpha subunit) (CBF-alpha 3) (Acute myeloid leukemia 2 protein) (Oncog AML-2) (Polyomavirus enhancer binding protein 2 alpha C subunit) (PEB2-alpha C) (SL3-3 enhancer factor 1 alpha C) subunit) (SL3/AKV core-binding factor alpha C subunit).
RUNX3 OR CBFA3 OR AML2 OR PEBP2A3.
                                                                                                                                                                                                                                                                                                                                                        Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: BINDS TO THE CORE SITE OF MURING LEUKENIA VIRUS, THE CORE SEQUENCES IN THE ENHANCER OF THE POLYOMAVIRUS, AND ALSO TO THE ENHANCERS OF THE T-CELL RECEPTOR GENES. MAY BE INVOLVED IN CONTROL OF CELLULAR PROLIFERATION AND/OR DIFFERENTIATION (BY
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Submitted (JUL-1999) to the
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MEDLINE=95331802; PubMed=7607690;
Wijmenga_C_, Speck N.A., Dracopoli N.C., Hofker M.H., Liu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Levanon D., Negreanu V., Groner Y.; "The mouse AML2/Cbfa3 cDNA sequence."; Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Identification of a new murine runt domain-containing gene, Cbfa3, and localization of the human homolog, CBFA3, to chromosome 1p35-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Locus.
                                                                                                                                                                                                                                                                                                                                                                                                                                             RUNX3 gene structure and function.";
               European Bioinformatics Institute. There are no restrictions by non-profit institutions as long as its content is in
                                                                                                  DOMAIN: A proline/serine/threonine rich region is necessary for transcriptional activation of SIMILARITY: Contains 1 Runt domain.
                                                                                                                                                                                                                                                                             SIMILARITY).

SUBUNIT: Heterodimer of an alpha and a beta subunit. The alpha subunit binds DNA as a monomer and through the runt domain. DNJ binding is increased by heterodimerization. Interacts with TLE
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                                                                                                                                                                                                                        Event=Alternative
                                               SWISS-PROT entry is copyright. It is produced through a collaboration sen the Swiss Institute of Bioinformatics and the EMBL outstation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ., Rhodes M., Williamson P., Boy
loation and chromosomal mapping
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rubins
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                                                                                                                                                                                     Sequence=Displayed;
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                                                                                                                                                                                                                      splicing; Named isoforms=2;
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                                   EMBL; AE013007, -; 1.
HAMAP; MF_01205; -; 1.
InterPro; IPR002589; Alpp.
InterPro; Alpp; 1.
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Bacteria; Firmicutes; Clostridia; Thermoanaerobacteriales;
Thermoanaerobacteriaceae; Thermoanaerobacter.
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                                                                                                                                                                                                                                                   STRAIN=MB4 / JCM 11007;

MEDLINE=21992816, PubMed=11997336;

Bao Q., Tian Y., Li W., Xu Z., Xuan Z., Hu S., Dong Bao Q., Tian Y., Li W., Xu Z., Xuan J., Dong X., Chen Y., Xu Y., Lai X., Huang L., Dong X., Tan H., Chen R., Wang J., Yu J., Yang H.;

"A complete sequence of T. tengcongensis genome.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
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EMBL; AF321443; AAK11181.1; -.
PIR; A56842; A56842.
                        Pfam; PF01661; Alpp; 1. SMART; SM00506; Alpp; 1.
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                                                                                 EMBL; AE013064; AAM24250.1;
                                                                                                               or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                           Genome Res. 12:689-700(2002).
-!- SIMILARITY: BELONGS TO THE UPF0189 FAMILY.
                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=119072;
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1 protein TTE0995.
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Hypothetical SEQUENCE 17

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Complete proteome. 8762 MW; C1FB4A03A8A1BB5A CRC64;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                transfer between Bacteria and Archaea.";
J. Mol. Microbiol. Biotechnol. 4:453-461(2002)
-!- SIMILARITY: BELONGS TO THE UPF0189 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=22120827; PubMed=12125824;
Deppenmeier U., Johann A., Hartsch T., Merkl R., Schmitz R.A.,
Martinez-Arrias R., Henne A., Ezezer A., Baeumer S., Jacobi C.,
Martinez-Arrias R., Lienard T., Christmann A., Boemecke M., Steckel S.,
Bhattacharyya A., Lykidis A., Overbeek R., Klenk H.-P., Gunsalus R.)
Fritz H.-J., Gottschalk G.;
        Archaea; Euryarchaeota; Euryarchaeota orders incertae sedis; Methanosarcinales; Methanosarcinaceae; Methanosarcina
                                                     Hypothetical MA1614.
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HAMAP; MF_01205; -; 1.
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STRAIN-GOel / GOI / ATCC BAA-199 / DSM 3647 / OCM
                                       Methanosarcina acetivorans.
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Hypothetical
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Pfam; Pro1861; Alpp; 1.
Hypothetical protein; Complete
SEQUENCE 187 AA; 20361 MW;
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Archaea; Euryarchaeota; Euryarchaeota orders incertae sedis;
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36.4%;
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8E125281358A1F62 CRC64;
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(See http://www.isb-sib.ch/announce/
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RESULT 6
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01-FEB-1996 (Rel. 33, 1
15-SEP-2003 (Rel. 42, I
Cop-coated vesicle memb
SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.

SEQUENCE FROM N.A., Craighead M.W., Hoe M.H., Lampen N., Geromanos S.,

Stamnes M.A., Craighead M.W., Hoe M.H., Lampen N., Geromanos S.,

Tempst P., Rothman J.E.,

Tempst P., Rothman J.E.,

"An integral membrane component of coatomer-coated transport vesicles
defines a family of proteins involved in budding.";

Proc. Natl. Acad: Sci. U.S.A. 92:8011-8015(1995).

-I- FUNCTION: Could have a role in the budding of coatomer-coated and
other species of coated vesicles. Could bind cargo.molecules to
collect them into budding vesicles.

-I- SUBUNIT: Interacts with ARFGAP1, inhibiting the GTPase-activating
activity of ARFGAP1 (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                      P49020;
01-FEB-1996
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HAMAP; MF 01205; -; 1.
InterPro; IPR002589; Alpp.
Pfam; PF01661; Alpp; 1.
SMART; SM00506; Alpp; 1.
Hypothetical protein; Complete proteome.
Hypothetical protein; Complete proteome.
                                                                                                                                                                                                                                                                                           Cricetulus griseus (Chinese hamster).
Eukaryota; Metazoa; Chordata; Craniat
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Mammalia; Eutheria;
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                                                                                                                                                                                                                                            NCBI_TaxID=10029;
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STRAIN=C2A / ATCC 35395 / DSM 2834;

    -!- SIMILARITY: BELONGS TO THE UPF0189 FAMILY.

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SEQUENCE
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       Hypothetical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nature 407:508-513(2000).
-!- SIMILARITY: BELONGS TO THE UPF0189 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ruepp A., Graml W., Santos-Martinez M.-L., Koretke K.K., Volker C., Mewes H.-W., Frishman D., Stocker S., Lupas A.N., Baumeister W.; "The genome sequence of the thermoacidophilic scavenger Thermoplasma"
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Ruepp A., Graml W., Santos-Martine
Mewes H.-W., Frishman D., Stocker
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Thermoplasmataceae; The
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SIMILARITY: BELONGS TO THE EMP24/GESIMILARITY: Contains 1 GOLD domain.
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Pred. No. 1.2e+02;
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J. Biol. Chem. 271:17183-17189(1996).
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15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation updat
                                                                                     DOMAIN
DOMAIN
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Blum R., Feick P., Puype M., Vandekerckhove J., Klengel R.,
Nastainczyk W., Schulz I.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (Human)
Eukaryota; Metazoa;
Mammalia; Butheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     בי-בצר-2003 (Rel. 42, Last annotation update)
Cop-coated vesicle membrane protein p24 precursor
RNP24
                                                                                                                                                                            CHAIN
DOMAIN
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                                                                                                                                                                                                                                                                                                                              GO; GO:0016021; C:integral to membrane; TAS.
GO; GO:0005792; C:microsome; TAS.
GO:0005886; C:plasma membrane; TAS.
GO; GO:0006886; P:intracellular protein transport; TAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=96291865; PubMed=8663407;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9606;
                                                                                                                                                     TRANSMEM
                                                                                                                                                                                                                        SIGNAL
                                                                                                                                                                                                                                             Transport;
                                                                                                                                                                                                                                                                                    Pfam; PF01105; EMP24 GP25L; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; X92098; CAA63069.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        entities requires a license agreement
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                                                                                                                                                                                                                                                                  PROSITE;
                                                                                                                                                                                                                                                                                                              InterPro; IPR000348;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   coatomer-coated vesicles.
SIMILARITY: BELONGS TO THE EMP24/GP25L FAMILY.
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4; Conserv
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                       Similarity
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Pred. No.
                                                                GOLD.
; C452370E459DC894 CRC64;
                    Score 21; DB 1;
Pred. No. 1.3e+02;
                                                                                                                                                                                                 POTENTIAL.

COP-COATED VESICLE MEMBRANE PROTEIN P24.
                                                                                                                                                     LUMENAL (POTENTIAL)
POTENTIAL.
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                                                                                                                                 CYTOPLASMIC
                                                                                                                                                                                                                                             Transmembrane; Signal; Golgi stack.
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                                           P24 RAT
Q63524;
15-DEC-1998
15-DEC-1998
15-SEP-2003
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Q9R0Q3;
16-OCT-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- SUBCELLULAR LOCATION: Type I membrane protein.
coatomer-coated vesicles (By similarity).
-!- SIMILARITY: BELONGS TO THE EMP24/GP25L FAMILY.
-!- SIMILARITY: Contains 1 GOLD domain.
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  Cop-coated RNP24.
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Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        fransport;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS50866; GOLD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 nterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     L6-OCT-2001
L5-SEP-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FUNCTION: Could have a role in the budding of coatomer-coated and other species of coated vesicles. Could bind cargo molecules to collect them into budding vesicles (By similarity).

SUBUNIT: Interacts with ARFGAP1, inhibiting the GTPase-activating activity of ARFGAP1 (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MGI:1929269; Rnp24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pro; IPR000348; Emp24_gp25L_p24.
PF01105; EMP24_GP25L; 1.
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                      8 (Rel. 37, Created)
8 (Rel. 37, Last sequence update)
3 (Rel. 42, Last annotation updat
vesicle membrane protein p24 pre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Protein transport;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                201 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (Rel. 40, Last sequence update)
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21
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                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BAA84689.1; -.
                      membrane protein p24 precursor (p24A) (RNP21.4).
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                                                                                                                                                                                                                                                                                                                                                                                                                36.8%;
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e protein p24 precursor
                                                                                                                                                                                                                                                                                                                                                                0
                                                                                                                                                                                                                                                                                                                                                                                       Score 21; DB 1;
Pred. No. 1.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GOLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POTENTIAL.
CYTOPLASMIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LUMENAL (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POTENTIAL.

COP-COATED VESICLE MEMBRANE PROTEIN P24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Transmembrane; Signal; Golgi stack.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
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                                             update)
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RESULT 11
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Best Local
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01-NOV-1995
28-FEB-2003
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DOMAIN
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YG26_HAEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                      the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed. entities requires a license agreement (See
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Sorting of Golgi resident proteins into different subpopulations COPI vesicles: a role for ArfGAP1.";
J. Cell Biol. 155:1199-1212(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Tmp21 and p24A, two type I proteins microsomal membranes, are members of vesicular trafficking.", J. Biol. Chem. 271:17183-17189(1996).
                         Hypothetical HI1626.
                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                       SIGNAL
                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR000348; Emp24_gp25L_p24.
Pfam; PF01105; EMP24_GP25L; 1.
                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; X92097; CAA63068.1;
                                                                                                                                                                                                                                                                                                                                                                                                                             or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               activity of ARFGAP1.
-I- SUBCELLULAR LOCATION: Type I membrane protein. Golgi-derived
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Weiss M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INTERACTION WITH AREGAP1.

MEDLINE=21629435; PubMed=11748249;
Lanoix J., Ouwendijk J., Stark A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Blum R., Feick P., Puyp
Nastainczyk W., Schulz
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=Wistar; TISSUE=Pancreas; MEDLINE=96291865; PubMed=8663407;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa;
Mammalia; Eutheria;
 Bacteria;
            Haemophilus influenzae
                                                                                                                                                                                                                                                                                                   TRANSMEM
                                                                                                                                                                                                                                                                                                                DOMAIN
                                                                                                                                                                                                                                                                                                                            CHAIN
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-!- SIMILARITY: Contains 1 GOLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- SUBUNIT: Interacts with ARFGAP1,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS50866; GOLD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FUNCTION: Could have a role in the budding of other species of coated vesicles. Could bind o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       coatomer-coated vesicles.
SIMILARITY: BELONGS TO THE EMP24/GP25L FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       collect them into budding vesicles
                                                                                                                                                                                      19
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                                                                                                                                                              FAAHMDGTYKF
                                                                                                                                                                                      FXXXXXGXYXF 29
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Proteobacteria; Gammaproteobacteria; Pasteurellales;
                                                                                                                                                                                                                                                              30
201 AA;
                                                                                                                                                                                                                                                                                                                                                    Protein
                                  (Rel. 32, Created)
(Rel. 32, Last sequence update)
(Rel. 41, Last annotation update)
protein HI1626.
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169
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22733 MW;
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                                                                                                                                                                                                                                                                                                                                                   transport;
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Rodentia;
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                                                                                                                                                                                                                        Score 21;
Pred. No.
                                                                                                                                                                                                                                                                         GOLD
                                                                                                                                                                                                                                                                                                                          POTENTIAL.
COP-COATED VESICLE MEMBRANE
                                                                                                                                                                                                                                                                                      CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                   POTENTIAL
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                                                                                                  PRT;
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                                                                                                                                                                                                                                                              E35A3816429DDF9A CRC64;
                                                                                                                                                                                                               Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  enriched in pancreatic a protein family involved
                                                                                                  238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       inhibiting the
                                                                                                                                                                                                                                                                                                                                                                                                                                       (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                         1.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         There
                                                                                                                                                                                                                                      DB 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                as its content
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Usage
                                                                                                                                                                                                                                     Length 201;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            restrictions
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Dejgaard K.,
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MEDLINE=21608550; PubMed=11743193; Wood D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima Okura V.K., Zhou Y., Chen L., Wood G.E., Almeida N.F. J. Chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Bovee D. Chapman P., Clendenning J., Deatherage G., Gillet W., G. Kutyavin T., Levy R., Li M.-J., McClelland E., Palmieri
                                                                                                                                                                                                                                                                                       15-SEP-2003 (Rel. 42, Created)
15-SEP-2003 (Rel. 42, Last sequence update)
15-SEP-2003 (Rel. 42, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Glucose-1-phosphate adenylyltransferase (EC 2.7.7.27) (ADP-glucose synthase) (ADP-glucose pyrophosphorylase) (ADPGlc PPase).
GLGC OR ATU4076 OR AGR L 1560.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F., Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M., McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D., Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M., Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D., Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C., Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S., Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O., Venter J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                            QBUBLS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rd. ";
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                                                                                                                                                                                                                 Agrobacterium tumefaciens (strain C58 / ATCC 33970)
Bacteria, Proteobacteria; Alphaproteobacteria; Rhiz
Rhizobiaceae; Rhizobium/Agrobacterium group; Agroba
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    entities requires a license agreement (S or send an email to license@isb-sib.ch).
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NCBI_TaxID=727;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; U32835; AAC23269.1;
PIR; I64038; I64038.
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                                                                                                                                                  EQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUBCELLULAR LOCATION: Integral membrane protein (Potential) SIMILARITY: TO B.SUBTILIS YWIC.
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39 POTENTIAL.
84 POTENTIAL.
05 POTENTIAL.
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Pred. No. 1.5e+02;
); Mismatches 7;
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     et W., Grant C., Palmieri A.,
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cent is in
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Best Local (
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InterPro; IPR005835; ANP dlu pyrop.
InterPro; IPR005835; NTP transferase.
Pfam; PF00483; NTP transferase; 1.
PR051TE; PS00808; ADP GLC PYROPHOSPH 1; 1.
PROSITE; PS00809; ADP GLC PYROPHOSPH 2; 1.
PR051TE; PS00810; ADP GLC PYROPHOSPH 3; 1.
Glycogen biosynthesis; Transferase; Nucleo
                                                                                                         P39669;
01-FEB-1995
01-FEB-1995
15-SEP-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "The genome of
                                                                                                                                                                                                                                                                                                                                                      Complete
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Raymond C
Zhang S.,
                                                                             01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Glucose-1-phosphate adenylyltransferase (EC 2.7.7.
Synthase) (ADP-glucose pyrophosphorylase) (ADPGlc
                       Agrobacterium tumefaciens:
Bacteria; Proteobacteria; Alphaproteoi
Rhizobiaceae; Rhizobium/Agrobacterium
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Genome sequence of the plant pathogen and biotechnology agent Agrobacterium tumefaciens C58."; Science 294:2323-2328(2001).
-!- CATALYTIC ACTIVITY: ATP + alpha-D-glucose 1-phosphate =
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M., Mullin Qurollo B., Goldman B.S., Cao Y., Askenazi M., Halling C., Mullin Houmiel K., Gordon J., Vaudin M., Tartchouk O., Epp A., Liu F., Wollam C., Allinger M., Doughty D., Scott C., Lappas C., Markelz B Flanagan C., Crowell C., Gurson J., Lomo C., Sear C., Strub G., Cielo C., Slater S.;
                                                                                                                                                                                   AGRTU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  entities requires a license agreement (S or send an email to license@isb-sib.ch).
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Gordon-Kamm
NCBI_TaxID=358;
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PIR; G98228; G98228.
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PATHMAY: Glycogen biosynthesis; first
SIMILARITY: BELONGS TO THE BACTERIAL
PHOSPHATE ADENYLYLTRANSFERASE FAMILY.
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AE008276;
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S., Yoo H., Tao Y.,
I-Kamm B., Liao L., F
Y F., Tingey S.V., J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   E.W.;
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4; Conserv
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420 AA;
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DO H., Tao Y., Biddle P., Jung

B., Liao L., Kim S., Hendrick

Tingey S.V., Tomb J.-F., Gord
                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                    STANDARD;
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                                      Alphaproteobacteria;
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0; Mismatches
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, Jung M., Kresp
ndrick C., Zhao
, Gordon M.P., (
                                                                                                                                                                                                                                                                                                                                                                                Nucleotidyltransferase;
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                          group;
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AND PLANTS
                          Agrobacterium
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Zhao Z.-Y., Dolan
.P., Olson M.V.,
                                         Rhizobiales
                                                                                                                                                                                                                                                                                                                           Length 420;
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R InterPro; IPR005835; NTP-transferase.

R InterPro; IPR005835; NTP-transferase.

R Ffam; PF00483; NTP-transferase; 1.

R PROSITE; PS00809; ADP_GLC_PYROPHOSPH 1; 1.

DR PROSITE; PS00809; ADP_GLC_PYROPHOSPH_2; 1.

DR PROSITE; PS00810; ADP_GLC_PYROPHOSPH_3; 1.

DR PROSITE; PS00810; ADP_GLC_PYROPHOSPH_3; 1.

R PROSITE; PS00810; ADP_GLC_PYROPHOSPH_2; 1.
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Best Local S
Matches 4
                                                                      15-SEP-2003 (Rel. 42, Created)
15-SEP-2003 (Rel. 42, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
15-SEP-2003 (Rel. 42, Last annotation update)
Glucose-1-phosphate adenylyltransferase (EC 2.7.7.27) (AD synthase) (ADP-glucose pyrophosphorylase) (ADPGlc PPase).
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Gene 150:117-122(1994).

-i- CAPALYTIC ACTIVITY: ATP + alpha-D-glucose 1-phosphate - idiphosphate + ADP-glucose.

-i- PATHWAY: Glycogen biosynthesis; first step.

-i- SIMILARITY: BELONGS TO THE BACTERIAL AND PLANTS GLUCOS PHOSPHATE ADENYLYLTRANSFERASE FAMILY.
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This SWISS-PROT entry is copyright. between the Swiss Institute of Bio.
                                                                                                                                                                                                                                                                 Marroqui S., Zorreguieta A., Megias M., Downie J.A.; "Enhanced symbiotic performar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiaceae; Rhizobium/Agrobacterium group; R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "A CHIOMOSOMAL Cluster of genes encoding glycogen synthase and phosphoglucomutase tumefaciene".
                                                                                                                                                                                                                                                mutants.";
                                                                                                                                                                                                                                                                                                                                                         MEDLINE=21142510; PubMed=11208782;
                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rhizobium tropici.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=398
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ERIAL AND PLANTS GLUCOSE-1-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        group; Rhizobium.
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                         produced through
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                                                                                                        PLANTS GLUCOSE-1-
                                                                                                                                                                                       1-phosphate
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RESULT 15
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Q985F3; Q93QE7;

15-SEP-2003 (Rel. 42, Created)

15-SEP-2003 (Rel. 42, Last sequence update)

15-SEP-2003 (Rel. 42, Last annotation update)

15-SEP-2003 (Rel. 42, Last annotation update)

Slucose-1-phosphate adenylyltransferase (EC 2.7.7.27) (ADP-glucose synthase) (ADP-glucose pyrophosphorylase) (ADPGlC PPase).
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InterPro; IPR005836; NTP_transferase.
InterPro; IPR005835; NTP_transferase.
InterPro; IPR005835; NTP_transferase.
Pfam; pF00483; NTP_transferase; 1.Ph. PR051TE; pS00808; ADP_GLC_pYROPHOSPH_1; 1.PR051TE; pS00808; ADP_GLC_pYROPHOSPH_2; 1.PR051TE; pS00801; ADP_GLC_pYROPHOSPH_3; 1.PR051TE; pS00810; ADP_GLC_pYROPHOSPH_3; 1.PR051TE; pS00800; ADP_GLC_pYROPHOSPH_3; 1.PR051TE; ADP_GLC_pYROPHOSPH_3; 1.PR051TE; ADP_GLC_pYROPHOSPH_3; 1.PR051TE; ADP_GLC_pYROPHOSPH_3; 1.PR051TE; ADP_GLC_pYROPHOSPH_3; ADP_GLC_pYROPHOSPH_3; ADP_GLC_pYROPHOSPH_3; ADP_GLC_pYROPHOSPH_3; ADP_GLC_pYROPHOSPH_3; A
                                                                                                                                                                                                                                                                                                                                   "Complete genome structure of the nitrogen-fixing symbiotic ba Mesorhizobium loti.";
DNA Res. 7:331-338(2000).
-!- CATALYTIC ACTIVITY: ATP + alpha-D-glucose 1-phosphate = diphosphate + ADP-glucose.
-!- PATHMAY: Glycogen biosynthesis; first step.
-!- SIMILBAITY: BELONGS TO THE BACTERIAL AND PLANTS GLUCOSE-1-PHOSPHATE ADENYLYLTRANSFERASE FAMILY.
This SWISS-PROT entry is copyright. It is produced through a clother the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and foentities requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto Watanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura T., Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M. Takeuchi C., Yamada M., Tabata S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lepek V.C., Tomatis P.E., Giambiagi S., Ugalde R.A.; "Partial characterization of R.loti gene cluster for glycogen metabolism: differences with A.tumefaciens."; Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rhizobium loti (Mesorhizobium loti).
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales.
Phyllobacteriaceae; Mesorhizobium.
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DR HAMAP; AF003012; BAB54019.1; -.

DR HAMAP; MF 00624; -; 1.

DR InterPro; TPR005836; ADP_GLU_pyroP.

DR InterPro; TPR005835; NTP_transferase.

DR PROSITE; PS00808; ADP_GLC_PYROPHOSPH_2; 1.

DR PROSITE; PS00810; ADP_GLC_PYROPHOSPH_3; 1.

PT CONFLICT 154 154 N -> G (IN REF. 1).

PT CONFLICT 201 201 D -> G (IN REF. 1).

PT CONFLICT 262 262 A -> M (IN REF. 1).

PT CONFLICT 383 338 T -> S (IN REF. 1).

PT CONFLICT 355 355 T -> A (IN REF. 1).

PT CONFLICT 355 355 A -> V (IN REF. 1).

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PT CONFLICT 367 366 A -> V (IN REF. 1).

PT CONFLICT 367 366
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Perfect score:
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Maximum Match 100%
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Copyright (c) 1993 - 2004 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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### ALIGNMENTS

dg VQ	Ma Ma	SQ.	DR	DR	DR	DR	DR	DR	DR	DR	S	RL	RT	RT	RA	RP	RN	o×	8	8	გ	SO	GN	DE	DT	DT	DT	AC	ID Q	RESULT
19 PXXXXXXXXXX 29 	Query Match 40.4%; Score 23; DB 13; Length 352; Best Local Similarity 36.4%; Pred. No. 5.1e+02; Matches 4; Conservative 0; Mismatches 7; Indels 0; Gaps 0;		PROSITE; PS00250; TGF BETA 1; 1.	SMART; SM00204; TGFB; 1.	ProDom; PD000357; TGFb; 1.	PRINTS; PR00669; INHIBINA.	Pfam; PF00019; TGF-beta; 1.	InterPro; IPR001839; TGFb.	InterPro; IPR002405; Inhibin_alpha.	EMBL; AB044566; BAB19272.1;	-!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.	Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.		and cellular local		SEQUENCE FROM N.A.	[1]	NCBI_TaxID=8022;	formes; Salı	pterygii; Teleostei; Euteleostei	Chordata; Crania	Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).	INH.	Inhibin.	(TrEMBLrel. 22, Last	01-MAR-2001 (TrEMBLrel. 16, Last sequence update)	2001 (TrEMBLrel.		Q9DED3 PRELIMINARY; PRT; 352 AA.	ILT 1

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A Boistard P., Becker A., Boutry M., Cadieu E., Dreano S., Gloux S.,
A Godrie T., Goffeau A., Kahn D., Kiss E., Lelaure V., Masuy D.,
A Pohl T., Portetelle D., Puehler A., Purnelle B., Ramsperger U.,
A Pohl T., Portetelle D., Puehler A., Purnelle B., Ramsperger U.,
A Renard C., Thebault P., Vandenbol M., Weidner S., Galibert F.;
T' "Analysis of the chromosome sequence of the legume symbiont
Sinorhizobium meliloti strain 1021.";
Froc. Natl. Acad. Sci. U.S.A. 98:9877-9882(2001).
EMBL; ALS91792; CAC47575.1; -.
EMBL; ALS91792; CAC47575.1; -.
RE Interpro; IPR001084; Bac, surfAg, D15.
Interpro; IPR001084; Bac, surfAg, D15.
Interpro; IPR001084; CryStallin.
Interpro; IPR001084; Rac, surfAg, D15.
REPGME, PF00103; Bac SurfAce, Ag; 1.
REPGME, PS00178; AA TRNA LIGASE I; 1.
REPGSITE; PS00178; AA TRNA LIGASE I; 1.
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Q92LN9;
Q1-DEC-2001
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Runt related transcription factor 3.
Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rhizobium meliloti (Sinorhizobium meliloti).
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Rhizobiaceae; Sinorhizobium.
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STRAIN=C57BL/6J; TISSUE=Eye;
MEDLINE=22354683; PubMed=12466851;
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                                                                                                                                60,770 full-length cDNAs.";
Nature 420:563-573(2002).
EMBL; AX053910; BAC35587 l; -.
SEQUENCE 144 AA; 14731 MW;
                                                                                                                                                                                                                                          The FANTOM Consortium,
the RIKEN Genome Exploration Research Group
"Analysis of the mouse transcriptome based o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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(TrEMBLrel. 23, Last annotation)
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65656 MW; E51276BB29B1FB78 CRC64;
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IEOgai T., Ota T., Nishikawa T., Hayashi K., Otsuki T., Suzuki Y., Nagai K., Sugano S., Ishii S., Kawai-Hio Y., Suzuki Y., Nagai K., Sugano S., Ishii S., Kawai-Hio Y., Yamamoto J., Wakamatsu A., Nakamura Y., Kojima S., Nagahi Masuho Y., Ono T., Okano K., Yoshikawa Y., Aotsuka S., S. Hattori A., Okumura K., Iwayanagi T., Ninomiya K.;
"MEDO human cDNA sequencing project.";
"MEDO human cDNA sequencing project.";
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
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01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
11-MAR-2003 (TrEMBLrel. 23, Last annotation update)
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01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation updat
Hypothetical protein FLJ90481.
Hymon sapiens (Human).
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Mammalia; Eutheria;
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Hypotherical market
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InterPro; IPROC
Pfam; PF01105;
                                                                        EMBL; BC019349; AAH19349.1; -.
EMBL; AK074962; BAC11318.1; -.
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IPR000348; Emp24_gp25L_p24
1105; EMP24_GP25L; 1.
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Pred. No. 4.9e+02;
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., Kawai-Hio Y., Saito K
KOjima S., Nagahari K.,
Y., Aotsuka S., Sasaki N
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Kawai-Hio Y., Saito K.,
ojima S., Nagahari K.,
, Aotsuka S., Sasaki N.,
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RESULT 7

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ID Q9KG
AC Q9KG
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DT 01-M
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DT 01-M
BACT
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Q9KGP4;
01-OCT-2000
01-OCT-2000
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Q96K51; O1-DEC-2001 (TrEMBLrel. 19, Created)
O1-DEC-2001 (TrEMBLrel. 19, Last sequence update)
O1-OCT-2002 (TrEMBLE). 22, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y., Mishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H., Wagatsuma M., Hosoixi T., Kaku Y., Kodaira H., Kondo H., Sugawara M., Takahashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi S., Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K., Yamamoro J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y., "Ninomiya K., Iwayanagi T.; "NEDO human CDNA sequencing project."; Submitted (MAY-201) to the EMBL/GenBank/DDBJ databases.
            "Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and genomic sequence comparison with Bacillus subtilis. Nucleic Acids Res. 28:4317-4331 (2000).
EMBL; AP001507; BAB03732.1; -.
                                                                        STRAIN=C-125 / JCM 9153;
MEDLINE=20512582; PubMed=11058132;
Takami H., Nakasone K., Takaki Y., Maeno G.
Fuji F., Hirama C., Nakamura Y., Ogasawara
                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hypothetical protein SEQUENCE 224 AA;
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Mammalia; Eutheria;
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Homo sapiens (Human)
                                                                                                                                                         NCBI_TaxID=86665;
                                                                                                                                                                     Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus
                                                                                                                                                                                  Bacillus halodurans.
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                                                                Horikoshi K.;
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Pfam; PF01105; EMP24_GP25L; 1.
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                                             Proc. Natl. Acad. Sci. U.S.A. 98:3460-3465(2001).
EMBL; AE006081; AAKO2539.1; -.
InterPro; IPR006314; Dyp_peroxidase.
TIGRRAMs; TIGR01413; Dyp_perox_fam; 1.
Hypothetical protein; Complete proteome.
SEQUENCE 296 AA; 32951 MW; C4B616FAB4E40197 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Zhang Y., Ren S., Li H., Fu G., Lu L., Lu G., Chen Z., Wen Y.;
Submitted (NOV-2002) to the EMBL/GenBank/DDBJ EMBL, AB016747; AA004603.1; -.
Hypothetical protein; Complete proteome.
SEQUENCE 290 AA; 33745 MW; Al3E6A424943B19
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01-JUN-2001 (TrEMBLrel. 17,
01-MAR-2003 (TrEMBLrel. 23,
Hypothetical protein PM0455
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01-MAR-2003 (TrEMBLrel. 23, Las
01-MAR-2003 (TrEMBLrel. 23, Las
Conserved hypothetical protein.
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                                                                                                     May B.J., Zhang Q., Li L.L., Paustian M.L., Whittam T.S., K "Complete genomic sequence of Pasteurella multocida Pm70.", Proc. Natl. Acad. Sci. U.S.A. 98:3460-3465(2001).
                                                                                                                                                      SEQUENCE FR
STRAIN=Pm70
                                                                                                                                                                                                Pasteurellaceae; Pasteurella.
                                                                                                                                                                                                             Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
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STRAIN=ATCC 12228;
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Al3E6A424943B195 CRC64;
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SEQUENCE FROM N.A.
STRAIN=El Tor N16961 / Serotype O1;
MEDLINE=20406833; PubMed=10952301;
Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton J.D., Umayam L.A.,
Dedson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,
Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Wayam L.A.,
Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,
Gill S.R., Nelson K.E., Read T.D., Bass S., Qin H., Dragoi I., Sellers P.,
Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,
McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O.,
McDonald C., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
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Q9KQ59;
01-OCT-2000
01-OCT-2000
01-MAR-2003
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Bacteria; Proteobacteria;
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Choy H.E.;
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                                                      InterPro; IPR006314; Dyp_peroxidase.
TIGRFAMs; TIGR01413; Dyp_perox_fam; 1.
                                                                                                                                                                                                            Nature 406:477-483(2000)
                                                                                                                                                                                                                                         cholerae
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Pred. No. 7.9e+02;
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STRAIN=Goel / Gol / ATCC BAA-199 / DSM 3647 / OCM 88.

STRAIN=Goel / Gol / ATCC BAA-199 / DSM 3647 / OCM 88.

MEDLINE=22120827; PubMed=12125824;

Deppenmeler U., Johann A., Hartsch T., Merkl R., Schr
Martinez-Arias R., Henne A., Wiezer A., Baeumer S., i

Brueggemann H., Lienard T., Christmann A., Boemecke I

Brueggemann H., Lienard T., Christmann A., Boemecke I

Brutz H.-J., Gottschalk G.;

"The genome of Methanosarcina mazei: evidence for lat

transfer between Bacteria and Archaea.";
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Deppenmeier U., Johann A., Hartsch T., Merkl R., Schmitz R.A., Martinez-Arias R., Henne A., Wiezer A., Baeumer S., Jacobi C., Brueggemann H., Lienard T., Christmann A., Boemecke M., Stecke Bhattacharyya A., Lykidis A., Overbeek R., Klenk H.-P., Gunsall Fritz H.-J., Gottschalk G.;
"The genome of Methanosarcina mazei: evidence for lateral gene
                                                                                                                                                                                                                                                                                                                                                                                                                                               Methanosarcina mazei (Methanosarcina i
Archaea; Euryarchaeota; Methanococci;
Methanosarcinaceae; Methanosarcina.
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                                                                                                                                                       Merkl R., Schmitz R.A.,
Baeumer S., Jacobi C.,
A., Boemecke M., Stecke
R., Klenk H.-P., Gunsal
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                                                                                                                                                                                                                           Q8EJZ4 PRELIMINARY; PRT; 384 AA.
Q8EJZ4;
Q1-MAR-2003 (TrEMBLrel. 23, Created)
O1-MAR-2003 (TrEMBLrel. 23, Last sequence update)
O1-MAR-2003 (TrEMBLrel. 23, Last annotation update)
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Q966G5 Q966G5 Q1
Q1-DEC-2001 (TrEMBLrel 19, Created)
01-DEC-2001 (TrEMBLrel 19, Last sequence update)
01-MAR-2003 (TrEMBLrel 23, Last annotation update)
Hypothetical protein R13D7.10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Direct Submission.";
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AC006680; ARX72298.1; -.
WormPep; R13D7.10; CE18155.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Murray J., Wohldmann P., Elliott G.;
"The sequence of C. elegans cosmid R13D7.";
Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
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STRAIN=Bristol N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium.", Science 282:2012-2018(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=Bristol N2;
MEDLINE=99069613; PubMed=9851916;
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Rhabditidae; Peloderinae;
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                                                                           Bacteria; Proteobacteria; Gammaproteobacteria; Alteromonadales;
                                                                                                                   Shewanella oneidensis.
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Alteromonadaceae; Shewanella.
NCBI_TaxID=70863;
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fam; PF01748; DUF32; 1.
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les 4; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              355 AA;
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A Heidelberg J.F., Paulsen I.T., Ward N., Methe B., Clayton R.A.,
A Read T.D., Eisen J.A., Seshadri R., Ward N., Methe B., Clayton R.A.,
A Meyer T., Tsapin A., Scott J., Beanan M., Brinkac L., Daugharty S.,
Daboy R.T., Dodson R.J., Durkin A.S., Haft D.H., Kolonay J.F.,
A Madupu R., Peterson J.D., Umayam L.A., White O., Wolf A.M.,
A Madupu R., Peterson J.D., Umayam L.A., White O., Wolf A.M.,
A Wamathevan J., Weidman J., Impraim M., Lee K., Berry K., Lee C.,
A Mueller J., Khouri H., Gill J., Utterback T.R., McDonald L.A.,
A Mueller J., Khouri H.O., Venter J.C., Nealson K.H., Fraser C.M.,
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57
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#### ALIGNMENTS

Human T1-receptor ligand III; T1-R ligand III; atherosclerosis; autoimmune disease; inflammation; metabolic dysfunction; immune-regulated disorder. 28-FEB-1997; 26-FEB-1998; WO9838311-A1 Human T1-receptor ligand III splice variant 1. (HUMA-) HUMAN GENOME SCI INC sapiens 97US-0039483. 98WO-US03483 Location/Qualifiers 25..163 /note= "Signal peptide" /note= "T1-R ligand III splice variant

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SXCCCCCCCCX BX PPTX R RXPI
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Best Local S
Matches 4
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11-JAN-2000;
The invention relates to primers for synthesising full length cDI clones, 830 cDNA molecules encoding a human protein have been isolated and nucleotide sequences of 5' and 3'-ends of the cDNA molecules have been determined. Primers for synthesising the full cDNA are useful for clarifying the function of the protein encode
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New human T1-receptor ligand III splice variant(s) - useful for, e.g. detecting and treating immune system related disorders such cancer and inflammation % \left( 1\right) =\left\{ 1\right\} =
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N-PSDB; AAK94557.
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2000JP-0183765.
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na T, Nagai
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Pred. No. 2.1e
0; Mismatches
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   Primers for synthesising the full length the function of the protein encoded by
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K, Kojima
                                                                                                                                                                                                                                      sequence listing;
                                                                                                                                                                                                                                                                                                                                                  full length cDNA clones
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2.1e+02;
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S, Otsuki
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                                    ligand III) splice variants and antibodies raised against these proteins. The present sequence represents the T1-R ligand III splice variant 2 protein sequence. The T1-R ligand III splice variants are claimed useful for screening agonists and antagonists. They are also claimed useful for treating disorders such as atherosclerosis, autoimmune disease, inflammation, metabolic dysfunction and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the cDNA. The full length clones were obtained by construction of full length enriched cDNA libraries that were synthesised by the oligo-capping method. The primers enable the production of the full length cDNA easily without any special methods. The present sequence is a polypeptide encoded by a full length human cDNA of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in CD-ROM format directly from EPO.
                                                                                                                                                              New human T1-receptor ligand III splice variant(s) e.g. detecting and treating immune system related cancer and inflammation
                                                                                                                                                                                                                                                                                                   28-FEB-1997;
                                                                                                                                                                                                                                                                                                                           26-FEB-1998;
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                                                                                                             The invention provides novel human T1-receptor ligand III (T1-R
                                                                                                                                      Claim 1; Fig 2; 115pp; English.
                                                                                                                                                                                                                                                                                                                                                                             WO9838311-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   immune-regulated disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 autoimmune
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Peptide
                           immune-regulated disorders
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DB; AAV33462.
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                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "Signal peptide'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Protein;
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                                                                                                                                                                                                    The present invention relates to methods for identifying genes and proteins that are implicated in a specific disease or physiological condition. The method comprises comparing the transcriptome/proteome of a specialised cell type implicated in a disease or condition with that of a second specialised cell type, under two experimental conditions, and identifying a gene that is differentially regulated in the two specialised cell types under experimental conditions. ABV7873-ABV78116 and ABB65061-ABB65257 were identified using the methods of the invention. The coding sequences and proteins are useful for treating a disease in a patient, for manufacture of a medicament for treating hypoxia-regulated conditions, and for regulating tumourigenesis, angiogenesis, apoptosis, biological response to hypoxia conditions or hypoxia-associated conditions in a patient who coding sequences and proteins are seculated.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            inclaiming atory; vulnerary; gynecological; ophthalmological; vaccine; hypoxia; tumourigenesis; angiogenesis; apoptosis; cancer; ischaemic condition; reperfusion injury; retinopathy; neonatal stress; preeclapmsia; atherosclerosis; inflammatory condition; wound healing; inflammation; erythropoiesis; hair loss: human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Identifying a gene involved in disease for treating hypoxia-regulated conditions, comprises comparing the transcriptome/proteome of two cel types under different conditions and identifying a differentially
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08-FEB-2001; 2001GB-0003156.
25-OCT-2001; 2001GB-0025666.
      Sequence
                                                                                       pathology in a patient. The coding sequences and proteins are also useful for monitoring the therapeutic treatment of a disease or physiological condition, such as cancer, ischaemic conditions, reperfusion injury, retinopathy, neonatal stress, preeclapmsia, atherosclerosis, inflammatory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2002-627238/67.
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                                                             inflammation,
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CC Sequences ABB10981-ABB12330 represent 1350 novel human polypeptides, and CC sequences ABA08225-ABA09574 represent nucleic acids encoding them. The CC invention also relates to vectors and recombinant host cells comprising a CC nucleotide of the invention, methods of producing the movel polypeptides, cantibodies against the polypeptides, methods of identifying compounds which CC or polypeptides in a sample, and methods of identifying compounds which CC bind to polypeptides of the invention. Although movel, many of the CC polypeptides of the invention have homology to known proteins, thereby CC giving an insight into their probable biological activities, and hence CC potential therapeutic applications. The polypeptides of the invention may have various activities; stem cell growth factivity; activity is tissue growth activity; CC haematopolesis regulatory activity; tissue growth activity; CC chemotactic or chemokinetic activities; are inhibin-related activities; or thrombotic or thrombolytic activities; cancer cell proliferation or metastasis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human proteins and DNA encoding sequences useful for preventing, treating or ameliorating a medical condition in a mammalian subject e.g. arthritis and cancer -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              myeloid cell disorder; lymphoid cell disorder; asthma; arthritis; chronic inflammatory condition; proliferative retinopathy; atherosclerosis; coronary heart disease; arterial ischaemia; bone disorder; osteoporosis; vascular growth disorder; tissue regeneration; wound healing; infection; immune disorder; cell culture; drug screening; gene therapy; antiinflammatory; antiasthmatic; antiarthritic; haemostatic; antiarteriosclerotic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 20; Page 245; 1963pp;
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27-APR-2000; 2000US-0560875.
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RESULT 6
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The invention relates to primers for synthesising full length cDNA clones. 830 cDNA molecules encoding a human protein have been isolated, and nucleotide sequences of 5'- and 3'-ends of the cDNA molecules have been determined. Primers for synthesising the full
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Depending on their biological activities, polypeptides and nucl the invention are useful for preventing, treating or ameliorati conditions, e.g., by protein or gene therapy. Such conditions i cancers, haematopoietic disorders (e.g., myeloid or lymphoid cel
                                                                                                                                                        Claim
                                                                                                                                                                                                              830 Primers useful for synthesizing use in genetic manipulation -
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02-MAY-2000;
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su A, Sugiyama
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2000JP-0118774.
2000JP-0183765.
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                                                                                                                                                     3923; 1380pp + sequence listing; English
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a T, Nagai
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Pred. No. 2.8e+02;
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K, Kojima
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                                                                                                                                                                                                                                                                                                                                                                                                 Kawai Y;
T, Koga
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Matches 4
the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end sequence and an oligonucleotide comprising a sequence complementary to a polynucleotide which comprises a 3'-end sequence, where the oligonucleotide which comprises a 15 nucleotides and the combination of the 5'-end sequence/3'-end sequence is selected from those defined in the specification. The primer sets can be used in antisense therapy and
                                                                                                                         The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dT primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the complementary strand of a polynucleotide which comprises one of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cDNA are useful for clarifying the function of the protein encoded by the cDNA. The full length clones were obtained by construction of full length enriched cDNA libraries that were synthesised by the oligo-capping method. The primers enable the production of the full length cDNA easily without any special methods. The present sequence is a polypeptide encoded by a full length human cDNA of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in CD-ROM format directly from EPO.
                                                                                                                                                                                                                                                                                                                                                                                                                                      29-JUL-1999; 99JP-0248036
27-AUG-1999; 99JP-0300253
11-JAN-2000; 2000JP-0118776
02-MAY-2000; 2000JP-0183767
09-JUN-2000; 2000JP-0241899
                                                                                                                                                                                                                                                                  Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human;
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                                                                                                                                                                                                                                                   diagnosis of the ength cDNAs -
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T, Wakamatsu
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                              Hayashi K, !
A, Nagai K,
                                                                                                                                                                                                                      ROM;
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2.9e+02;
                                                                                                                                                                                                                    English
                                                                                                                                                                                                                                                                                                                                                              Saito K,
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RESULT 8
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                                                                                                                                                                                                               Dufour GE, Hillim.

Daughtery SC, Dam T

David P
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29-MAR-2001;
16-MAY-2001;
17-MAY-2001;
17-MAY-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cancer; cell proliferative disorder; autoimmune disorder; inflammatory disorder; infection; hormonal disorder; metabolic disorder; neurological disorder; gastrointestinal disorder; transport disorder; connective tissue disorder; drug screening; proteome analysis; gene therapy; antisense therapy; genotyping; transgenic animal; knock in; disease model; toxicological testing; transcript imaging;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   in gene therapy. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs easily without any specialised methods. AAH03166 to AAH13628 and AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to AAH3630 to AAH13632 and AAH95893 represent human amino acid sequences; and AAH13632 to AAH13632 and AAH95893 represent oligonucleotides, all of which are used in the exemplification
Novel human diagnostic and therapeutic polypeptide useful for identifying test compound which specifically binds to a polypeptide encoded by human diagnostic and therapeutic polynucleotide, and to induce antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; dithp; diagnostic and therapeutic polynucleotide; diagnosis;
                                                                                                                           N-PSDB;
                                                                                                                                                  WPI; 2003-129518/12.
                                                                                                                                                                                                                                                                                                     Daffo A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28-MAR-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27-MAR-2002; 2002WO-US10056
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human DITHP cell membrane protein.
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                                                                                                                           ACC46611.
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                                                                                                                                                                                                                                                                                                     Jones AL,
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                                                                                                                                                                                                                                                                   Hillman JL,
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2001US-291849P.
2001US-299428P.
2001US-299776P.
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2001US-280068P.
2001US-291280P.
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                                                                                                                                                                                                                                                                                                   Tran AB,
                                                                                                                                                                                                          an AB, Dahl CR, Gieuz
, Yu JY, Tuason O, Ya
Liu TF, Nguyen DA,
----- SA, Chen AJ,
                                                                                                                                                                                                  Lo A,
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Pred. No.
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2.9e+02;
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O, Yap PE, A
DA, Kleefeld
                                                                                                                                                                                                                            Panzer
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                                                                                                                                                                                                                                            Amshey SR;
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                                                                                                                                                                                                                                                                           SR;
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RESULT 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   or cell type and to induce antibodies. The dithp nucleic acids are additionally useful in somatic or germline gene therapy of the disorders mentioned above, as a source of antisense sequences, as a source of probes and primers, in genotyping and identification of individuals, in the generation of transgenic animal models of human disease or knock in humanised animals, in toxicological testing, and in transcript imaging. The present sequence represents a DITHP protein which is a cell membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 disorders; neurological disorders; gastrointestinal disorders; transport disorders; and connective tissue disorders. They may also be used to screen for modulators of protein activity or gene expression. DITHP proteins can additionally be used in analysis of the proteome of a tissue
                                                   Kimmerly WJ;
                                                                                                                                                                                                  09-NOV-2000; 2000WO-US30782
                                                                                                                                                                                                                                                                                                    WO200134809-A2
                                                                                                                                                                                                                                                                                                                                                   Staphylococcus
                                                                                                                                                                                                                                                                                                                                                                                                    Staphylococcus epidermidis SR1 strain; infection; diagnosis; vaccination; endocarditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             S. epidermidis open reading frame protein sequence SEQ ID NO:2066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAG82486;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAG82486 standard; Protein; 266 AA
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                                                                                                                                                                                                                                                      17-MAY-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The sequence data for this patent did not fication, but was obtained in electronic for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           27; SEQ
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                                                                                                     GROUP LTD
                                                                                                                                                                                                                                                                                                                                                   epidermidis
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Pred. No. 3e+0
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3e+02;
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WPI; 2001-316495/33

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RESULT 10
ABP392927
ID ABP39
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  in vaccination. The nucleic acids (I) may be used to produce the S. epidermidis polypeptides (II) via the production of vectors containing them which are used to produce hosts cells which express the polypeptides. The polypeptides (II) (and/or nucleic acids) may then be used to vaccinate subjects and to raise antibodies against the bacteria. The polypeptides may also be used to assay for other inhibitors of their activity and therefore identify compounds that may be used for the treatment of S. epidermidis infections, e.g. endocarditis. AAH53971 to AAH55090 represent specifically claimed S. epidermidis genomic DNA polynucleotide sequences from the present invention. AAH55091 to AAH55098 represent oligonucleotide sequences and primers which are used in the exemplification of the present invention.

N.B. The present invention specifically claims all the polynucleotide sequences given in the present invention. The present invention, bewever the sequence listing only goes up to SEO ID NO:4454 so even though sequences are given in the disclosure for SEO ID NO:4455 to 4472, no sequences are present for SEO ID NO:4455 to 4472,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
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Best Local :
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                          Novel isolated nucleic acid encoding a Staphylococcus epidermidis polypeptide, useful for diagnosing and treating bacterial infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Staphylococcus antibacterial;
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                                                                                                                                                                                                                                                                                                                     14-AUG-1997;
08-NOV-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Staphylococcus
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                                                                                                                   2002-381255/41
DB; ABN91842.
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                                                                                                                                                                                                                                                               GENOME
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Page 560; 2188pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         266 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    epidermidis ORF amino acid sequence SEQ ID NO:4142.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 epidermidis;
gene therapy.
                                                                                                                                                                                                    Ę,
                                                                                                                                                                                                                                                               THERAPEUTICS CORP
                                                                                                                                                                                                                                                                                                                     97US-055779P.
97US-064964P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               epidermidis.
                                                                                                                                                                                                                                                                                                                                                                                                        98US-0134001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     38.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               represent nucleic acids (I) encoding polypeptides 454 to AAG83120, from Staphylococcus epidermidis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        polypeptides from Staphylococcus epidermidis, against infections, e.g. endocarditis -
                                                                                                                                                                                                       ū
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  open
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 292 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 22; DB 22;
Pred. No. 3.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               reading
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  frame; ORF; bacterial infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 266;
                             bacterial infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
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Best Local
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N.B. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the
                                                                                                                               Propionibacterium acnes vaccinating against and treating acne vulgaris
                                                                                                                                                                                                                                                                                                                                                                                                                                                       SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteoruveitis; endophthalmitis; bone; joint; central nervous system; inflammatory lesion; acne vulgaris; enzyme linked immunosorbeni dermatological; osteopathic; neuroprotectant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                              21-APR-2000; 2000US-199047P
02-JUN-2000; 2000US-208841P
07-JUL-2000; 2000US-216747P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; SEQ ID 4142; 267pp; English
                                                                                                        Example 1; SEQ ID No 18249; 1069pp; English
                                                                                                                                                                                                                             L'maisonneuve J,
                                                                                                                                                                                                                                          Skeiky YAW,
                                                                                                                                                                                                                                                                                                                                                   20-APR-2001; 2001WO-US12865
                                                                                                                                                                                                                                                                                                                                                                             01-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                 Propionibacterium acnes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Propionibacterium acnes immunogenic protein #17950.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAU57054;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAU57054 standard;
                                                                                                                                                                                                                                                                     (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                   2001-616774/71.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FKTTRSGVYTF 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             site.
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                                                                                                                                                                                                                             Persing DH,
e J, Zhang Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           38.6%;
                                                                                                                                             polypeptides and nucleic acids useful diagnosing infections, especially uses
                                                                                                                                                                                                                              Mitcham JL, Wang SS,
, Jen S, Carter D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          540
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 22;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                pustulosis; hypertosis; osteomyelitis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 23;
3.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 292;
                                                                                                                                                                                                                                            Bhatia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         immunosorbent
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                                                                                                                                                   for
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Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogen polypeptides. The proteins and their associated DNA sequences are used the treatment, prevention and diagnosis of medical conditions caused by P. acnes. The disorders include SAPHO syndrome (synovitis, acne, pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis. P. acnes is also involved in infections of bone, joints and the central nervous system, however it is particularly involved in the inflammatory

s immunogenic s are used in s caused by

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RESULT 12
AAB73384
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Matches 4
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Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                           Montero
Llobell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  antifungal; microbial cell wall degradation; antimicrobial; yeast extract production; disinfection; anti-biofilm; textile treatment; N-terminal peptide.
The invention relates to novel Trichoderma harzianum CECT 2413 beta-(1,6) endoglucanases, designated BGN16.1 and BGN16.3 (AAB73382 and AAB73383, respectively) and to nucleic acids encoding them (AAF76368 and AAF76269, respectively). The enzymes of the invention have antifungal activity, being able to degrade degrade beta-(1,6)-glucan components in microbial cell walls. The beta-(1,6)-endoglucanases are used as antifungal agents for the treatment and/or prevention of infections on
                                                                                                                                                                                                                                                                                                    New enzyme with beta-(1,6)-endoglucanase act antifungal agent in animals or plants, from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     31-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Trichoderma harzianum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Beta-(1,6)-endoglucanase; BGN16.1; strain CECT 2413;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     05-JUN-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                   Example 13; Page 32; 62pp; Spanish.
                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-182948/18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (NEWB-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28-JUL-2000; 2000WO-ES00293.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (UYSA-)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            harzianum beta-(1,6)-endoglucanase BGN16.1 N-terminal peptide.
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Macarro M,
Gonzalez A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NEWBIOTECHNIC SA.
UNIV SEVILLA.
UNIV SALAMANCA.
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                                                                                                                                                                                                                                                                              nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99ES-0001747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rey Barrera M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     38.6%;
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Pred.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Monte Vazquez
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6.9e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 22;
                                                                                                                                                                                                                                                                                                       activity, useful e.g. as rom Trichoderma harzianum,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 540;
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                                                                                                                                                                                                                                                                                                       also
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Matches 4
         The present sequence represents a Helicobacter pylori antigenic protein that is characterised by immunoreactivity with H. pylori-positive antisera. The proteins are highly immunogenic and induce a long-lasting immune response that persists even after antimicriobial treatment. In antibody-detection assays, on sera, plasma, urine, saliva etc., they are highly sensitive and specific. The specification also describes 69 previously unrecognised immunogenic cluster families. H. pylori antigens are used to detect H. pylori-specific antibodies, for diagnosing infection or to confirm eradication of infection, and in vaccines to protect against H. pylori infection and related diseases (gastritis, peptic ulcer, gastric adenocarcinoma/lymphoma).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                or harvested crops. They may also be used for disinfection of livestock installations and to prevent contamination of samples for analysis. Other applications of the beta-(1,6)-endoglucanases include the production of protoplasts and yeast extracts, extraction of mannoproteins; production of wine and fruit juices (improving filtration); eliminating dental plaque, cleaning teeth, dentures and contact lenses; removal of biofilms or fungi from coatings; and for the treatment of textiles, e.g., to remove excess dye. The present sequence represents a Trichoderma harzianum CECT 2413 beta-(1,6)-endoglucanase BGN16.1 N-terminal peptide used in the design of a degenerate PCR primer for the isolation of
                                                                                                                                                                                                                              New Helicobacter pylori - useful in serological long-lasting immune resp
                                                                                                                                                                                                                                                                                        WPI;
                                                                                                                                                                                                   Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Helicobacter
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                                                                                                                                                                                                                                                                                                                                                                             14-OCT-1997;
25-APR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     05-NOV-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO9849314-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Antigen; immunogenic cluster family; vaccine; gastritis; peptic ulcer; gastric adenocarcinoma; gastric lymphoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Antigen from cluster 60.
                                                                                                                                                                                                                                                                                                                                                                                                                        25-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20-MAR-2003
18-FEB-1999
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                                                                                                                                                                                                   Page 272; 402pp; English.
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(first en
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         pylori.
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                                                                                                                                                                                                                                                                                                                                                                             97US-0061958
97US-0045107
                                                                                                                                                                                                                                                                                                                                                                                                                        98WO-US08487
                                                                                                                                                                                                                                                                                                                    Lim MY,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             entry)
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36.4%;
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                                                                                                                                                                                                                                           antigens and related nucleic acid sequences diagnosis and protective vaccines. providing
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                                                                                                                                                                                                                      The invention relates to a human monoclonal antibody or its antigen binding fragments, which exhibit immunological binding affinity for a hepatitis C virus (HCV) El antigen, comprising an amino acid sequence homologous to the binding portion of a human antibody Fab molecule from combinatorial antibody library. The vaccine composition comprising the antibodies or antigen binding fragments against HCV El or E2 antigen or its hypervariable region is useful in treating or preventing HCV infection in a subject. Sequences ABG76513-ABG76568 represent human monoclonal antibodies against HCV El antigen.
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             AAY37071
                                                                                                                                                                                                                                                                                                                                                   Disclosure; Page 55-56; 64pp; English.
                                                                                                                                                                                                                                                                                                                                                                                      Vaccine comprising a human monoclonal antibody against hepatitis C virus (HCV) El or E2 antigen, useful for treating or preventing HCV
                                     AAY37071 standard;
                                                                                                                                                                                                   Sequence
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Search completed: January 12, Job time : 6.67166 secs

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Matches 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Vaccine; eye disease; conventional trachoma; nonendemic trachoma; paratrachoma; inclusion conjunctivitis; genital disease; perihepatitis; nongonococcal uretritis; epidymitis; cervicitis; salpingitis;
                                                                                                           Sequence
                                                                                                                                      may be
                                                                                                                                                                                                                                                                                                       Disclosure; Page 883-884; 1755pp; English.
                                                                                                                                                                                                                                                                                                                                  Genome sequence of Chlamydia trachomatis
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28-NOV-1997;
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97FR-0015041.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     specific to Chlamydia trachomatis
                                                                  36.8%;
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Pred. No.
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US-09-030-847-2
US-10-215-088-2
US-09-030-847-4
US-10-215-088-4
US-10-029-386-29069
US-10-039-865-7
US-10-060-255-68
US-10-060-255-68
US-10-060-255-68
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US-10-215-088-2
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CURRENT FILING DATE: 1998-02-26
EARLIER APPLICATION NUMBER: 60/039,483
EARLIER FILING DATE: 1997-02-28
NUMBER OF SEQ ID NOS: 16
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2
LENGTH: 163
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Best Local Similarity
Matches 4; Conserv
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TITLE OF INVENTION: T1-R Ligand III
FILE REFERENCE: PF357
FILE REFERENCE: WINNER: US/09/0
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## ALIGNMENTS

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Sequence 2, Application US/10215088
Publication No. US20030069409A1
GENERAL INFORMATION:
APPLICANT: Ni et al.
TITLE OF INVENTION: T1-R Ligand III
FILE REFERENCE: PF357C1
CURRENT APPLICATION NUMBER: US/10/215,088
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; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 215
; TYPB: PRT
; ORGANISM: Homo sapiens
US-09-030-847-4
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Patent No. US20020111472A1
GENERAL INFORMATION:
APPLICANT: Ni, Jian
TITLE OF INVENTION: T1-R Ligand III
FILE REFERENCE: PF357
CURRENT APPLICATION NUMBER: US/09/030,847A
CURRENT FILING DATE: 1998-02-26
EARLIER APPLICATION NUMBER: 60/039,483
EARLIER FILING DATE: 1997-02-28
UNUMBER OF SEQ ID NOS: 16
COPTMANDE: DOTORTON NUMBER: 05/039,483
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US-10-215-088-4
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US-10-215-088-4
                              SEQ ID NO 4
LENGTH: 215
TYPE: PRT
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Matches 4
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                                                                           PRIOR FILING DATE: 1998-02-26
PRIOR APPLICATION NUMBER: 60/039,483
PRIOR FILING DATE: 1997-02-28
NUMBER OF SEQ ID NOS: 16
SOFTWARE: Patentin version 3.1
                                                                                                                                                              APPLICANT: Ni et al.
TITLE OF INVENTION: T1-R Ligand III
FILE REFERENCE: PF357C1
CURRENT APPLICATION NUMBER: US/10/215,088
CURRENT FILING DATE: 2002-08-09
PRIOR APPLICATION NUMBER: 09/030,847
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PRIOR APPLICATION NUMBER: 09/030,847
PRIOR FILING DATE: 1998-02-26
PRIOR APPLICATION NUMBER: 60/039,483
PRIOR FILING DATE: 1997-02-28
NUMBER OF SEQ ID NOS: 16
SOPTWARE: Patentin version 3.1
            ORGANISM: Homo sapiens
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ilarity 36.4%;
Conservative
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Pred. No.
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Pred. No.
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2.7e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 6
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                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 6, Application US/10039865 Publication No. US20020132999A1 GENERAL INFORMATION:
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Best Local
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Best Local
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APPLICANT: Rank, David R.
APPLICANT: Hanzel, David R.
APPLICANT: Hanzel, David K.
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR GI
TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
FILE REFERENCE: ABOMICA-X-2
CURRENT APPLICATION NUMBER: US/10/029,386
CURRENT APPLICATION DATE: 2001-12-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 34288
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
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OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.75

OTHER INFORMATION: EXPRESSED IN BEART, SIGNAL = 1.2

OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.8

OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.2

OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.65

OTHER INFORMATION: SWISSPROT HIT: P34562, EVALUE 6.20e+00
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          COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: 1EM Compartable

OPERATING SYSTEM: DOS

SOFTWARE: FastSEQ for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/039,865

FILING DATE: 19-Oct-2001

CLASSIFICATION. (Thrown)
                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc
STREET: 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                     Bandman, Olga
TITLE OF INVENTION: NOVEL P24 VESICLE PROTEINS
NUMBER OF SEQUENCES: 8
                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Goli, Surya K.
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CLASSIFICATION: <Unknown>
                                                                                                                                                                                      COUNTRY: USA
ZIP: 94304
                                                                                                                                                                                                                                 STATE: CA
                                                                                                                                                                                                                                                   CITY: Palo Alto
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36.4%;
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Pred. No. 1.7e+02;
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Pred. No. 3.5e+02;
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      INFORMATION FO
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                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION UNMBER: US/10/039,865
FILING DATE: 19-Oct-2001
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: PF-0189 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: 08/801,740 FILING DATE: <Unknown> ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 94304
COMPUTER READABLE FORM:
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ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
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TITLE OF INVENTION: NOVEL P24 VESICLE PROTEINS
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IMMEDIATE SOURCE:
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                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA
                                                                                                TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 8
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TELEX: <Unknown>
)N FOR SEQ ID NO: 7:
ENCE CHARACTERISTICS:
                                                                                                                                                                                           APPLICATION NUMBER: US/09/215,736
FILING DATE: <Unknown>
APPLICATION NUMBER: 08/801,740
FILING DATE: <Unknown>
                                                                                                                    REFERENCE/DOCKET NUMBER: PF-0189 US
                                                                                                                                     NAME: Billings, Lucy J. REGISTRATION NUMBER: 36,749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE: CA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Palo Alto
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FILING DATE: <Unknown>
                                                            TELEFAX: 415-845-4166
                                                                              TELEPHONE: 415-855-0555
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TITLE OF INVENTION: 25 Human secreted proteins
FILE REFERENCE: P2042P1
CURRENT APPLICATION NUMBER: US/10/060,255
CURRENT FILING DATE: 2002-02-01
PRIOR PELICATION NUMBER: 09/781,417
PRIOR FILING DATE: 2001-02-13
PRIOR APPLICATION NUMBER: PCT/US00/22325
PRIOR APPLICATION NUMBER: 60/149,182
PRIOR APPLICATION NUMBER: 60/149,182
PRIOR APPLICATION NUMBER: 60/149,182
PRIOR APPLICATION NUMBER: 60/149,182
PRIOR PILING DATE: 1999-08-17
NUMBER OF SEQ ID NOS: 86
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 68
LENGTH: 201
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Publication No. US20030113840A1

GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: 25 Human secreted proteins
FILE REFERENCE: P2042P1

CURRENT APPLICATION NUMBER: US/10/060,255

CURRENT FILING DATE: 2002-02-01

PRIOR APPLICATION NUMBER: 09/781,417

PRIOR APPLICATION NUMBER: 07/91,417

PRIOR APPLICATION NUMBER: DCT/US00/22325

PRIOR APPLICATION NUMBER: PCT/US00/22325

PRIOR FILING DATE: 2000-08-16
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SEQ ID NO 59
LENGTH: 201
TYPE: PRT
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                                                                                                                                                                                                                                                                                                     Sequence 68, Application US/100 Publication No. US20030113840A1 GENERAL INFORMATION:
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Best Local Similarity' 36.4%;
Matches 4; Conservative
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 201 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE DESCRIPTION: SEQ ID NO: 7:
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Pred. No.
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Pred. No.
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RESULT 11
US-09-769-736-86
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-060-255-69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Rosen et al.
TITLE OF INVENTION: 25 Human secreted proteins
FILE REFERENCE: PZ042P1
CURRENT APPLICATION NUMBER: US/10/060,255
CURRENT FILLING DATE: 2002-02-01
PRIOR APPLICATION NUMBER: 09/781,417
PRIOR FILING DATE: 2001-02-13
PRIOR APPLICATION NUMBER: PCT/US00/22325
PRIOR APPLICATION NUMBER: PCT/US00/22325
PRIOR FILING DATE: 1090-08-16
PRIOR FILING DATE: 1999-08-17
NUMBER OF SEQ ID NOS: 86
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US-10-060-255-68
Query Match
Best Local S
Matches 4
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                                                                         SEQ ID NO 86
LENGTH: 300
TYPE: PRT
ORGANISM: Streptococcus agalactiae
S-09-769-736-86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 86, Ap
Publication No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQ ID NO 69
                                                                                                                                                                                                                                           APPLICANT: Wells, Jeremy M
APPLICANT: Hanniffy, Sean B
TITLE OF INVENTION: Proteins
FILE REFERENCE: PWC/P21089w0
CURRENT APPLICATION NUMBER: US/09/769,736
CURRENT FILING DATE: 2003-02-14
PRIOR APPLICATION NUMBER: GB 9816335.5
PRIOR FILING DATE: 1998-07-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Microbial Technics Limited APPLICANT: Le Page, Richard WF APPLICANT: Wells, Jeremy M
                                                                                                                                                                     SOFTWARE: PatentIn Ver. 2.1
                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 212
                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: US 60/125163 PRIOR FILING DATE: 1999-03-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      / Match 36.8%;
Local Similarity 36.4%;
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No. US20030138775A1
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36.8%; Score 21; DB larity 36.4%; Pred. No. 8.60 Conservative 0; Mismatches
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36.4%;
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Pred. No. 5.9e 
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Pred. No. 5.9e+02;
Pred. No. 5.9e+02;
                 DB 12; Length 300;
8.6e+02;
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5.9e+02;
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US-10-369-493-11376
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US-10-369-493-14778
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                                                                                                                                                                     ; ORGANISM: Agrobacterium tumefaciens US-10-369-493-14778
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APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10 (52052) B
FILE REFERENCE: 38-10 (52052) B
CURRENT APPLICATION NUMBER: US/10/369, 493
CURRENT FILING DATE: 2003-02-28
                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 14778
LENGTH: 420
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PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 11376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 14778, Application US/10369493 Publication No. US20030233675A1
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                                                                                    Matches
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APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
ITTLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
ITTLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10 (52052) B
FILE REFERENCE: 38-10 (52052) B
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4; Conservative
FALASMGIYVF 211
                                          FXXXXXGXYXF 29
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36.4%;
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                                                                                                     Score 21; DB 12;
Pred. No. 1.2e+03;
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Pred. No. 1.2e+03;
                                                                                    Mismatches
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RESULT 14

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SEQ ID NO 14932

LENGTH: 420

TYPE: PRT

ORGANISM: Agrobacterium tumefaciens
US-10-369-493-14932
Search completed: January 12, 2004, 08:33:42
Job time : 5.77445 secs
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                                                                                                                                                                                                                                                                                              ; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 15269
; LENGTH: 420
; TYPE: PRT
; ORGANISM: Agrobacterium tumefaciens
US-10-369-493-15269
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US-10-369-493-15269
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Publication No. US20030233675A1

GENERAL INFORMATION:
APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(52052)B
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
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Best Local Similarity
Matches 4; Conserva
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APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.

APPLICANT: Slater, Steven C.

APPLICANT: Slater, Steven C.

APPLICANT: Goldman, Barry S.

APPLICANT: Goldman, Barry S.

APPLICANT: Chen, Xianfeng

IIILE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF

IIILE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES

FILE REFERENCE: 38-10(52052)B

CURRENT APPLICATION NUMBER: US/10/369,493

CURRENT APPLICATION NUMBER: US/10/369,493

PRIOR APPLICATION NUMBER: US 60/360,039

PRIOR PILING DATE: 2003-02-21
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Result
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      Pred. No.
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/cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/BCTUS_COMB.pep:*
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US-09-328-352-6069
US-09-328-352-6182
US-09-198-452A-698
US-08-801-740-6
US-08-801-740-7
US-08-801-740-7
US-08-801-740-7
US-09-252-991A-30813
US-09-071-035-404
US-09-071-035-402
US-08-637-759B-501
US-08-637-759B-501
US-08-637-759B-501
US-08-997-080-47
US-08-997-080-47
US-08-997-080-47
US-08-997-362-47
US-08-997-362-47
US-08-997-362-47
US-08-998-855-47
US-08-998-855-47
US-08-998-856-47
US-08-685-808-2
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Sequence 4142,
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402, App
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29 20 35.1 469 4 US-09-198-452A-793 30 20 35.1 479 4 US-09-996-243-216 31 20 35.1 492 4 US-09-252-991A-27863 32 20 35.1 498 3 US-09-232-466A-18 33 20 35.1 498 3 US-09-232-466A-24 34 20 35.1 498 3 US-09-232-466A-24 35.1 498 4 US-09-784-984B-52 36 20 35.1 498 4 US-09-784-984B-52 36 20 35.1 498 4 US-09-784-984B-52 36 20 35.1 498 4 US-09-784-994B-54 38 20 35.1 546 2 US-09-667-35.1 38 20 35.1 546 3 US-09-67-35.1 39 20 35.1 546 3 US-09-36-643A-10 40 20 35.1 546 4 US-09-36-643A-15 41 20 35.1 1430 3 US-09-210-361-6 42 20 35.1 1430 3 US-09-210-361-6 43 20 35.1 1430 3 US-09-210-361-6 44 20 35.1 3177 2 US-08-477-451-4 45 19 33.3 32 4 US-08-525-539A-35																		
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US-09-198-452A-793 US-09-996-243-216 US-09-996-243-218 US-09-9252-991A-27853 US-09-232-468A-18 US-09-232-468A-24 US-09-232-468A-24 US-09-324-984B-52 US-09-784-984B-54 US-09-784-984B-54 US-09-784-984B-54 US-09-360-490-1 US-09-360-490-1 US-09-360-490-1 US-09-360-490-1 US-09-360-490-1 US-09-360-490-1 US-09-360-491-6 US-09-360-491-6 US-09-360-491-6 US-09-360-491-6 US-09-360-491-6 US-09-198-452A-15 US-09-210-361-6 US-09-210-361-6 US-09-210-361-6 US-09-210-361-6 US-09-210-361-6 US-09-210-361-6 US-09-210-361-6 US-09-210-361-6 US-09-210-361-6	32	3177	1430	1430	1430	922	646	546	546	498	498	498	498	498	492	479	469	
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	35, Appl	4, Appli	6, Appli	6, Appli	2, Appli	15, Appl	10, Appl	<ol> <li>Appli</li> </ol>	<ol> <li>Appli</li> </ol>	54, Appl	52, Appl	231, App	24, Appl	18, Appl	27853, A	216, App	793, App	

#### ALIGNMENTS

RESULT 1 US-09-252-991A-18273

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Sequence 4142, Application US/09134001C
PATCHI NO. 6380370
GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: BEIDERMIDIS FOR DIAGNOST
FILE REFERENCE: GTC-007
FILE REFERENCE: GTC-007
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
SEQ ID NO 4142
LENGTH: 292
TYPE: PRT
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US-09-134-001C-4142
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PATENT NO. 6551795
GENERAL INFORMATION:
APPLICANT: MATC J. Rubenfield et al.
APPLICANT: MATC J. Rubenfield et al.
TITLE OF INVENTION: ACCUEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: ACRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 18273
LENGTH: 268
TYPE: PRT
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Pseudomonas aeruginosa
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Pred. No.
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                                                                                  US-09-198-452A-698
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US-09-328-352-8182
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Sequence 698, Application US/09198452A
Patent No. 6559294
GENERAL INFORMATION:
APPLICANT: Griffais, R.
APPLICANT: Griffais, R.
TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: GARY L. Breton et al.
APPLICANT: GARY L. Breton et al.
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 6069
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 6069, Application US/09328352
Patent No. 6562958
GENERAL INFORMATION:
APPLICANT: GRATY L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC99-03PA
                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 8182
LENGTH: 404
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Patent No. 6562958
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Pred. No. 1.5e+02;
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Pred. No. 1
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Pred. No. 1.1e+02;
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1.1e+02;
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Query Match
Best Local Similarity
Watches 4; Conserva
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CURRENT FILING DATE: 1998-11-24
NUMBER OF SEQ ID NOS: 6849
SEQ ID NO 698
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 6, Application US/08801740 Patent No. 5869639
                              Matches
                                                          Query Match
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                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:

NAME: Billings, Lucy J.

REGISTRATION NUMBER: 36,749

REFERENCE/DOCKET NUMBER: PF-C
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
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                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 201 amino acids
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FILING DATE: Herewith
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                            OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Diskett
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Goli, Surya K. APPLICANT: Bandman, OlgaTITLE OF INVENTION: NOVEL
                                                                                                                                  IMMEDIATE SOURCE:
                                                                                           LIBRARY: Ge...
1212965
                                            Local
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19 FXXXXXGXYXF 29
                             Similarity 36. 4; Conservative
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                           Score 21; DB 2; LC
Pred. No. 1.4e+02;
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Pred. No. 1.1e+02
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82 FAAHMDGTYKF 92

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RESULT 8
US-08-801-740-6
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                                                                                                          Sequence 6, Application US/08801740
Patent No. 6130325
GENERAL INFORMATION:
APPLICANT: Goli, Surya K.
                                                                                                                                                                                                                                                                                                          Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/801,740
FILING DATE: Herewith
                                                                                                                                                                                                                                                                                                                                                                                                                          IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 514
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Bandman, Olga
TITLE OF INVENTION: NOVEL P24 VESICLE PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                       Match 36.8%; Local Similarity 36.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: STRANDEDNESS: 811
                                                                                                                                                                                                                                                                                                                                                                                         LIBRARY: GenBank
CLONE: 1213221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 94304
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Palo Alto
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ENGTH:
          Bandman, Olga
TITLE OF INVENTION: NOVEL P24 VESICLE PROTEINS
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
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                                                                                                                                                                                                                                                                          19 FXXXXXGXXXF 29
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                                                                                                                                                                                                                                             FAAHMDGTYKF 92
STREET: 3174 Po
CITY: Palo Alto
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3174 Porter Drive
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                                                                                                                                                                                                                                                                                              Score 21; DB 2; Pred. No. 1.4e+02; Indels
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Sequence 7, Application US/08801740

; Patent No. 6130325

; GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
                                                  COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/801,740
FILING DATE: 14-Feb-1997
CLASSIFICATION: CUNKnown>
PRIOR APPLICATION DATA:
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FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0
APPLICATION NUMBER: <Unknown>
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
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FILING DATE: 14-Feb-1997
CLASSIFICATION: «Unknown»
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                   Bandman, Olga
TITLE OF INVENTION: NOVEL P24 VESICLE PROTEINS
NUMBER OF SEQUENCES: 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LIBRARY: GenBank
CLONE: 1212965
SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: FastSEQ for CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Goli, Surya K.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                         STATE: CA
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ilarity 36.4%;
Conservative
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Pred. No. 1.4e+02;
0; Mismatches 7
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US-09-071-035-404
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US-09-252-991A-30813
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APPLICANT: Marc J. Rubenfield et al.

APPLICANT: Marc J. Rubenfi
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SEQ ID NO 30813
LENGTH: 252
                                                                                                                                                                                                                                             Patent No. 6448043
GENERAL INFORMATION:
APPLICANT: Gil H. Choi
TITLE OF INVENTION: En
                                                                                                                                                                                                                                                                                                                                                                                      Sequence 404, Application US/09071035
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Pseudomonas aeruginosa
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INFORMATION FOR SEQ ID NO: 7:
                                                                                                                                                                      NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local
COUNTRY:
                                                                                                    STREET:
                                                                                                                                     ADDRESSEE:
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Similarity 36.4%;
4; Conservative
                      9410 Key West Avenue
Rockville
Maryland
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STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                         Human Genome Sciences, Inc
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Pred. No. 1.8e+02;
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Pred. No. 1.4e+02;
0; Mismatches 7;
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RESULT 12
US-09-071-035-402
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NAME: A. Anders Brookes
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB36
TELECOMMUNICATION INFORMATION:
TELEFAX: (301) 309-8514
INFORMATION FOR SEQ ID NO: 404:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 402, Application US/09071035
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Patent No. 6448043
GENERAL INFORMATION:
INFORMATION FOR SEQ ID NO:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
                                                            FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: A. Anders Brookes
RECISTRATION NUMBER: 36,
REFERENCE/DOCKET NUMBER:
                                                                                                                                               PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                CURRENT APPLICATION DATA: APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM: MEDIUM TYPE: Diskette,
                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: Enterococcus faecalis Polynucleotides and Polypeptides NUMBER OF SEQUENCES: 496
CORRESPONDENCE ADDRESS:
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MEDIUM TYPE: Diskette, 3.50 inch, 1.

COMPUTER: HP Vectra 486/33

OPERATING SYSTEM: MSDOS version 6.2
                           TELEPHONE: (301) 309-8504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Gil H.
                                                                                                                                                                                                                                                 OPERATING SYSTEM: MS
SOFTWARE: ASCII Text
                                                                                                                                                                                                                                                                                  COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                   STREET: 9410 Key West Avenue CITY: Rockville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS:
                                                                                                                                                                                CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
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                 (301) 309-8512
                                                                                                                                                                                                                                                                              HP Vectra 486,
                                                                                                                                                                                                                                                                                                                                                                                                                    Human Genome Sciences, Inc
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                                                                              36,373
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Pred. No.
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1e+03;
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US-08-637-759B-501
RESULT 14
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                                                                                     Query Match
Best Local Similarity 36.7
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APPLICANT: David
                                                                                                                                                                                                                                                                               TELEFAX: (404) 873-8795
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: FILING DATE: 11-DEC-1
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION UNMBER: US/08/637,759B
FILING DATE: 03-MAY-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: USA
ZIP: 30309-3450
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 1448 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                          MOLECULE TYPE:
                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 63 amino acids
                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: RP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404) 873-8794
                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION:
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Local Similarity 36.4%;
les 4; Conservation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC
OPERATING SYSTEM:
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                                         FQSIVAGYYYF 14
                                                                       FXXXXXGXYXF 29
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2800 One Atlantic Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1201 West Peachtree Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   David William Holden
//ENTION: Identification of Genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       E: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                        linear
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NO
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                                                                                                               35.1%;
36.4%;
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                                                                                                 Score 20; DB Pred. No. 85; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                            RPMS 101
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Pred. No. 1.1e+03;
                                                                                                                               DB 2; Length 63;
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                                                                                                                                                                                                                                                               Sequence 501, Application US/09201945 Patent No. 6342215
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APPLICANT: David
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: 1i
MOLECULE TYPE:
HYPOTHETICAL:
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FILING DATE: 09-JUN-177,
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: PCT/GB95/02875
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                       NUMBER OF SEQUENCES: 5
                                                                                                                                                                                                           TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION: TELEPHONE: (404) 873-8794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
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CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: David William Holden
                                                                                                                    ADDRESSEE: Patrea L. Pabst
STREET: 2800 One Atlantic Center
STREET: 1201 West Peachtree Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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STREET: 2800 One Atlantic Center
STREET: 1201 West Peachtree Street
                                                     COUNTRY: USA
ZIP: 30309-3450
                                                                                                       CITY: Atlanta
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: RPI
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FILING DATE: 11-DEC
CLASSIFICATION: 435
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                                                                                                                                                                                                                             David William Holden
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36.4%;
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Pred. No.
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/09/201,945
FILING DATE:
CLASSIFICATION NUMBER: US/09/201,945
FILING DATE:
PRIOR APPLICATION NUMBER: 08/637,759
FILING DATE:
CLASSIFICATION NUMBER: 08/637,759
FILING DATE:
CLASSIFICATION:
APPLICATION NUMBER: 08/637,759
FILING DATE:
CLASSIFICATION:
APPLICATION NUMBER: 08/637,759
FILING DATE:
CLASSIFICATION:
APPLICATION NUMBER: 08/637,759
FILING DATE:
CLASSIFICATION: NUMBER: S1.284
REFIGENCE/DOCKET NUMBER: RPMS 101
FELEPAXI: (404) 873-8794
FELEPHONE: (404) 873-8794
FELEPHONE: (404) 873-8795
INFORMATION FOR SEQ ID NO: 501:
SEQUENCE CHARACTERISTICS:
LENGTH: 63 amino acids
TYPE: protein
HYPOTHETICAL: NO
US-09-201-945-501
Search completed: January 12, 2004, 08:20:09 Job time: 3.57784 secs
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                                                                                                                                                                                                        Query Match 35.1%; Score 20; DB 4; Length 63; Best Local Similarity 36.4%; Pred. No. 85; Matches 4; Conservative 0; Mismatches 7; Indels
                                                                                                                                                         19 FXXXXXGXYXF 29
                                                                                                        4 FOSIVAGYYYF 14
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                                                                                                                                                                                                        Gaps
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